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CC EMBL; J03171; AAA52730.1;
 CC EMBL; X60459; AAA42992.1;
 CC PIR: A32694; A32694.
 CC PIR: S17112; S17112.
 CC MIM: 107450;
 CC Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 CC Phosphorylation.
 CC CHAIN 1 27
 CC SIGNAL 1 27
 CC DOMAIN 28 436
 CC TRANSMEM 437 457
 CC DOMAIN 458 557
 CC DISULFID 79 87
 CC DISULFID 199 220
 CC MOD_RES 461 466
 CC MOD_RES 481 481
 CC CARBOHYD 50 50
 CC CARBOHYD 58 58
 CC CARBOHYD 81 81
 CC CARBOHYD 88 88
 CC CARBOHYD 110 110
 CC CARBOHYD 172 172
 CC CARBOHYD 254 254
 CC CARBOHYD 313 313
 CC CARBOHYD 314 314
 CC CARBOHYD 376 376
 CC CARBOHYD 416 416
 CC CARBOHYD 433 433
 CC CARBOHYD 433 433
 CC VARIANT 168 168
 CC CONFLICT 17 17
 CC SEQUENCE 557 AA; 63525 MW; 0f6744c8ba1adeb73 CRC64;
 SO Query Match 100.0%; Score 3178; DB 1; Length 557;
 SO Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 SO Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 ID INR1 SHEEP STANDARD: PRF: 560 AA.
 AC Q28589; Q95206;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
 DE (INTERFERON ALPHA/BETA RECEPTOR-1)
 GN IFNARI OR IFNAR
 OS Ovis aries (Sheep)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 [1]
 RN RP SEQUENCE FROM N.A.
 RC TISSUE-ENDOMETRIUM;
 RX MEDLINE: 9713690.
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
 RT "Structure of an ovine interferon receptor and its expression in
 RT endometrium."
 RL J. Mol. Endocrinol. 17:207-215(1996).
 [2]
 RN RP SEQUENCE FROM N.A.
 RC TISSUE-ENDOMETRIUM;
 RX MEDLINE: 98006426.
 RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
 RT "Molecular cloning of ovine and bovine type I interferon receptor
 RT subunits from uteri, and endometrial expression of messenger
 RT ribonucleic acid for ovine receptors during the estrous cycle and
 RT pregnancy."
 RL Endocrinology. 138:4757-4767(1997).
 CC -1 FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC -1 I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
 CC CONCEPTUS AT DAY 15 OF PREGNANCY.
 CC -1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1 SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@sdb.ch).

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CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE II-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@sdb.sdb.ch).
CC -----
DR EMBL; X68443; CAA0484.1; -
DR EMBL; L06520; AAA02571.1; -
DR PIR; S33770; S33770.
DR PIR; S27387; S27387.
DR PIR; PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
FT CHAIN 25 560 CHAIN.
FT DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 438 458 POTENTIAL.
FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
FT DISULFID 76 84 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT CARBOHYD 47 47 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 109 109 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 254 254 POTENTIAL.
FT CARBOHYD 313 313 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 434 434 POTENTIAL.
FT CONFLICT 422 422 F -> V (IN REF. 2).
SQ SEQUENCE 560 AA; 63818 MW; 66D76B72861E1D11 CRC64;

Query Match 66.2%; Score 2103; DB 1; Length 560;
Best Local Similarity 65.2%; Pred. No. 0.00e+00;
Matches 287; Conservative 78; Mismatches 67; Indels 8; Gaps 8;

DB 1 MALLGATTMLVA-GRVVLPAASGEANLK-PENVEIHIIIDNPFLLKNSSSESYKNTF 58
QY 2 MYVLLGATTLVAVGVPMVLSAAGSKNLSPQKEVDIIDDNFLIKRNRDSDEIGNTF 61
DB 59 SADVOIIGTDWKKSLSGCQHITSTKCNFSVELNEVFETELRIAEAGNNTSTWEYEP 118
QY 62 SEDFOCKGMDDMMIKLSGCQNTSTKCNFSISLT-NVYEELIKRLRAEK-ENTSSWEYDS 119
DB 119 FVPLELAOIGPDVHLEEDKAIIISTSPPTKSIIMAMRSSPRYSVTAKNSSLEE 178
QY 120 FTTPRKAOIGPEVHLEEDKAIVIHISP-CFKOSVMALDGLSTYSLSLTKNSSGYEE 178
DB 179 RTEVYPEDKIKLSPETLYCLKVAERKLQS-RVGCYSPYCINTERRHVPSPENIOI 237
QY 179 RLENITSNHKIYKLSPETTYCLAKYKVAL-LTSMKIGVSPVHCRTKYENELPREPENIEV 237
DB 238 NADNOIYLAKMDYYENATFOAMLRAFFKIIPGNHSDKMKQIPNCENATYSTHCFFREY 297
QY 238 SVQNOMNYVKMDYYANNTFOVWLAFKLKPNNHLYKMQOIPDCCEVNTKOCVFPONY 297
DB 298 SSRGIYYVRVASNGNSGFSEKENTERTKTIIFPVLSYKSVTODSLHVSAGASEES 357
QY 298 FOKEITLRVAVASGANNITSEISEIKADTELQALLPVENIRSLSD-SPIITYIGAPROS 356
DB 358 ENNSVNOLLYPIYIVIVEMENTSNAERVULEKTETFIIPDLKPLLVYCVKRALLENRRN 417
QY 357 GNPVVIDGYDIYIIEIEMENTSNAERKTIIEKTDVYTPNLKPLLVYCYVKAHAHMDEKLN 416
DB 418 KGSFSDVCYEKTRPGNTSK 437
QY 417 KSVYFSDVAYCEKTRPGNTSK 436
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Db      181 NSIYYVEKILPELLEPTTYCLEFKALHPSLKRSNSTVOCISITVTANKPVPAGNLOYDAQ 240
Oy      181 ENITSNHAKITYKLSPETTYCYLKAVALLSWKGIVSPPHCITTYENELPPENLESVO 240
Db      241 GRSYLVAKMPOYIASADVLFAFOMLPGRSKSSGSHSDKMPPIPCANVOTRCVFESODRY 300
Oy      241 NQNYVATKMXY-YYANNFPQVOWHLAFKNRPNCHLYXMKQIPDCENVKTTCQVFPQN-VF 298
Db      301 -TGFPLHYQASGECHNTSWSEE-KFIDSOKHILPPPYIYTVAMSDLLVAVNC--QDS 356
Oy      299 ORGIYVILLRQADSDGNNTSWSEEIF-DEIDQFLFPLPFNFNRSLSDSFHIYGAPKQSG 357
Db      357 -T-C-D-GLANEIFFEMTSMT-TISMKEQDEPTLNIOPLYVCQARY-LERALLN 409
Oy      358 NRPYVDIYLIIEIFEMTSNAEKYIEKK-TDVTVPMLPLTVYCVAKRHMDXEN 416
Db      410 KTSNSEKLCERTRGGS 426
Oy      417 KSVFSDAVCECKTKPGN 433

RESULT 5
ID      CRF4_HUMAN STANDARD; PRT; 325 AA.
AC      Q08334;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, last sequence update)
DT      01-OCT-1996 (Rel. 34, last annotation update)
DE      CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
GN      CRFB4.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
[1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=FETAL BRAIN;
RX      MEDLINE; 93300510.
RA      Lutfalla G., Gardiner K., Uze G.;
RT      "A new member of the cytokine receptor gene family maps on chromosome
RT      21 at less than 35 kb from IFMAR."
RL      Genomics 16:366-373(1993).
[2]
RN      RN
RM      SEQUENCE FROM N.A.
RX      MEDLINE; 96054036.
RA      Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT      "Structure of the human CRFB4 gene: comparison with its IFMAR
RT      neighbor ".
RL      J. Mol. Evol. 41:338-344(1995).
CC      -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: CONTAINS 2 FIBROBLASTIC TYPE III-LIKE DOMAINS.
CC      -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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Cc      or send an email to: license@isb-sib.ch).
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DR      EMBL; Z17227; CAAY8933.1;
DR      EMBL; U08986; AAA86872.1;
DR      PIR; A47003; AA7003.
DR      HSSP; R13726; 1DAN.
DR      MIT; 123889.
KW      Receptor; Transmembrane; Glycoprotein; Signal.
FT      SIGNAL 1..19 POTENTIAL.
FT      CHAIN 20..325 CYTOKINE RECEPTOR CLASS-II CRF2-4.
FT      DOMAIN 20..220 EXTRACELLULAR (POTENTIAL).
FT      TRANSEM 221..249 POTENTIAL.
FT      DOMAIN 250..325 CYTOPLASMIC (POTENTIAL).
FT      DYSLEPID 66..74 BY SIMILARITY.
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FT DISULFID 188 209 BY SIMILARITY.
 FT CARBOHYD 49 49 POTENTIAL.
 FT CARBOHYD 68 68 POTENTIAL.
 FT CARBOHYD 102 102 POTENTIAL.
 FT CARBOHYD 161 161 POTENTIAL.
 FT CARBOHYD 124 124 A-> D (IN REF. 2).
 FT CONFLICT 269 273 FLGHP -> VGRME (IN REF. 2).
 FT CONFLICT 274 325 MISSING (IN REF. 2).
 FT SEQUENCE 325 AA; 37011 MM; 66706C79P8514B33 CMC64;
 Query Match 8.6%; Score 274; DB 1; Length 325;
 Best Local Similarity 30.1%; Pred. No. 2,52e-35;
 Matches 62; Conservative 55; Mismatches 75; Indels 14; Gaps 10;
 Db 23 PPNVBNMSVNFKNILQWESAPAKNITFAQY---LSRIFQDKCMNTLTLECDSS 78
 Oy 32 SPQVEVDIIDNFIIRNRDESGVNTFSPDYOKTGMMDMIRKISGCONITSTKCNSS 91
 Db 79 LS-K-YGDHTRVRAFEHSDWVNI-TFCPVDTIIGPGMOVEYLAIDLHRLAPK 135
 Oy 92 LKLVYEIKLRIRAE-KENTSSWEVDSEFPFKRAQIGPEVHLLEDAKIVIH-ISP 149
 Db 136 IENEYETWTKMKNVNSWTYNYQWKNGTDEKFOITPODFEVLNLEPWTYCYQVGRFL 195
 Oy 150 T-KDSVMAALDGL--SFYSLILKNSGVBERIENIYSRRIKIKLSPETTYCLAKVNAAL 206
 Db 196 PDRKAGWSEPV-CEQTHDETVPS 220
 Oy 207 LITWKIGVYS-PVHCITVENEELP 231
 RESULT 6
 ID INGS_HUMAN STANDARD; PRT; 337 AA.
 AC P38484;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
 DE RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
 GN IINGR2 OR IINGR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG FIBROBLAST;
 RX MEDLINE; 94170380.
 RA Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R.,
 RA Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.,
 RT Identification and sequence of an accessory factor required for
 RT activation of the human interferon gamma receptor.
 RL Cell 76:793-802(1994).
 RN [2]
 RP SEQUENCE OF 1-24 FROM N.A.
 RX MEDLINE; 97067142;
 RA Rhee S., Ebensperger C., Dembic Z., Pestka S.,
 RT The structure of the gene for the second chain of the human
 RT interferon gamma receptor.
 RL J. Biol. Chem. 271:28947-28952(1996).
 CC 1-FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR
 CC SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
 CC THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO
 CC INTERACT WITH GAF, JAK1, AND/OR JAK2.
 CC 1-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC 1-SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
 CC 1-SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC EMBL; 005875; AAA1695.1;
 DR EMBL; 005877; AAA1695.1;
 DR EMBL; 068755; AAC52066.1;
 DR MIM; 147569;
 DR PIRAM; PF00041; fn3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 27
 FT CHAIN 28 337
 FT DOMAIN 28 247 INTERFERON-GAMMA RECEPTOR BETA CHAIN.
 FT TRANSMEM 248 268 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 269 337 POTENTIAL.
 FT CARBOHYD 56 56 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 85 85 POTENTIAL.
 FT CARBOHYD 110 110 POTENTIAL.
 FT CARBOHYD 137 137 POTENTIAL.
 FT CARBOHYD 219 219 POTENTIAL.
 FT CARBOHYD 231 231 POTENTIAL.
 FT VARIANT 64 64 R->Q.
 FT SEQUENCE 337 AA; 37834 MM; 18C61B10AD90E509 CRC64;
 Query Match 5.8%; Score 183; DB 1; Length 337;
 Best Local Similarity 23.7%; Pred. No. 6.08e-16;
 Matches 56; Conservative 60; Mismatches 95; Indels 25; Gaps 22;
 Db 1 MRPTLL-WSLLILGVFAAAAPDPLSQLPAPHQRIKRIYNAEVLSPYALNSTR 59
 Oy 1 MAVVLLGATVTLVAVGVWLSAAGG-KIKSPQKVEVDIIDNFIIRNR-S-DSVG 57
 Db 60 PNVYRQKDYDSKMTADIMSIGVCTQIATCEDPFAASGAFPMDFVTLRLREL 119
 Oy 58 NVFYS-FDYOKTG-MONMIR-LS-GGQNTSTKCNSSLKLVY--E-EIKLRIRAEK 108
 Db 120 GALSAVNTMPFQHNVTAVGPPENIEVTPGESLIIRSSPP-D-IA-DTSTAFCY 176
 Oy 109 ENT-SSWEVDSEFPFKRAQIGPE-VHLEDAKIVIHISPGKDSVMAALDGLSPTYS 166
 Db 177 VHYWKG-GIQQ-VKGFRRNSISLDMLKRSRYCLOVOQLT--NKSNIFFRGH 228
 Oy 167 LITKNSGVBERIENIYSRRI-Y-KLSPETTYCLAKVNAALTSW-KIGVSPVH 219
 RESULT 7
 ID INGR_HUMAN STANDARD; PRT; 489 AA.
 AC P15260;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).
 GN IINGR1
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89003065;
 RA Aguet M., Dembic Z., Melin G.,
 RT Molecular cloning and expression of the human interferon-gamma
 RT receptor.
 RL Cell 55:273-280(1988).
 RN [2]
 RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
 RX MEDLINE; 93183911;
 RA Stueber D., Friedlein A., Fountoulakis M., Lahm H.W., Garotta G.,
 RT Alignment of disulfide bonds of the extracellular domain of the
 RT interferon gamma receptor and investigation of their role in
 RT biological activity.
 RL Biochemistry 32:2423-2430(1993).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
 RX MEDLINE; 95342235.

RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lynn C.A.,
 RA Zaodny P.J., Narula S.K.,
 RT "Crystal structure of a complex between interferon-gamma and its
 RT soluble high-affinity receptor.";
 RL Nature 376:230-235(1995).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 26-122 COMPLEX WITH ANTIBODY.
 RA MEDLINE: 98035727.
 RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
 RA Winkler F.K., Robinson J.A.,
 RT "Neutralizing epitopes on the extracellular interferon gamma receptor
 RT (IFNGAMMAR) alpha-chain characterized by homolog scanning mutagenesis
 RT and X-ray crystal structure of the A6 fab-IFNGAMMAR1-108 complex.";
 RL J. Mol. Biol. 273:882-897(1997).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
 CC INTERFERON-GAMMA DIMER.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PM: PHOSPHORYLATED AT SER/THR RESIDUES.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC
 DR EMBL: J03143; AAA52731.1;
 DR PIR: A31553; A31553.
 DR PDB: 1JRH; 25-MAR-98.
 DR MIM: 107470;
 DR MIM: 209950;
 KM Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
 KM Immunoglobulin domain; 3D-structure.
 FT SIGNAL 1 17
 FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
 FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 246 265 POTENTIAL.
 FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 77 85
 FT DISULFID 122 167
 FT DISULFID 195 200
 FT DISULFID 214 235
 FT CARBOHYD 34 34 POTENTIAL.
 FT CARBOHYD 79 79 POTENTIAL.
 FT CARBOHYD 86 86 POTENTIAL.
 FT CARBOHYD 179 179 POTENTIAL.
 FT CARBOHYD 240 240 POTENTIAL.
 SQ SEQUENCE 489 AA; 54404 MW; DCP9E5740BF47400 CRC64;
 Query Match 4.4%; Score 140; DB 1; Length 489;
 Best Local Similarity 25.3%; Pred. No. 9.41e-08;
 Matches 37; Conservative 38; Mismatches 68; Indels 3; Gaps 3;
 DB 1 MALLFLPLPMGVSAEAGTADLGPSSVPTNTIETSYNMPYVVEYQIMPPVY-F 59
 OY 3 VLLGATTLVLAAGPWLISALA-GGKRLKSPQKEVDIIDNFIILNRSDSESVGNVTF 61
 DB 60 TVEAVNYGVKSEWIDACINISHYCNISDHGDPSSNSLWVYKARVQKESAVKSEEF 119
 OY 62 SEDYQKGTGDMNKLKSGCNITSTKCNSSSLKANYEEIKLIRAKREKTSWYE-VDSF 120
 DB 120 AVCRGKICPPKLDIRKEKQIMDI 145
 OY 121 TPFKRAOIGPPEVHLEADKAIVIH 146
 RESULT 8
 ID IL10R_MOUSE STANDARD; PRT; 575 AA.

AC 061727;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
 GN IL10RA OR IL10R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X AJ F1; TISSUE=HEMATOPOIETIC;
 RA MEDLINE: 94068585.
 RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
 RT "A receptor for interleukin 10 is related to interferon receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
 CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC
 DR EMBL: L12120; AAA16156.1;
 DR MGD: MGI:96538; IL10RA.
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 575 INTERLEUKIN-10 RECEPTOR.
 FT DOMAIN 17 241 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 242 262 POTENTIAL.
 FT DOMAIN 263 575 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 204 225
 FT DISULFID 263 575 POTENTIAL.
 FT CARBOHYD 50 50 POTENTIAL.
 FT CARBOHYD 66 66 POTENTIAL.
 FT CARBOHYD 113 113 POTENTIAL.
 FT CARBOHYD 182 182 POTENTIAL.
 FT CARBOHYD 238 238 POTENTIAL.
 SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;
 Query Match 4.2%; Score 132; DB 1; Length 575;
 Best Local Similarity 20.5%; Pred. No. 2.43e-06;
 Matches 33; Conservative 48; Mismatches 65; Indels 15; Gaps 13;
 DB 69 WNDHICRAQALSCDLFTFLDLYHSYGRARAVDANSQYSNMTTETRTVD-EVI 127
 OY 277 WKQIDPCENVKTQC-V--FPQNVFQKI-YLLRVAQASDGNSTSMSE-EIKFDIEIOAF 331
 DB 128 LTVDSVTLKAMDGIITGTHPPRP-ITPAGDVEQVQRDLRVYISIRKSELMKARR 186
 OY 332 LIPVFNIRLSDSPHYIIGAPKQSGNPNPDIYPLIY-ET-IFEMNTSN-AERKTIERK 388
 DB 187 VQOEFTFLVPVIGVRRFCVKVLP-RLESRINKA-WSEEC 225
 OY 389 IDVTPNKL-PLTV--YCYKARAHNDKLNKSSVPSAVC 426
 RESULT 9
 ID IL10B_HUMAN STANDARD; PRT; 918 AA.
 AC P40189;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATIN M
 DE RECEPTOR) (CDM130) (CD130 ANTIGEN).
 GN IL6ST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE-MYELOMA, AND PLACENTA;
 RX MEDLINE: 91084844.
 RA Hibi M., Murakami M., Saito M., Hirano T., Tago T., Kishimoto T.;
 RT "Molecular cloning and expression of an IL-6 signal transducer,
 RT gp130.";
 RL Cell 63:1149-1157(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE: 98169383.
 RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130.";
 RL EMBO J. 17:1665-1674(1998).
 CC -1 FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
 CC IL-6, LIF, OSM, CNP, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6R (ALPHA CHAIN) COMPLEX,
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1 SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1 TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES
 CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
 CC -1 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1 SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1 DATABASE: NAME-PROW; NOTE-CD guide CD130 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm"
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M57230; AAA59155.1;
 DR PIR: A36337; A36337.
 DR PDB: 1BGU; 26-AUG-98.
 DR MIM: 600694;
 DR PFAM: PF00041; fn3; 3.
 DR PRINTS: PRO0014; FNTYPE11.
 DR PROSITE: PS00340; RECEPTOR CYTOKINES_2; 1;
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 KW Repeat; 3D-structure.
 CC FT SIGNAL 1 22
 CC FT CHAIN 23 918
 CC FT DOMAIN 23 619
 CC FT TRANSMEM 620 641
 CC FT DOMAIN 642 918
 CC FT DOMAIN 26 120
 CC FT DOMAIN 124 222
 CC FT DOMAIN 223 324
 CC FT DOMAIN 325 423
 CC FT DOMAIN 424 517
 CC FT DOMAIN 518 613
 CC FT DOMAIN 725 755
 CC FT DISULFID 134 144
 CC FT DISULFID 172 182
 CC FT CARBOHYD 43 43
 CC FT CARBOHYD 83 83
 CC FT CARBOHYD 131 131
 CC FT CARBOHYD 157 157
 CC FT CARBOHYD 227 227
 CC FT CARBOHYD 379 379
 CC FT CARBOHYD 383 383
 CC FT CARBOHYD 390 390
 CC FT CARBOHYD 553 553
 CC FT CARBOHYD 564 564
 CC FT SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;

Query Match 4.0%; Score 128; DB 1; Length 918;
 Best Local Similarity 22.9%; Pred. No. 1,19e-05;
 Matches 19; Conservative 25; Mismatches 36; Indels 3; Gaps 3;
 DB 231 INSEELSLIKLTWNPISIKSYIILKYNIOYTKDASTWSQIP-EDTASTSFTVODL 289
 QY 36 VEVDIIDNFIILRW-NRSESGVNTFSFDYKTDGMDNMIKISGCONITSTCNFSSLTL 94
 DB 290 KPTEYVPIRCKEDGKQMSD 312
 QY 95 NYEEIKIRIRAKEKNTSS-WYE 116
 RESULT 10
 ID 110R-HUMAN STANDARD; PRT; 578 AA.
 AC Q13651;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 15-DEC-1998 (rel. 37, Last annotation update)
 DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
 GN IL10RA OR IL10R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOMA;
 RX MEDLINE: 94165477.
 RA Liu Y., Wei S.H., Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;
 RT "Expression cloning and characterization of a human IL-10 receptor";
 RL J. Immunol. 152:1821-1828(1994).
 CC -1 FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PBMC. FAINT EXPRESSION
 CC IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENTA,
 CC LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,
 CC LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF IL-
 CC 10R.
 CC -1 SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U00672; AAA17896.1;
 DR MIM: 146933;
 DR Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; 3D-structure.
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 578
 CC FT DOMAIN 22 235
 CC FT TRANSMEM 236 236
 CC FT DOMAIN 257 578
 CC FT DOMAIN 202 223
 CC FT DISULFID 50 50
 CC FT CARBOHYD 74 74
 CC FT CARBOHYD 110 110
 CC FT CARBOHYD 154 154
 CC FT CARBOHYD 177 177
 CC FT CARBOHYD 189 189
 CC FT SEQUENCE 578 AA; 62903 MW; E81B29064338157C CRC64;
 Query Match 3.7%; Score 116; DB 1; Length 578;
 Best Local Similarity 20.9%; Pred. No. 1,17e-03;
 Matches 49; Conservative 68; Mismatches 96; Indels 21; Gaps 19;
 DB 1 MLCPLVILALSLRSGDAHGTELPSPVFEAEFFH-H-ILMTPIPNSESTCYE 58
 QY 5 LIGATITVLAIVAGVWVLSAAAGKNTLSPKRV-EVDIIDNFIILRW-NRSESGVNTFS 62

DB 59 VALLRYGIESMNSISNCSC-TLS-YDLTAVTLDLYHSNGYRARVAVGSRHSNM-TVTN 115
 OY 63 FYQYTGMDNWKISGCCQITSTKCNFSLKLVYE-E-IKLRIR-A-EKENTSSWEYDS 119
 DB 116 -TRFVDEYTLTVGSYNLEHNGFLIKQIDPRKAPAPNDYESTFSEFRETAKRV 174
 OY 120 FPFPRKAOIG-D-PEVHEDEKRAIV-TIHISPTKDSYVMAALDGI-S-FT-YSLIIMN 172
 DB 175 PCNFETHKKV-KHENFSLTSGEVEPCVOYKPSVANSNNGMSKECISLT 227
 OY 173 SSCVEERLENTYSRKHTYKLP-ETT-YCLVKVAAALITSMKIGVSPVHCIT 224

RESULT 11
 ID 112R HUMAN STANDARD: 662 AA.
 AC P42701.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN PRECURSOR (IL-12R).
 GN IL12RB1 OR IL12RB OR IL12R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 94267217.
 RA Chua A.O., Chizzonite R., Desai B.B., Trullit T.P., Nunes P., Miretti L.J., Marlier R.R., Presky D.H., Levine J.F., Gately M.R., Gubler U.;
 RA "Expression cloning of a human IL-12 receptor component. A new member of the cytokine receptor superfamily with strong homology to gp130.";
 RT J. Immunol. 153:128-136(1994).
 RL -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION.
 CC -1- SUBUNIT: MAY FORM DIMERS OR OLIGOMERS. REQUIRES AN UNIDENTIFIED SUBUNIT TO GENERATE A HIGH AFFINITY IL-12R COMPLEX.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING MAY GIVE RISE TO A SECOND PROTEIN 2 AMINO ACIDS SHORTER.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC
 DR EMBL: U03187; AAA21340.1;
 DR MIM: 601604;
 DR PFM: PF00041; fn3; 1;
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing; Repeat.
 FT SIGNAL. 1 23
 FT CHAIN. 24 662
 FT DOMAIN. 24 545
 FT TRANSMEM 546 570
 FT DOMAIN. 571 662
 FT DOMAIN. 43 133
 FT DOMAIN. 143 236
 FT DOMAIN. 237 337
 FT DOMAIN. 338 444
 FT DOMAIN. 445 540
 FT DISULFID 52 62
 FT CARBOHYD 121 121
 FT CARBOHYD 329 329
 FT CARBOHYD 346 346
 FT CARBOHYD 352 352
 FT CARBOHYD 442 442
 FT POTENTIAL.
 FT INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT FIBRONECTIN TYPE-III.
 FT FIBRONECTIN TYPE-III.
 FT FIBRONECTIN TYPE-III.
 FT FIBRONECTIN TYPE-III.
 FT FIBRONECTIN TYPE-III.
 FT BY SIMILARITY.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.

FT CARBOHYD 456 456 POTENTIAL.
 FT VANSPLIC 659 662 KAKM -> DE (IN A SHORTER FORM).
 SQ SEQUENCE 662 AA; 73108 MM; 541A060820A1EF CAC64;
 Query Match 3.7%; Score 118; DB 1; Length 662;
 Best Local Similarity 28.4%; Pred. No. 5,54e-04;
 Matches 23; Conservative 17; Mismatches 35; Indels 6; Gaps 5;
 DB 146 IKVSLAGLRLMEETPNQVCAEV-QPR-HETPSSPW-KLDCGPODDDTESC-LCPLE 201
 OY 36 VEVDIIDNFIILNRSDSSVGNVTFSPDYQKTDGMDNWKISGC--QNTSTKCNFSSLK 93
 DB 202 NNVAQEPQLRRRLSGSGSSW 222
 OY 94 LVNVEIKRLRIAEKENTSSW 114

RESULT 12
 ID 116R RAT STANDARD: 918 AA.
 AC P40190.
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
 GN IL6ST.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 93052397.
 RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
 RA "Molecular cloning and characterization of the rat liver IL-6 signal transducing molecule, gp130.";
 RT Genomics 14:666-672(1992).
 RL -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC
 DR EMBL: M92340; -; NOT_ANNOTATED_CDS.
 DR PIR: A44257; A44257.
 DR HSSP: P40189; 1BOU.
 DR PFM: PF00041; fn3; 3.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.
 FT SIGNAL. 1 22
 FT CHAIN. 23 918
 FT DOMAIN. 23 618
 FT TRANSMEM 619 640
 FT DOMAIN. 641 918
 FT DOMAIN. 26 120
 FT DOMAIN. 124 221
 FT POTENTIAL.
 FT INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE C2-TYPE DOMAIN.
 FT FIBRONECTIN TYPE-III.

FT DOMAIN 222 323 FIBRONECTIN TYPE-III
 FT DOMAIN 324 422 FIBRONECTIN TYPE-III
 FT DOMAIN 423 516 FIBRONECTIN TYPE-III
 FT DOMAIN 517 612 FIBRONECTIN TYPE-III
 FT DOMAIN 724 754 SER-RICH
 FT DISULFID 134 144 BY SIMILARITY
 FT DISULFID 172 181 BY SIMILARITY
 FT CARBOHYD 43 43 POTENTIAL
 FT CARBOHYD 61 61 POTENTIAL
 FT CARBOHYD 83 83 POTENTIAL
 FT CARBOHYD 131 131 POTENTIAL
 FT CARBOHYD 157 157 POTENTIAL
 FT CARBOHYD 205 205 POTENTIAL
 FT CARBOHYD 226 226 POTENTIAL
 FT CARBOHYD 382 382 POTENTIAL
 FT CARBOHYD 389 389 POTENTIAL
 FT CARBOHYD 477 477 POTENTIAL
 FT CARBOHYD 552 552 POTENTIAL
 SQ SEQUENCE 918 AA; 102450 MW; 9E18B6FECF087F7 CRC64;

Query Match 3.7%; Score 119; DB 1; Length 918;
 Best Local Similarity 23.3%; Pred. No. 3.80e-04;
 Matches 21; Conservative 27; Mismatches 36; Indels 6; Gaps 5;

Db 223 PPHLSTNSSELSIILKLVNGSLKSDIQRKTDASTWIOVPL-EDTSPRT 281
 QY 32 SPOKVEVDIIDD-NFILLR--WNRSD-ESVGNVTFSDYOKGDMWIKSGCONITSTKC 87
 Db 282 SFIVQDLKPFTEYVIRISIRKNGKYMSD 311
 QY 88 NFSLKLVYIEIRIKIRAKENKTS-WYE 116

RESULT 13
 ID EPAS_MOUSE STANDARD; PRT; 877 AA.

AC 060629;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1) (BRAIN-SPECIFIC KINASE) (CEK-7).
 DE EPHAS OR EHK1 OR CEK7 OR BSK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE; 94194581.
 RA Zhou R., Copeland T.D., Kromer L.F., Schulz N.T.;
 RT Isolation and characterization of bsk, a growth factor receptor-like tyrosine kinase associated with the limbic system.*
 RL J Neurosci. Res. 37:129-143(1994).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN-TYPE III-LIKE DOMAIN.
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 CC EMBL; 007357; AAA17038.1;

DR HSPD; P00523; 2PTK.
 DR MSD; MG1;99654; EPHAS.
 DR PFAM; PF01404; EPH_1bd; 1.
 DR PFAM; PF00536; SAM; 1.
 DR PFAM; PF00041; fn3; 1.
 DR PFAM; PF00069; Pkinase; 1.
 DR PRINTS; PR00014; ENTPETIT.
 DR PRINTS; PR00109; TYRKINASE.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 FT SIGNAL 1 26
 FT CHAIN 27 877
 FT DOMAIN 27 412
 FT TRANSMEM 413 433
 FT DOMAIN 434 877
 FT DOMAIN 305 399
 FT DOMAIN 514 775
 FT NP_BIND 520 528
 FT BINDING 546 546
 FT ACT_SITE 639 639
 FT CARBOHYD 266 266
 FT CARBOHYD 301 301
 SQ SEQUENCE 877 AA; 97115 MW; 54AD2C864178214 CRC64;

Query Match 3.4%; Score 108; DB 1; Length 877;
 Best Local Similarity 40.0%; Pred. No. 2.11e-02;
 Matches 18; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

Db 338 LEVIRKPEKQETSYTIISKETSTIRAEGLKPSVYVQIRAT 382
 QY 367 LIVRIEIMENTSNAERIKIERK-TDYVTPNLKPLTYCVKARAT 410

RESULT 14
 ID EPAS_RAT STANDARD; PRT; 1005 AA.

AC P54757;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1).
 DE EPHAS OR EHK1 OR EHK-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 94067777.
 RA Maisonneville P.C., Barrezaeta N.X., Yancopoulos G.D.;
 RT Ehk-1 and Ehk-2: two novel members of the eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression.*
 RL Oncogene 8:3277-3288(1993).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
 CC SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X78689; CAA55357.1;
 CC DR HSSP: P00523; 2PRK.
 CC DR PFAM: PF01404; EPH_Lbd. 1.
 CC DR PFAM: PF00536; SAM. 1.
 CC DR PFAM: PF00041; In3. 2.
 CC DR PFAM: PF00069; PKINASE. 1.
 CC DR PRINTS: PR00014; FNTYPEIII.
 CC DR PRINTS: PR00109; TYRKINASE.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR. 1.
 CC DR PROSITE: PS00011; PROTEIN_KINASE_DOM. 1.
 CC DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V. 1.
 CC DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2. 1.
 CC DR PROSITE: PS01186; EGF_2; UNKNOWN.1.
 CC DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
 CC FT SIGNAL 1
 CC FT CHAIN 1
 CC FT DOMAIN 1
 CC FT TRANSMEM 576
 CC FT DOMAIN 597
 CC FT DOMAIN 677
 CC FT NP_BIND 683
 CC FT BINDING 709
 CC FT ACT_SITE 802
 CC FT CARBOHYD 266
 CC FT CARBOHYD 301
 CC FT CARBOHYD 371
 CC FT CARBOHYD 425
 CC FT CARBOHYD 438
 CC FT CARBOHYD 463
 CC FT VARSPLIC 10
 CC FT VARSPLIC 306
 CC FT VARSPLIC 358
 CC FT VARSPLIC 470
 CC FT VARSPLIC 597
 CC FT VARSPLIC 621
 CC FT CONFLICT 170
 CC FT CONFLICT 566
 CC FT CONFLICT 578
 CC FT CONFLICT 669
 CC FT CONFLICT 708
 CC FT CONFLICT 799
 CC FT SEQUENCE 1005 AA; 111007 MW; 1AED42C99693C574 CRC64;
 Query Match 3.4%; Score 107; DB 1; Length 1005;
 Best Local Similarity 40.0%; Pred. No. 3.00e-02;
 Matches 18; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

RESULT 15
 ID UFE1_YEAST STANDARD; PRT; 346 AA.
 AC P41834;
 DT 01-NOV-1995 (Rel. 32, Created)
 DE 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE UFE1 PROTEIN.
 GN UFE1 OR YOR075W OR YOR29-26.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AH22;
 RX MEDLINE: 97074230.
 RA Downing T.A., Storms R.K.;
 RT "Molecular analysis of UFE1, a Saccharomyces cerevisiae gene
 RT essential for spore formation and vegetative growth."
 RL Curr. Genet. 30:396-403(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97357290.
 RA Lewis M.J., Rayner J.C., Pelham H.R.B.;
 RT "A novel SNARE complex implicated in vesicle fusion with the
 RT endoplasmic reticulum."
 RL EMBO J. 16:3017-3024(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97279235.
 RA Valens M., Bohn C., Dainan-Formier B., Dang V., Bolotin-Fukuhara M.;
 RT "The presence of a 54.7 kb fragment of yeast chromosome XV reveals
 RT the presence of two tRNAs and 24 new open reading frames."
 RL Yeast 13:379-390(1997).
 CC -1- FUNCTION: T-SNARE FOR ENDOPLASMIC RETICULUM. MEDIATES RETROGRADE
 CC TRANSPORT FROM THE GOLGI COMPLEX TO THE ER.
 CC -1- SIMILARITY: TO S.POMBE SPC895.04C.
 CC
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 CC EMBL: L15081; AAC13730.1;
 CC DR EMBL: U53416; AAB50196.1;
 CC DR EMBL: Z74983; CAA99268.1;
 CC DR EMBL: Z70678; CAA94560.1;
 CC DR SGD: L0002637; UFE1.
 CC DR Transp. Protein transport; Endoplasmic reticulum; Colled coil.
 CC FT DOMAIN 222
 CC FT SEQUENCE 346 AA; 40539 MW; DDC164793510A897 CRC64;
 Query Match 3.3%; Score 104; DB 1; Length 346;
 Best Local Similarity 23.0%; Pred. No. 8.47e-02;
 Matches 17; Conservative 26; Mismatches 26; Indels 5; Gaps 5;
 DB 91 DMECLQLOQY-FK-KFELE-NYEMERINLSLKRFQGS-HRMSKILSNKDKRKHVH 146
 OY 234 NIEVSQNONNYLAKNDYTAANTFOVWLHAFKRNPNHLYKKWQIDPCENVKTKOCF 293
 DB 147 PODI-ENGVEERFL 159
 OY 294 PONVFOKGYILARV 307
 Search completed: Mon Aug 21 10:26:14 2000
 Job time: 18 secs.

 RELEASE

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MSPrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 10:26:31 2000; Maspar time 35.95 Seconds

Tabular output not generated. 840.922 Million cell updates/sec

Title: >US-09-240-675-2

Description: (1-436) from US09240675.pep

Sequence: 3178 1 MMTVLGATTLVAVGVPMV.....KSSVSDAVCEKTKPGNTSK 436

Scoring table: PAM 150

Gap 11

Searched: 225678 segs, 69334122 residues

Post-processing: Minimum match 0%

Listing first 45 summaries

Database:

sptrembl12
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 48.339; Variance 79.116; scale 0.611

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	899	28.3	569 13	Q9YHMO	INTERFERON ALPHA/BETA	5.53e-186
2	284	8.9	349 11	Q61190	CYTOKINE RECEPTOR FAMI	5.09e-37
3	241	7.6	332 11	Q63953	INTERFERON GAMMA RECEPTOR	1.25e-27
4	243	7.6	341 13	Q9YGC8	INTERLEUKIN-10 RECEPTOR	4.66e-28
5	140	4.4	484 4	Q10496	INTERFERON-GAMMA RECEPTOR	1.77e-07
6	123	3.9	26926 4	Q10466	TIRIN HEART ISOFORM N	1.52e-04
7	118	3.7	349 5	Q9XK66	Y102AKC.31 PROTEIN	1.01e-03
8	114	3.6	349 5	Q45849	T27C5.5 PROTEIN	4.46e-03
9	114	3.6	198 13	Q9W609	GLYCOPROTEIN 130 PRECURSOR	4.46e-03
10	114	3.6	1493 11	P97798	NEOGENIN (NEOGENIN PRO)	4.46e-03
11	113	3.6	6875 6	Q28733	TIRIN (FRAGMENT)	6.43e-02
12	111	3.5	1056 14	Q57161	PURATIVE REPLICASE	1.33e-02
13	112	3.5	1471 5	Q18825	C27B7.7 PROTEIN	9.25e-03
14	108	3.4	505 1	Q93662	CATALASE (EC-1.11.1.6)	3.87e-02
15	107	3.4	817 13	Q00784	TIRIN (FRAGMENT)	5.50e-02
16	109	3.4	979 2	Q9X155	CLOSTRIDIUM-RELATED PR	2.71e-02
17	104	3.3	666 5	Q9XU75	RII1A5.7 PROTEIN	1.56e-01
18	104	3.3	837 14	Q36406	PRIMASE	1.56e-01
19	102	3.2	192 5	Q77232	ADPOFERRITIN-2	3.09e-01
20	101	3.2	215 2	Q45207	VARIABLE OUTER MEMBRAN	4.33e-01

21	102	3.2	1055 14	Q98701	REPLICASE.	3.09e-01
22	102	3.2	1825 5	Q61210	H19M22.1 PROTEIN (FRAG	3.09e-01
23	101	3.2	2606 14	Q36414	LARGE TEGUMENT PROTEIN	4.33e-01
24	103	3.2	6048 5	Q23020	TWITCHIN.	2.20e-01
25	103	3.2	6831 5	Q23550	UNC-22 PROTEIN.	2.20e-01
26	103	3.2	7160 5	Q23551	ZK617.1B PROTEIN.	2.20e-01
27	100	3.1	287 2	Q50549	ESTERASE.	6.05e-01
28	99	3.1	310 2	Q47735	ORF13.	8.43e-01
29	99	3.1	327 3	Q94614	HYPOTHETICAL.36.8 KD P	8.43e-01
30	100	3.1	356 10	Q920N3	T13118.1 PROTEIN.	6.05e-01
31	99	3.1	356 2	Q72901	HYPOTHETICAL.41.6 KD P	8.43e-01
32	99	3.1	402 4	Q9Y6V4	KIF3 (FRAGMENT).	8.43e-01
33	98	3.1	449 1	Q27677	CHORISMATE MUTASE.	1.17e+00
34	99	3.1	688 14	Q9WBD4	LARGE T ANTIGEN.	8.43e-01
35	99	3.1	688 14	Q9WAZ2	LARGE T ANTIGEN.	8.43e-01
36	99	3.1	688 14	Q9WMO8	LARGE T ANTIGEN.	8.43e-01
37	99	3.1	688 14	Q9WMO7	LARGE T ANTIGEN.	8.43e-01
38	99	3.1	688 14	Q55871	LARGE T ANTIGEN.	8.43e-01
39	99	3.1	688 14	Q82950	LARGE T ANTIGEN.	8.43e-01
40	99	3.1	688 14	Q42051	LARGE T ANTIGEN.	8.43e-01
41	99	3.1	688 14	Q92721	LARGE T ANTIGEN.	8.43e-01
42	99	3.1	688 14	Q92722	LARGE T ANTIGEN.	8.43e-01
43	99	3.1	688 14	Q55875	LARGE T ANTIGEN.	8.43e-01
44	99	3.1	688 14	Q90457	LARGE T ANTIGEN.	8.43e-01
45	99	3.1	688 14	P88898	LARGE T ANTIGEN.	8.43e-01

ALIGNMENTS

RESULT ID	Q9YHMO	PRELIMINARY	PRT	569 AA.
AC	Q9YHMO			
DT	01-MAY-1999 (Trembl)	10, Created		
DT	01-MAY-1999 (Trembl)	10, Last sequence update		
DT	01-MAY-1999 (Trembl)	10, Last annotation update		
DE	INTERFERON ALPHA/BETA RECEPTOR 1.			
GN	IFNAR1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;			
OC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RA	REBOUL J., GARDINER K., MONNERON D., UZE G., LUTPALLA G.;			
RT	"Comparative genomic analysis of the interferon/interleukin-10			
RT	receptor gene cluster."			
RL	Genome Res. 0:0-0(1999).			
DR	EMBL; AF082664; AAD13669.1;			
KW	Receptor.			
SO	SEQUENCE	569 AA; 64055 MW; F99BC099 CMC32;		

Query Match	28.38;	Score 899;	DB 13;	Length 569;
Best Local Similarity	38.48;	Pred. No. 5.53e-186;		
Matches	163;	Conservative	90;	Mismatches 149; Indels 23; Gaps 20;
Db	27	AGCTNLSKSPDIDVAVANTNTLMVNTGCT-NPTFSAYOCFDDLOTEPEMKELSGC	85	
QY	25	AGGNTLKSPOKVEVDIIDNFILRMNSDESQVTFPS--FD-YQ-KTGMDWMILSGC	79	
Db	86	QNSHTCEDPSAATVYDTHIRIRAEKRSKPSISPEMIPYELAIGPEALQSI	145	
QY	80	QNTTSKCNFSSKLKLVYEIKRIRAEK-ENTSSVYEDVSPFRKAQIGPEVLENE	138	
Db	146	NGAKINISPEPNQVRKRM-LISVFKNVIVMDSNANE-KVRSILPIDVINDLAPET	203	
QY	139	DKAIVHISPGTDSV--MVALDGLSEFTSLIMKNSGVEERIEIYSHKIKYKLSPEP	196	
Db	204	TYLAKVQATVPLED--GGLESPHCHIKTRKVDLCPNVRPALNMFYLLMDNHYE	262	
QY	197	TYLAKKALD-LTSMKIGVSPHCHIKTIVE-NELPPEITEFVSQNVNIVLKMDTYA-	253	
Db	263	HTYTVQVYLTGLYKLNLDYSSKMWQVSCENTSKCNLSVYKFTSAYFRVQANNE	322	

OY 254 NMFOVOMLHAFKRNPNHLYKWKQIPDCENYKTCQVEPQWVFGKI-YLLRVQASDG 312
 DB 323 YSSCSLSKQVNDVPVYNEIGPPDVAK-DISDVLHHTKIPPGPGKIMSDLYDSYQI 361
 OY 313 NNTSPSEETKPTETIOAFLPPFNRSLSDSF-HIYIGAPQSGTPIYIDPLIYEI 371
 DB 382 LYKNSSDNEEYKMKETQIATVSDIAPSTLYCVQVAFS-EA-YNKSDDSRECCIG 439
 OY 372 IFWENNS-NMER-KIIEKTKDY-TVPLKPLTYCYVARAHYHDEKLKSSVSDAVCEK 428
 DB 440 TAGCK 444
 OY 429 TKPGN 433

RESULT 2
 ID 061190 PRELIMINARY; PRT: 349 AA.
 AC 061190;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
 GN IL10RB OR CRF4 OR CRF2-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 RN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97199375.
 RA GIBBS V.C., PENNICA D.;
 RT CRF-4: Isolation of cDNA clones encoding the human and mouse
 RT proteins.
 RL Gene 186:97-101(1997).
 DR EMBL; U53696; AAC53062.1;
 DR MGD; MGI:109380; 1110rb.
 DR PFAM; PF00041; fn3; 1.
 SQ SEQUENCE 349 AA; 39774 MW; 4AC1802A CRC32;

Query Match 8.9%; Score 284; DB 11; Length 349;
 Best Local Similarity 28.5%; Pred. No. 5, 09e-37;
 Matches 59; Conservative 60; Mismatches 73; Indels 15; Gaps 14;

DB 23 PREKVMNSVFNKILLOWEPAPKNTLFTAQESY-R-S-PQ-DHCKRTASTOODFSH 78
 OY 32 SPOKVEVDIIDDNFILKMNKSDSGVNTFSFYQTKGDMNKLKSGCONITSTKCNFS 91
 DB 79 LS-K-YGDYTVRVRALADEHESEWAV-TFCPEVEDTIGPPEKQISLAEHLRFSAPO 135
 OY 92 LKLNVEEIKLRIRAE-KENTSSMYEVDFTPRKAOIGPEVHLAEKAIYHIS-PG 149
 DB 136 IENEPTWTLKNIYDSWAVRVOIKNGINEKFOVSPYDSEYLRNLEPTTCIOYQVPL 195
 OY 150 T-KDSYVMALDGL-SFYSLIMKNSGVEERIEYIRHRIKISPETCYLAKVAML 206
 DB 196 LQNRGSESEPI-CERTG-NDEITPS 220
 OY 207 LTSWKIGVTS-FVHCICKTVEVELPP 232

RESULT 3
 ID 063953 PRELIMINARY; PRT: 332 AA.
 AC 063953;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
 GN IFNGR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN SEQUENCE FROM N.A.
 RP MEDLINE; 94170381.

RA HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;
 RT "A novel member of the interferon receptor family complements
 RT functionality of the murine interferon gamma receptor in human
 RT cells".
 RL Cell 76:803-810(1994).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-129SV/72
 RX MEDLINE; 97128072.
 RA EBENSBERGER C., RIEE S., MUTHUKUMARAN G., LEMBO D., DONNELLY R.,
 RA PESTKA S., DEMBIC Z.;
 RT "Genomic organization and promoter analysis of the gene Ifng2.
 RT encoding the second chain of the mouse interferon gamma receptor".
 RL Scand. J. Immunol. 44:599-606(1996).
 DR EMBL; U69599; AAC52938.1; JOINED.
 DR EMBL; U69594; AAC52938.1; JOINED.
 DR EMBL; U69595; AAC52938.1; JOINED.
 DR EMBL; U69596; AAC52938.1; JOINED.
 DR EMBL; U69597; AAC52938.1; JOINED.
 DR EMBL; U69598; AAC52938.1; JOINED.
 DR EMBL; S69336; AAB30165.1;
 DR MGD; MGI:107654; Ifng2.
 DR PFAM; PF00041; fn3; 1.
 SQ SEQUENCE 332 AA; 37471 MW; 0BF24E9E CRC32;

Query Match 7.6%; Score 241; DB 11; Length 332;
 Best Local Similarity 27.8%; Pred. No. 1, 25e-27;
 Matches 60; Conservative 56; Mismatches 80; Indels 20; Gaps 16;

DB 10 SLILCLGA-MASSPFSQALAPLRLHLINDEOILTWEPSSNDPRPVYQVEYSF 68
 OY 10 TLVLAVGPGWVLSAAGKNNLSPOVEVDIIDDNFILKMNKSDSGV-N-VTFSPDYOK 67
 DB 69 ID-GSWHRLPEPCDITETKCDLTGCGRLKLPHPFVFLRARGNLTSMVLEPF 127
 OY 68 TGMDMYIKL--SGCONITSTKCNFSSL-KLNVEE-IR--LNRAREN-TSMVEVDSF 120
 DB 128 QHENVTVGPPKNISVTPGKSLVHFSPF-D-V---FHGATFOYLVYWEKSETOQDO 182
 OY 121 TFERKAOIIPP-EVHLAEADKAIYHISPGTDSYVMALDGLSFYSLIMKNSGVEER 179
 DB 183 VEGPFSKNSIVLGNLKPVRYCLOTEOILNKRI 218
 OY 180 IENITSRRI-Y-KLSPETCYLAKVAML-LTSWKI 212

RESULT 4
 ID 091C8 PRELIMINARY; PRT: 341 AA.
 AC 091C8;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE INTERLEUKIN-10 RECEPTOR 2.
 GN IL10R2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN SEQUENCE FROM N.A.
 RP REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;
 RT "Comparative genomic analysis of the interferon/interleukin-10
 RT receptor gene cluster".
 RL Genome Res. 0:0-0(1999).
 DR EMBL; AF082667; AAD13678.1;
 DR EMBL; AF082666; AAD13671.1;
 DR KX Receptor.
 SQ SEQUENCE 341 AA; 39062 MW; 743D3364 CRC32;

Query Match 7.6%; Score 243; DB 13; Length 341;
 Best Local Similarity 26.1%; Pred. No. 4, 66e-28;
 Matches 54; Conservative 52; Mismatches 86; Indels 15; Gaps 12;

DB 24 PRNARISVNFRRSVLLMDPGVRKGNLSYVQAKSIFPKQNFNNVT--NLNVTCEVSS 81

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OY 33 POKVEVDIIDNFILRNKRSDESGVNTFSDYDQKT-GADNWITLSCQNTITKCNFSS 91
DB 82 L-SVYGATYALRVTEMEDEHSDV-AVYRKPMDVYIGPSSVNVKSESGTLHVDFTGPA 138
OY 92 LKLVNEYIKLRIRAE-KENTSSVYEVDSFPFRKAQGPPEVLEHEDKAIVIHIS-PG 149
DB 139 ADREHDMKSLKQYTGSMYIRLLYKKSGNKKVHIIDPKHNSIIISOLEPWTYICVOG- 197
OY 150 T-KDSVWALDGL--SEFYSLILKNSGVGE-RIENIYSHKIKYKLSPEPTYCLAKYAA 205
DB 198 VIFEMNKTGERSQELCEQT-HNGVTP 223
OY 206 LITSM-KIGVYSPVHCITTYENELP 231

RESULT 5
ID 014936 PRELIMINARY; PRT: 484 AA.
AC 014936;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89003065.
RA AGUET M., DEMBIC Z., MERLIN G.;
RT "Molecular cloning and expression of the human interferon gamma
RT receptor."
RT Cell 55:273-280(1988).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE; 97246734.
RA MERLIN G., VAN DER LEEDE B.-J.M., MCKUNE K., KNEZEVIC N.,
RA BANNAWARTH W., ROMODIN N., VIEGAS-PEQUIGNOT E., KIEFER H., AGUET M.,
RA DEMBIC Z.;
RT "The gene for the ligand binding chain of the human interferon gamma
RT receptor."
RT Immunogenetics 45:413-421(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA DEMBIC Z.;
RT Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL; 019247; AAC52064.1;
DR EMBL; 019241; AAC52064.1; JOINED.
DR EMBL; 019242; AAC52064.1; JOINED.
DR EMBL; 019243; AAC52064.1; JOINED.
DR EMBL; 019244; AAC52064.1; JOINED.
DR EMBL; 019245; AAC52064.1; JOINED.
DR EMBL; 019246; AAC52064.1; JOINED.
SQ SEQUENCE 484 AA; 53818 MW; EEC99DIF CRC32;

Query Match 4.4%; Score 140; DB 4; Length 484;
Best Local Similarity 25.3%; Pred. No. 1.77e-07;
Matches 37; Conservative 38; Mismatches 68; Indels 3; Gaps 3;

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ID 010466 PRELIMINARY; PRT: 26926 AA.
AC 010466;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TTIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-HEART.
RX MEDLINE; 96026330.
RA LABELT S., KOLMER B.;
RT "Titins: giant proteins in charge of muscle ultrastructure and
RT elasticity."
RT Science 270:293-296(1995).
RN [2]
RP SEQUENCE OF 22277-25376 FROM N.A.
RX MEDLINE; 92258380.
RA LABELT S., GAUTIEL M., LAKEY A., TRINICK J.;
RT "Towards a molecular understanding of titin."
RT EMBO J. 11:1711-1716(1992).
RN [3]
RP SEQUENCE OF 1976-2014 FROM N.A.
RA LABELT S.;
RT Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE; 95331314.
RA GAUTIEL M., CASTIGLIONE-MORELLI M.A., PEUHL M., MOTTA A., PASTORE A.;
RT "A calmodulin-binding sequence in the C-terminus of human cardiac
RT titin kinase."
RT Eur. J. Biochem. 230:752-759(1995).
CC -1- FUNCTION: THIS GIANT MUSCLE PROTEIN MAY BE INVOLVED IN MUSCLE
CC ASSEMBLY AND IN MAINTAINING THE STRUCTURAL INTEGRITY OF
CC SARCOMERES. MAY HAVE PROTEIN KINASE ACTIVITY.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE
CC PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE
CC DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN ANY
CC ONE TISSUE. THE SEQUENCE SHOWN HERE IS THAT OF THE HEART ISOFORM
CC N2-B.
CC -1- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
CC -1- SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
CC KINASES.
CC -1- SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 112
CC IMMUNOGLOBULIN C2-LIKE DOMAINS AND 132 FIBRONECTIN TYPE III-LIKE
CC DOMAINS.
DR EMBL; X64698; CAA45939.1;
DR EMBL; X83270; CAA58243.1;
DR EMBL; X64697; CAA45938.1;
DR EMBL; X90568; CAA62188.1;
DR EMBL; X64699; CAA45940.1;
DR HSSP; P56276; IYTK.
DR PFAM; PF00041; fn3; 132.
DR PFAM; PF00047; 19; 59.
DR PFAM; PF00069; kinase; 1.
DR PRINTS; PR00014; FMYVEPRTI.
DR PRINTS; PR00726; LEXASERFAS.
KW Muscle protein; cytoskeleton; Structural protein; Calmodulin-binding;
KW Serine/threonine-protein kinase; Alternative splicing; Repeat;
KW Immunoglobulin domain; Phosphorylation.
FT DOMAIN 1370 1389 4 X 5 AA TANDEM REPEATS OF R-W-S-P-A.
FT DOMAIN 4429 4614 GEL/LYS/PRO/VAL-RICH.
FT DOMAIN 24731 25070 CATALYTIC.
FT DOMAIN 25030 25056 CALMODULIN-BINDING.
FT MOD_RES 1372 1372 PHOSPHORYLATION (BY PDK) (POTENTIAL).
FT MOD_RES 1377 1377 PHOSPHORYLATION (BY PDK) (POTENTIAL).
FT MOD_RES 1382 1382 PHOSPHORYLATION (BY PDK) (POTENTIAL).
FT MOD_RES 1387 1387 PHOSPHORYLATION (BY PDK) (POTENTIAL).
FT MOD_RES 26171 26171 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 26178 26178 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 26184 26184 PHOSPHORYLATION (POTENTIAL).

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FT MOD.RES 26190 26190 PHOSPHORYLATION (POTENTIAL).
 FT CONFLICT 22277 22277 T->P (IN REF. 2).
 FT CONFLICT 22449 22449 E->G (IN REF. 2).
 FT CONFLICT 22454 22454 T->Q (IN REF. 2).
 FT CONFLICT 23324 23324 S->L (IN REF. 2).
 FT SEQUENCE 26926 AA; 2993428 MW; 0214E3A3 CRC32;

Query Match
 Best Local Similarity 27.18; Score 123; DB 4; Length 26926;
 Matches 29; Conservative 34; Mismatches 35; Indels 9; Gaps 8;

DB 21139 VILDMN-VCRIVATVITGIPSPK-KGPIRED-EIKADSVLSDVDEGGEGITCY 21195
 4 VILGATTVVAVGVAVLAAAGKMKSPQKVEYIIDNFTLRNRSDESYG-NVT-P 61

DB 21196 STEKRETSQTNW-KNV-CSSVANT--FKVPIVYKDAEYOFVRAEN 21238
 62 SFQYQTKGDMNWKILSGCONITSTKCNFSIKMAYEEIKLRIRAK 108

RESULT 7
 ID 09XX66 PRELIMINARY; PRT: 349 AA.

AC 09XX66:
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE Y102A5C.31 PROTEIN.
 GN Y102A5C.31.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditiia; Rhabditidae;
 OC Rhabditiina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA GARDNER A.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSICOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRATON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH R., SONNHAMMER E., STADEN R., SULLSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: AL031627; CA20969.1;
 SO SEQUENCE 349 AA; 4019 MW; FD45B68 CRC32;

Query Match
 Best Local Similarity 29.7%; Score 118; DB 5; Length 349;
 Matches 17; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

DB 6 NSSEYDFAPYLHFAVEIPHLVLAIVIFTPSPMAVKNMMPFLHRCASFL 62
 112 SSMYEDSTPRKAOIGPPEVHLAEADKAIVIHISPGKDSVMALDGLSTYSIL 168

RESULT 8
 ID 045849 PRELIMINARY; PRT: 349 AA.
 AC 045849:
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE T27C5.5 PROTEIN.

GN T27C5.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditiia; Rhabditidae;
 OC Rhabditiina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CUMMINGS P.;
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSICOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRATON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH R., SONNHAMMER E., STADEN R., SULLSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: 282058; CAB04866.1;
 DR PFM; PF01604; 7em.5; 1.
 SO SEQUENCE 349 AA; 40102 MW; 5FD9517 CRC32;

Query Match
 Best Local Similarity 31.6%; Score 114; DB 5; Length 349;
 Matches 18; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

DB 6 NSSEYDFAPYLHFAVEIPHLVLAIVIFTPSPMAVKNMMPFLHRCASFL 62
 112 SSMYEDSTPRKAOIGPPEVHLAEADKAIVIHISPGKDSVMALDGLSTYSIL 168

RESULT 9
 ID 09MEU9 PRELIMINARY; PRT: 918 AA.
 AC 09MEU9:
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE GLYCOPROTEIN 130 PRECURSOR.
 GN GP130.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7, E8);
 RX MEDLINE: 99026068.
 RA GEISSEN M., HELLER S., PENNICA D., ERNSENBERGER U., ROHRER H.;
 RT "The specification of sympathetic neurotransmitter phenotype depends
 on gp130 cytokine receptor signaling.";
 RL Development 125:4791-4801(1998).
 DR EMBL: AJ011688; CAB42084.1;
 KW Signal.
 FT SIGNAL 1
 SO SEQUENCE 918 AA; 102495 MW; 9DC128C3 CRC32;

Query Match
 Best Local Similarity 3.6%; Score 114; DB 13; Length 918;
 Matches 21; Conservative 23; Mismatches 36; Indels 3; Gaps 3;

DB 235 VNSGILPVLKLSWENOISTVYMELEKFNIRIRISSDINWMEVP-EDTASPTSFSGGL 293
 36 VEVDIIDNFTLRN-NRDESYGVNVTSEFDYQKGMWIKILSGCONITSTKCNFSIKL 94
 DB 294 RPYEYVPSIRCKMEKEDGVGMSD 316
 95 NYVEIKLRIRAKENTSS-NYE 116

[illegible]

 WIRELESS
 (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Aug 21 10:24:36 2000; Maspar time 13.95 Seconds
 Tabular output not generated. 740.422 Million cell updates/sec

Title: >US-09-240-675-2
 Description: (1-436) from US09240675.pep
 Perfect Score: 3178
 Sequence: 1 MMVVLGATLVVAAGPWV.....KSSVFSDAVCEKTRKPGTSK 436

Scoring table: PAM 150
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: a-geneseq36
 1:geneseqp

Statistics: Mean 35.309; Variance 151.609; scale 0.233

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	3178	100.0	436	1	R28495	Sequence of a soluble	4.64e-300
2	3178	100.0	436	1	R14487	Soluble Interferon- α	4.64e-300
3	3178	100.0	557	1	R14488	Complete Interferon- α	4.64e-300
4	3178	100.0	557	1	R11958	Human α -Interferon	4.64e-300
5	3178	100.0	557	1	R42635	Human Interferon recep	4.64e-300
6	3178	100.0	557	1	R28496	Sequence of a soluble	4.64e-300
7	3171	99.8	557	1	R75356	Human IFN receptor	2.33e-299
8	3171	99.8	557	1	R21804	Transmembrane Interfe	2.33e-299
9	3163	99.5	436	1	R71233	IFN-receptor extracell	1.48e-298
10	3117	98.1	434	1	R21805	Spliced-deleted interf	5.96e-294
11	3025	95.2	496	1	R21806	CRPB4 protein.	5.65e-14
12	274	8.6	332	1	W52296	IFN-gamma receptor: bet	4.95e-11
13	243	7.6	332	1	W79159	Zcytor7 cytokine recep	3.29e-11
14	243	7.6	332	1	W79159	Human IFN-gamma access	5.21e-06
15	183	5.8	337	1	R75783	Human cytokine recepto	2.02e-04
16	183	5.8	337	1	R75783	Human cytokine recepto	2.02e-04
17	164	5.2	574	1	W97861	Human cytokine recepto	1.94e-03
18	152	4.4	211	1	W97864	Human cytokine recepto	1.94e-03
19	139	4.4	17	1	R47008	IFN- α receptor: pos	2.15e-02
20	140	4.4	489	1	R70469	Plasmod falciparum huma	1.79e-02
21	132	4.2	575	1	W41803	Mouse IL-10 receptor	9.15e-02
22	131	4.1	245	1	R62023	Soluble human Interfer	1.10e-01
23	130	4.1	575	1	R57139	Interleukin-10 recepto	1.10e-01

24	128	4.0	329	1	W17859	Rheumatoid arthritis a	1.57e-01
25	128	4.0	332	1	W70799	Human gp130-delta-3f1b	1.57e-01
26	128	4.0	658	1	R94576	Human gp130 splice var	1.57e-01
27	128	4.0	708	1	R85811	gp130 N-terminal fragm	1.57e-01
28	128	4.0	708	1	R37804	Human gp130 N-terminal	1.57e-01
29	128	4.0	859	1	W70796	Human gp130-Fc-His6 am	1.57e-01
30	128	4.0	918	1	R75368	Human gp130 protein	1.57e-01
31	128	4.0	918	1	R46233	Human soluble glycopro	1.57e-01
32	128	4.0	918	1	R10545	Recombinant human gp13	1.57e-01
33	128	4.0	951	1	W70798	Human gp130-C-gamma-1	1.57e-01
34	125	3.9	227	1	R14642	Gamma interferon recep	2.67e-01
35	125	3.9	231	1	R14641	Gamma interferon recep	2.67e-01
36	125	3.9	473	1	R55749	Extracellular domain o	2.67e-01
37	125	3.9	942	1	R70113	Gamma-IFN-R-GPB 130 fn	2.67e-01
38	119	3.7	210	1	R14643	Gamma Interferon recep	7.70e-01
39	116	3.7	578	1	R57138	Interleukin-10 recepto	1.30e+00
40	116	3.7	578	1	W41804	Human IL-10 receptor	1.30e+00
41	118	3.7	660	1	R65633	Human Interleukin-12 r	9.17e-01
42	118	3.7	662	1	R65632	Human Interleukin-12 r	9.17e-01
43	118	3.7	662	1	W12772	Human Interleukin-12 b	9.17e-01
44	113	3.6	180	1	W00404	Interleukin-6 antagoni	2.18e+00
45	108	3.4	877	1	W71628	Mouse Bsk receptor-11k	5.11e+00

ALIGNMENTS

RESULT	1	R28495	standard; Protein; 436 AA.
ID	AC	R28495	
AD	31-MAR-1993	(first entry)	
DT	DE	Sequence of a soluble form of the interferon (IFN) receptor	
DE	DE	with a high affinity for IFN- α and - β .	
KW	Interferon receptor; α -Interferon; β -Interferon.		
OS	Synthetic.		
PN	WO9218626-A.		
PD	29-OCT-1992.		
PF	17-APR-1991; WO-F00318.		
PR	17-APR-1991; WO-F00318.		
PA	(EUBI-) LAB EURO BIOTECHNOLOGIE.		
PI	Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,		
PI	Tovey M, Uze G;		
DR	WPI: 92-382110/46.		
DR	N-PSDB: 030532.		
PT	Water soluble polypeptide(s) strongly bind interferon(s) α and β		
PT	and β - useful as immunosuppressants, for treating auto-immune		
PT	diseases and transplant rejection		
PS	Claim 2; Fig 1; 58pp; English.		
CC	DNA encoding the water-soluble polypeptide with a high affinity for		
CC	IFN- α and - β 15 isolated by PCR, using appropriate		
CC	oligonucleotides as primers and cloned cDNA as template. For example,		
CC	bacteriophage lambda ZAP, containing the entire coding sequence of		
CC	the IFN- α and - β receptor (Q30533), was incubated with oligos		
CC	Q30534 and Q30535. R28496 represents the complete receptor. R28495		
CC	lacks the transmembrane and cytoplasmic domains. Both forms bind		
CC	IFN in the same way as antibodies so are immunosuppressants e.g. for		
CC	treating autoimmune diseases and graft rejection. They lack the		
CC	toxic side-effects of known immunosuppressants such as steroids.		
CC	Sequence 436 AA.		
CC	Sequence 436 AA.		

Query Match: 100.0%; Score 3178; DB 1; Length 436;
 Best local similarity 100.0%; Pred. No. 4.64e-300;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB	1	MMVVLGATLVVAAGPWVLSAAGGKNIKSPQKVEVDIIDDPIIRMRSDSYVNT	60
DB	1	MMVVLGATLVVAAGPWVLSAAGGKNIKSPQKVEVDIIDDPIIRMRSDSYVNT	60
DB	61	FSDYDQKTDNWKISGCONITSTKCNSSKLNTVEETKIRAREKENTSSWYEDSF	120
DB	61	FSDYDQKTDNWKISGCONITSTKCNSSKLNTVEETKIRAREKENTSSWYEDSF	120
DB	121	TPPRKAOIGPPEVHEAEKRAIYTHISPGKDSVMAALDLSPTYSILITKNSGVEERI	180
DB	121	TPPRKAOIGPPEVHEAEKRAIYTHISPGKDSVMAALDLSPTYSILITKNSGVEERI	180

OY 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKNSGVEERI 180
DB 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
OY 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKOIPDCENVTTCQVFPQNVFOR 300
OY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKOIPDCENVTTCQVFPQNVFOR 300
DB 301 GIVILRQASDGNNTSFWESEIKFDTEIOAFLLPPVENIRLSDFSFIHYIGAPKOSGNTP 360
OY 301 GIVILRQASDGNNTSFWESEIKFDTEIOAFLLPPVENIRLSDFSFIHYIGAPKOSGNTP 360
DB 361 VIODYPLIYEIIFWENTSMARKIIIEKKTDTVTYNLKLPLVYCYKARAHMDEKLNTSSV 420
OY 361 VIODYPLIYEIIFWENTSMARKIIIEKKTDTVTYNLKLPLVYCYKARAHMDEKLNTSSV 420
DB 421 FSDAVCEKTRKGNNTSK 436
OY 421 FSDAVCEKTRKGNNTSK 436

RESULT 2

ID R14487 standard; Protein; 436 AA.
AC R14487;
DE 16-JAN-1992 (first entry)
DT Soluble interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eid P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tover MG, Uze G;
PI WPI; 91-319778/44.
DR N-PSDB; Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 45; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also Q14240.
SQ Sequence 436 AA;

Query Match 100.0%; Score 3178; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 4.64e-300;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVVLGATLVLVAVGPVWLSAAGGKNLKSPOKVEVDIIDNFIIRNRSDSEGVNT 60
OY 1 MMVVLGATLVLVAVGPVWLSAAGGKNLKSPOKVEVDIIDNFIIRNRSDSEGVNT 60
DB 61 FSPDYQKTGMDNNIKISGCCNITSTKCNFSSKLANTYEEIKLIRAEKENTSSMYEVDSE 120
OY 61 FSPDYQKTGMDNNIKISGCCNITSTKCNFSSKLANTYEEIKLIRAEKENTSSMYEVDSE 120
DB 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKNSGVEERI 180
OY 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKNSGVEERI 180
DB 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
OY 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKOIPDCENVTTCQVFPQNVFOR 300
OY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKOIPDCENVTTCQVFPQNVFOR 300

OY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKOIPDCENVTTCQVFPQNVFOR 300
DB 301 GIVILRQASDGNNTSFWESEIKFDTEIOAFLLPPVENIRLSDFSFIHYIGAPKOSGNTP 360
OY 301 GIVILRQASDGNNTSFWESEIKFDTEIOAFLLPPVENIRLSDFSFIHYIGAPKOSGNTP 360
DB 361 VIODYPLIYEIIFWENTSMARKIIIEKKTDTVTYNLKLPLVYCYKARAHMDEKLNTSSV 420
OY 361 VIODYPLIYEIIFWENTSMARKIIIEKKTDTVTYNLKLPLVYCYKARAHMDEKLNTSSV 420
DB 421 FSDAVCEKTRKGNNTSK 436
OY 421 FSDAVCEKTRKGNNTSK 436

RESULT 3

ID R14488 standard; Protein; 557 AA.
AC R14488;
DE 16-JAN-1992 (first entry)
DT Complete interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eid P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tover MG, Uze G;
PI WPI; 91-319778/44.
DR N-PSDB; Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Disclosure; Page 47; 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also Q14239.
CC See also Q14239.
SQ Sequence 557 AA;

Query Match 100.0%; Score 3178; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 4.64e-300;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVVLGATLVLVAVGPVWLSAAGGKNLKSPOKVEVDIIDNFIIRNRSDSEGVNT 60
OY 1 MMVVLGATLVLVAVGPVWLSAAGGKNLKSPOKVEVDIIDNFIIRNRSDSEGVNT 60
DB 61 FSPDYQKTGMDNNIKISGCCNITSTKCNFSSKLANTYEEIKLIRAEKENTSSMYEVDSE 120
OY 61 FSPDYQKTGMDNNIKISGCCNITSTKCNFSSKLANTYEEIKLIRAEKENTSSMYEVDSE 120
DB 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKNSGVEERI 180
OY 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKNSGVEERI 180
DB 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
OY 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKOIPDCENVTTCQVFPQNVFOR 300
OY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKOIPDCENVTTCQVFPQNVFOR 300

Db 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLPPVFNIRSLSDSFHYIYIGAPKOSGNT 360
 OY 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLPPVFNIRSLSDSFHYIYIGAPKOSGNT 360
 Db 361 VIODPLIYEIIFEMENTSNAERKIIIEKTDVTPMLKPLTYCYVARAHATDEKLNKSSV 420
 OY 361 VIODPLIYEIIFEMENTSNAERKIIIEKTDVTPMLKPLTYCYVARAHATDEKLNKSSV 420
 Db 421 FSDVACERTKPGNTSK 436
 OY 421 FSDVACERTKPGNTSK 436

RESULT 4

ID R11958 standard; Protein 557 AA.
 AC R11958:
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein.
 KW Human alpha IFN, IFN agonists; antiviral; anti tumour agent;
 OS Homo sapiens.
 FH Key
 FT peptide
 FT 1. 27
 PN WO9105862-A.
 PD 02-MAY-1991.
 PF 19-OCT-1990; F00758.
 PR 20-OCT-1989; FR-013770.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Mogensen KE, Uze G, Lutfalla G, Gresser I;
 DR WPI: 91-148740/20.
 DR N-PSDB: Q11701.
 PT New human alpha-interferon receptor protein - useful for testing
 PS Interferon agonists and in treatment or diagnosis
 CC Disclosure: fig 4; 30pp; French.
 CC This recombinant human alpha-interferon (IFN) receptor protein is
 CC useful for the testing of IFN agonists and for treatment and diag-
 CC nosis of viral diseases and tumours. Antibodies raised against
 CC this protein can be used for blocking the receptor when required,
 CC or where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the protein,
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 SO Sequence 557 AA.

Query Match 100.0%; Score 3178; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 4,64e-300;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMYVLGATTLVAVGPWVLSAAGKRLKSPQKVEVDIIDDFFILRNRSDESNGNT 60
 OY 1 MMYVLGATTLVAVGPWVLSAAGKRLKSPQKVEVDIIDDFFILRNRSDESNGNT 60
 Db 61 FSDYQGTGDMNFKISGCONITSTKCNFSLKLNVEEIKLRIRAEKETSWMYEDSF 120
 OY 61 FSDYQGTGDMNFKISGCONITSTKCNFSLKLNVEEIKLRIRAEKETSWMYEDSF 120
 Db 121 TPRKAOIGPEVHLEAEDKAIYIHISPGKDSVMALDGLSTYSLLIMKSSGVEERI 180
 OY 121 TPRKAOIGPEVHLEAEDKAIYIHISPGKDSVMALDGLSTYSLLIMKSSGVEERI 180
 Db 181 ENYSRHKIKYKSPETTYCLAKVAALLTSMKIGVSPVHCITTYENELPPENIEVSQ 240
 OY 181 ENYSRHKIKYKSPETTYCLAKVAALLTSMKIGVSPVHCITTYENELPPENIEVSQ 240
 Db 241 NONTYAKMDYTYANNFTFOVOMLHAFKRNPGNHLKWKQIPDCEVNTKTCVFPONVOK 300
 OY 241 NONTYAKMDYTYANNFTFOVOMLHAFKRNPGNHLKWKQIPDCEVNTKTCVFPONVOK 300
 Db 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLPPVFNIRSLSDSFHYIYIGAPKOSGNT 360
 OY 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLPPVFNIRSLSDSFHYIYIGAPKOSGNT 360

Db 361 VIODPLIYEIIFEMENTSNAERKIIIEKTDVTPMLKPLTYCYVARAHATDEKLNKSSV 420
 OY 361 VIODPLIYEIIFEMENTSNAERKIIIEKTDVTPMLKPLTYCYVARAHATDEKLNKSSV 420
 Db 421 FSDVACERTKPGNTSK 436
 OY 421 FSDVACERTKPGNTSK 436

RESULT 5

ID R42635 standard; Protein 557 AA.
 AC R42635:
 DT 20-APR-1994 (first entry)
 DE Human interferon receptor
 KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
 KW cell proliferation; allograft rejection; systemic lupus erythematosus;
 KW psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;
 OS Immunodeficiency; measles virus; Interferon-alpha-beta.
 FH Key
 FT domain
 FT 1. 436
 PN BP-563487-A.
 PD 06-OCT-1993.
 PF 31-MAR-1992; 400902.
 PR (Euhel) LAB EURO BIOTECHNOLOGIE SA.
 PA Benoit P, Maguette D, Meyer F, Plavec I, Torey MG;
 DR WPI: 93-312951/40.
 DR P-PSDB: R42635.
 PT Monoclonal antibody to human interferon type-I receptor - having
 PS neutralising activity against human type I interferon, used for
 PS therapy and diagnosis
 CC Disclosure: fig 3; 21pp; English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC interferon alpha-beta receptor based on the full-length human IFN-R
 CC sequence are claimed. The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 SO Sequence 557 AA.

Query Match 100.0%; Score 3178; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 4,64e-300;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMYVLGATTLVAVGPWVLSAAGKRLKSPQKVEVDIIDDFFILRNRSDESNGNT 60
 OY 1 MMYVLGATTLVAVGPWVLSAAGKRLKSPQKVEVDIIDDFFILRNRSDESNGNT 60
 Db 61 FSDYQGTGDMNFKISGCONITSTKCNFSLKLNVEEIKLRIRAEKETSWMYEDSF 120
 OY 61 FSDYQGTGDMNFKISGCONITSTKCNFSLKLNVEEIKLRIRAEKETSWMYEDSF 120
 Db 121 TPRKAOIGPEVHLEAEDKAIYIHISPGKDSVMALDGLSTYSLLIMKSSGVEERI 180
 OY 121 TPRKAOIGPEVHLEAEDKAIYIHISPGKDSVMALDGLSTYSLLIMKSSGVEERI 180
 Db 181 ENYSRHKIKYKSPETTYCLAKVAALLTSMKIGVSPVHCITTYENELPPENIEVSQ 240
 OY 181 ENYSRHKIKYKSPETTYCLAKVAALLTSMKIGVSPVHCITTYENELPPENIEVSQ 240
 Db 241 NONTYAKMDYTYANNFTFOVOMLHAFKRNPGNHLKWKQIPDCEVNTKTCVFPONVOK 300
 OY 241 NONTYAKMDYTYANNFTFOVOMLHAFKRNPGNHLKWKQIPDCEVNTKTCVFPONVOK 300
 Db 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLPPVFNIRSLSDSFHYIYIGAPKOSGNT 360
 OY 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLPPVFNIRSLSDSFHYIYIGAPKOSGNT 360
 Db 361 VIODPLIYEIIFEMENTSNAERKIIIEKTDVTPMLKPLTYCYVARAHATDEKLNKSSV 420
 OY 361 VIODPLIYEIIFEMENTSNAERKIIIEKTDVTPMLKPLTYCYVARAHATDEKLNKSSV 420

OY 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420
 DB 421 FSDAVCEKTPGNTSK 436
 OY 421 FSDAVCEKTPGNTSK 436

RESULT 6
 ID R28496 standard; Protein; 557 AA.
 AC R28496;
 DT 31-MAR-1993 (first entry)
 DE Sequence of a soluble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta
 KM Interferon receptor; alpha-interferon; beta-interferon
 OS Synthetic.
 PN WO9218626-A.
 PD 29-OCT-1992.
 PF 17-APR-1991; F00318.
 PR 17-APR-1991; WO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE.
 PI Tovey M, Uze G.
 DR MPI: 92-382110/46.
 DR N-PSDB: 030533.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating, auto-immune diseases and transplant rejection
 PS Claim 3; Fig 2; 58pp; English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 3178; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 4,64e-300;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMYVLLGATTLVAVAGPWLISAAGGNLKSPOKYEVDIIDNFI LRNRSDSESGNT 60
 OY 1 MMYVLLGATTLVAVAGPWLISAAGGNLKSPOKYEVDIIDNFI LRNRSDSESGNT 60
 DB 61 FSDYQKGTGDMNKLKSGCONITSTKCNFSLKLNVEEIKLIRAEKENTSSMYEVSF 120
 OY 61 FSDYQKGTGDMNKLKSGCONITSTKCNFSLKLNVEEIKLIRAEKENTSSMYEVSF 120
 DB 121 TPRKAOIGPEVHLAEDEKAIYIHISPGTKDSVMALDGLSTYSLLIKNSSGVEER 180
 OY 121 TPRKAOIGPEVHLAEDEKAIYIHISPGTKDSVMALDGLSTYSLLIKNSSGVEER 180
 DB 181 ENIYSRHKIYKLSPEYTCYKVAALLTSWKIGVSPHCIKTVENELPPENIEVSQ 240
 OY 181 ENIYSRHKIYKLSPEYTCYKVAALLTSWKIGVSPHCIKTVENELPPENIEVSQ 240
 DB 241 NQNTYVAKMDYTYANMTFOVOMLAFLKRNNGNHLKWKQIPDCENVTTCQVPONVFK 300
 OY 241 NQNTYVAKMDYTYANMTFOVOMLAFLKRNNGNHLKWKQIPDCENVTTCQVPONVFK 300
 DB 301 GIYLLRVOASDGNNTSFWSEIKFDTEIOAFLLPPVFNIRSLSDSHIYIGAKOSGNT 360
 OY 301 GIYLLRVOASDGNNTSFWSEIKFDTEIOAFLLPPVFNIRSLSDSHIYIGAKOSGNT 360
 DB 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420
 OY 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420
 DB 421 FSDAVCEKTPGNTSK 436

OY 421 FSDAVCEKTPGNTSK 436

RESULT 7
 ID R75356 standard; Protein; 557 AA.
 AC R75356;
 DT 16-OCT-1995 (first entry)
 DE Human IFN receptor.
 KM IFN receptor; Interferon receptor; Interferon-alpha; Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT domain 1..436
 FT /label- Extracellular_domain
 FN WO9507716-A.
 PD 23-MAR-1995.
 PF 16-SEP-1994; E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benizrl EJ, Tovey MG.
 PI MPI: 95-131187/17.
 DR N-PSDB: 086458.
 PT Composn. of monoclonal antibodies against interferon receptor
 PS useful as immunomodulator, eg. for treating AIDS
 CC The amino acid sequence of human interferon class I receptor is given in R75356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monoclonal antibodies.
 SQ Sequence 557 AA;

Query Match 99.8%; Score 3171; DB 1; Length 557;
 Best Local Similarity 99.8%; Pred. No. 2.33e-299;
 Matches 435; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMYVLLGATTLVAVAGPWLISAAGGNLKSPOKYEVDIIDNFI LRNRSDSESGNT 60
 OY 1 MMYVLLGATTLVAVAGPWLISAAGGNLKSPOKYEVDIIDNFI LRNRSDSESGNT 60
 DB 61 FSDYQKGTGDMNKLKSGCONITSTKCNFSLKLNVEEIKLIRAEKENTSSMYEVSF 120
 OY 61 FSDYQKGTGDMNKLKSGCONITSTKCNFSLKLNVEEIKLIRAEKENTSSMYEVSF 120
 DB 121 TPRKAOIGPEVHLAEDEKAIYIHISPGTKDSVMALDGLSTYSLLIKNSSGVEER 180
 OY 121 TPRKAOIGPEVHLAEDEKAIYIHISPGTKDSVMALDGLSTYSLLIKNSSGVEER 180
 DB 181 ENIYSRHKIYKLSPEYTCYKVAALLTSWKIGVSPHCIKTVENELPPENIEVSQ 240
 OY 181 ENIYSRHKIYKLSPEYTCYKVAALLTSWKIGVSPHCIKTVENELPPENIEVSQ 240
 DB 241 NQNTYVAKMDYTYANMTFOVOMLAFLKRNNGNHLKWKQIPDCENVTTCQVPONVFK 300
 OY 241 NQNTYVAKMDYTYANMTFOVOMLAFLKRNNGNHLKWKQIPDCENVTTCQVPONVFK 300
 DB 301 GIYLLRVOASDGNNTSFWSEIKFDTEIOAFLLPPVFNIRSLSDSHIYIGAKOSGNT 360
 OY 301 GIYLLRVOASDGNNTSFWSEIKFDTEIOAFLLPPVFNIRSLSDSHIYIGAKOSGNT 360
 DB 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420
 OY 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420
 DB 421 FSDAVCEKTPGNTSK 436
 OY 421 FSDAVCEKTPGNTSK 436
 RESULT 8
 ID W21804 standard; Protein; 557 AA.
 AC W21804;
 DT 23-SEP-1997 (first entry)

F1	/label= Extracellular-domain
F1	/note= * comprises amino acids 1-427 of the
F1	transmembranial IFMAR*
F1	428..434
F1	/label= S.-domain
PN	AU9475977-A.
PD	11-MAY-1995.

PF 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 2; Fig 7; 46pp; English.
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1
 CC (W21805) is characterised by a new domain (S) which follows an
 CC end-deleted extracellular domain when compared to transmembrane
 CC IFNAR (W21804). There is no transmembrane domain. The amino acid
 CC sequence is predicted from a cDNA clone (see also T73520) obd-
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
 CC the response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating the activity of the multiple IFN
 CC subtypes. They can be expressed in host cells and used to inhibit,
 CC modulate or modify the activities of IFNs alpha and beta in cells,
 CC tissues and organisms, or for diagnostic purposes.
 SQ Sequence 434 AA;

Query Match 98.1%; Score 3117; DB 1; Length 434;
 Best Local Similarity 99.5%; Pred. No. 5,966-294;
 Matches 426; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 MAAVLLGATTLVLAAGVFWLSAAAGKRLKSPQVEVDIIDNFILRMNSDESVCNT 60
 QY 1 MAAVLLGATTLVLAAGVFWLSAAAGKRLKSPQVEVDIIDNFILRMNSDESVCNT 60
 DB 61 FSPDYORTGMDNMIRKLSGCCNITSTKCNFSSKLNTVEIKLRIRAEKENTSSWEYDSF 120
 QY 61 FSPDYORTGMDNMIRKLSGCCNITSTKCNFSSKLNTVEIKLRIRAEKENTSSWEYDSF 120
 DB 121 TPFRAKQIGPEVHLEADKAIYHISPGTDSVMALDGLSTFYSLILWNSGVEERI 180
 QY 121 TPFRAKQIGPEVHLEADKAIYHISPGTDSVMALDGLSTFYSLILWNSGVEERI 180
 DB 181 ENTYSRHKIYKLSPEYTYCLAKVKAALLTSMKIGVSPVHCITVTENELPPENIEVSQ 240
 QY 181 ENTYSRHKIYKLSPEYTYCLAKVKAALLTSMKIGVSPVHCITVTENELPPENIEVSQ 240
 DB 241 NONTVLKMDITYANMTFOVOMLAFLKRNPGNHLKWKQIPDCENVTTCVFPQNVFOK 300
 QY 241 NONTVLKMDITYANMTFOVOMLAFLKRNPGNHLKWKQIPDCENVTTCVFPQNVFOK 300
 DB 301 GIVLLRVOASGNTSFWSEIEIKFDTELOAFLLPPVFNIRLSDFHLYIGAPROSGNTP 360
 QY 301 GIVLLRVOASGNTSFWSEIEIKFDTELOAFLLPPVFNIRLSDFHLYIGAPROSGNTP 360
 DB 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTYNLKLPLVYCYKARAHMTDEKLKSSV 420
 QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTYNLKLPLVYCYKARAHMTDEKLKSSV 420
 DB 421 FSDAVCEN 428
 QY 421 FSDAVCER 428

RESULT 11:
 ID W21806 standard; Protein; 496 AA.
 AC W21806;
 DT 23-SEP-1997 (first entry)
 DE Spliced-deleted interferon alpha-receptor form 2.
 KW Interferon alpha-receptor; IFNAR.
 OS Homo sapiens.
 FH Key
 FT domain 1..419
 FT /label- Extracellular domain
 FT /note- "comprises amino acid residues 1-413 and
 FT 422-427 of transmembrane IFNAR"
 FT domain 420..496

FT /label- Intracellular domain
 FT /note- "comprises amino acids 481-557 of
 FT transmembrane IFNAR"
 PN AU9475977-A.
 PD 11-MAY-1995.
 PF 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of interferon(s)
 PS Example 3; Fig 7; 46pp; English.
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
 CC (W21806) is characterised by a double deletion when compared to
 CC transmembrane IFNAR (W21804). The extracellular domain is
 CC shortened by 6 amino acid residues and is followed by a truncated
 CC intracellular domain. There is no transmembrane region. The amino
 CC acid sequence is predicted from a cDNA clone (see also T73521) obd-
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
 CC response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating IFN activities. They can be expressed
 CC in host cells and used to inhibit, modulate or modify the
 CC activities of IFNs alpha and beta in cells, tissues and organisms,
 CC or for diagnostic purposes.
 SQ Sequence 496 AA;

Query Match 95.2%; Score 3025; DB 1; Length 496;
 Best Local Similarity 97.9%; Pred. No. 9,716-285;
 Matches 414; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

DB 1 MAAVLLGATTLVLAAGVFWLSAAAGKRLKSPQVEVDIIDNFILRMNSDESVCNT 60
 QY 1 MAAVLLGATTLVLAAGVFWLSAAAGKRLKSPQVEVDIIDNFILRMNSDESVCNT 60
 DB 61 FSPDYORTGMDNMIRKLSGCCNITSTKCNFSSKLNTVEIKLRIRAEKENTSSWEYDSF 120
 QY 61 FSPDYORTGMDNMIRKLSGCCNITSTKCNFSSKLNTVEIKLRIRAEKENTSSWEYDSF 120
 DB 121 TPFRAKQIGPEVHLEADKAIYHISPGTDSVMALDGLSTFYSLILWNSGVEERI 180
 QY 121 TPFRAKQIGPEVHLEADKAIYHISPGTDSVMALDGLSTFYSLILWNSGVEERI 180
 DB 181 ENTYSRHKIYKLSPEYTYCLAKVKAALLTSMKIGVSPVHCITVTENELPPENIEVSQ 240
 QY 181 ENTYSRHKIYKLSPEYTYCLAKVKAALLTSMKIGVSPVHCITVTENELPPENIEVSQ 240
 DB 241 NONTVLKMDITYANMTFOVOMLAFLKRNPGNHLKWKQIPDCENVTTCVFPQNVFOK 300
 QY 241 NONTVLKMDITYANMTFOVOMLAFLKRNPGNHLKWKQIPDCENVTTCVFPQNVFOK 300
 DB 301 GIVLLRVOASGNTSFWSEIEIKFDTELOAFLLPPVFNIRLSDFHLYIGAPROSGNTP 360
 QY 301 GIVLLRVOASGNTSFWSEIEIKFDTELOAFLLPPVFNIRLSDFHLYIGAPROSGNTP 360
 DB 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTYNLKLPLVYCYKARAHMTDESDAVCEY 420
 QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTYNLKLPLVYCYKARAHMTDEKLKSSV 420
 DB 421 FSE 423
 QY 421 FSD 423

RESULT 12:
 ID W52296 standard; Protein; 325 AA.
 AC W52296;
 DT 23-JUN-1998 (first entry)
 DE CRP4 protein.
 KW CRP4; Interleukin-10; IL-10; IL-10 receptor; allograft rejection;
 KW vaccine; photosensitivity; inflammation; autoimmune disease;

This represents the zcytor7 cytok

This represents the zcytor7 cytokine receptor

CC This represents the 20vtext7 sub-11. 12pp; Engl15h.

CC binding receptor polypeptide and is a novel member of the type 2 cytokine
CC receptor family (Ccr2). An expression vector containing the Zcytor
CC polynucleotide, operably linked to transcription promoter, a sequence
CC encoding a transmembrane and intracellular domain, or both, and a
CC transcriptional terminator can be used to transform host cells for the
CC recombinant production of the polypeptide. The sequences can be used to
CC study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is
CC preferentially expressed in the kidney, pancreas, prostate or nervous
CC tissue. Agonists of Zcytor7 can be used to stimulate proliferation and
CC differentiation of cell in these organs. The antagonists and agonists can
CC also be used in the treatment of renal, neural, pancreatic and prostate
CC diseases.

Sequence 553 AA;

TELEFAX: (202)672-5399
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE 436 AA: 45723 MW: 1061275 CN;

Query Match 100.0%; Score 3178; DB 2; Length 436;
 Best Local Similarity 100.0%; Pred. No. 1,47e-277;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MAMVLLGATTLVAVAGPVVLSAAGGNLKSPOKVEVDIIDNFIILRNKSDSEYGVNT 60
 |||||||
 QY 1 MAMVLLGATTLVAVAGPVVLSAAGGNLKSPOKVEVDIIDNFIILRNKSDSEYGVNT 60
 |||||||
 DB 61 FSPDYOKTGMNWKIKSGCONITSTKCNFSSKLNYEEIKLRIRAEKNTSSWYEVDSF 120
 |||||||
 QY 61 FSPDYOKTGMNWKIKSGCONITSTKCNFSSKLNYEEIKLRIRAEKNTSSWYEVDSF 120
 |||||||
 DB 121 TFFRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSGVEERI 180
 |||||||
 QY 121 TFFRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSGVEERI 180
 |||||||
 DB 181 ENIYSRHKIYKLSPEPTYCLAKVAALLTSWKIGVSPVHCITTYENELPPPENIEVSQ 240
 |||||||
 QY 181 ENIYSRHKIYKLSPEPTYCLAKVAALLTSWKIGVSPVHCITTYENELPPPENIEVSQ 240
 |||||||
 DB 241 NONVYLKMDITYANMTFOVOMLHAFKRNPNHLYKMKOIPDCENKTKTQCVFPQNVOK 300
 |||||||
 QY 241 NONVYLKMDITYANMTFOVOMLHAFKRNPNHLYKMKOIPDCENKTKTQCVFPQNVOK 300
 |||||||
 DB 301 GYLLRVAQSDNNSTFMSSEIKFDEIOAFLPPVFNIRISLSDSFHYIGAPKOSGNTP 360
 |||||||
 QY 301 GYLLRVAQSDNNSTFMSSEIKFDEIOAFLPPVFNIRISLSDSFHYIGAPKOSGNTP 360
 |||||||
 DB 361 VIODYPLIYEIIFWENTSNAEKIIEKTDVVPNLKPLTYVCVAKAHMTDEKLKSSV 420
 |||||||
 QY 361 VIODYPLIYEIIFWENTSNAEKIIEKTDVVPNLKPLTYVCVAKAHMTDEKLKSSV 420
 |||||||
 DB 421 FSDAVCEKTRPGNTSK 436
 |||||||
 QY 421 FSDAVCEKTRPGNTSK 436
 |||||||

RESULT 2
 ID US-08-471-454-2 STANDARD; PRT: 557 AA.
 AC xxxxxx
 XX
 XX
 DE Sequence 2, Application US/08471454
 CC Patent No. 5731169
 CC GENERAL INFORMATION:
 CC APPLICANT: MOGENSEN, Knud E.
 CC APPLICANT: UZE, Gilles
 CC APPLICANT: LUTFALLA, Georges
 CC APPLICANT: GRESSER, Ion
 CC TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
 CC TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
 CC TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
 CC NUMBER OF SEQUENCES: 2
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: NIXON & VANDERHAYE P. C.
 CC STREET: 1100 NORTH GLEBE ROAD
 CC CITY: ARLINGTON
 CC STATE: VIRGINIA
 CC COUNTRY: U.S.A.
 CC ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,454
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/900,642
 FILING DATE: 15-JUN-1992
 APPLICATION NUMBER: FR 89/13770
 FILING DATE: 20-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: BYRNE, THOMAS E.
 REGISTRATION NUMBER: 32,205
 REFERENCE/DOCKET NUMBER: 960-7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 TELEX: 200797 NIXN UR
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 557 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE 557 AA: 65525 MW: 1717510 CN;

Query Match 100.0%; Score 3178; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1,47e-277;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MAMVLLGATTLVAVAGPVVLSAAGGNLKSPOKVEVDIIDNFIILRNKSDSEYGVNT 60
 |||||||
 QY 1 MAMVLLGATTLVAVAGPVVLSAAGGNLKSPOKVEVDIIDNFIILRNKSDSEYGVNT 60
 |||||||
 DB 61 FSPDYOKTGMNWKIKSGCONITSTKCNFSSKLNYEEIKLRIRAEKNTSSWYEVDSF 120
 |||||||
 QY 61 FSPDYOKTGMNWKIKSGCONITSTKCNFSSKLNYEEIKLRIRAEKNTSSWYEVDSF 120
 |||||||
 DB 121 TFFRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSGVEERI 180
 |||||||
 QY 121 TFFRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSGVEERI 180
 |||||||
 DB 181 ENIYSRHKIYKLSPEPTYCLAKVAALLTSWKIGVSPVHCITTYENELPPPENIEVSQ 240
 |||||||
 QY 181 ENIYSRHKIYKLSPEPTYCLAKVAALLTSWKIGVSPVHCITTYENELPPPENIEVSQ 240
 |||||||
 DB 241 NONVYLKMDITYANMTFOVOMLHAFKRNPNHLYKMKOIPDCENKTKTQCVFPQNVOK 300
 |||||||
 QY 241 NONVYLKMDITYANMTFOVOMLHAFKRNPNHLYKMKOIPDCENKTKTQCVFPQNVOK 300
 |||||||
 DB 301 GYLLRVAQSDNNSTFMSSEIKFDEIOAFLPPVFNIRISLSDSFHYIGAPKOSGNTP 360
 |||||||
 QY 301 GYLLRVAQSDNNSTFMSSEIKFDEIOAFLPPVFNIRISLSDSFHYIGAPKOSGNTP 360
 |||||||
 DB 361 VIODYPLIYEIIFWENTSNAEKIIEKTDVVPNLKPLTYVCVAKAHMTDEKLKSSV 420
 |||||||
 QY 361 VIODYPLIYEIIFWENTSNAEKIIEKTDVVPNLKPLTYVCVAKAHMTDEKLKSSV 420
 |||||||
 DB 421 FSDAVCEKTRPGNTSK 436
 |||||||
 QY 421 FSDAVCEKTRPGNTSK 436
 |||||||

RESULT 3
 ID US-08-466-974-2 STANDARD; PRT: 557 AA.
 AC xxxxxx
 XX
 XX

SQ SEQUENCE 557 AA; 63525 MW; 1717510 CN;
 Query Match 100.0%; Score 3178; DB 2; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1,47e-277;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMVVLGATTLVAVAGPWLSAAGKNIKSPQKVEVDIIDNFTLRNRSDSEVGNVT 60
 1 MMVVLGATTLVAVAGPWLSAAGKNIKSPQKVEVDIIDNFTLRNRSDSEVGNVT 60
 Oy 1 MMVVLGATTLVAVAGPWLSAAGKNIKSPQKVEVDIIDNFTLRNRSDSEVGNVT 60
 Db 61 FSDYORTGDMNWKILSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120
 Oy 61 FSDYORTGDMNWKILSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120
 Db 121 TPRRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180
 Oy 121 TPRRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180
 Db 181 ENIYSRHKIKYKLSPEPTYCLKVAKAAITTSKIGVSPVHCIKTYVENELPPENIEVSQ 240
 Oy 181 ENIYSRHKIKYKLSPEPTYCLKVAKAAITTSKIGVSPVHCIKTYVENELPPENIEVSQ 240
 Db 241 NONTVLKMDYTYANMTFOYOMLHAFKRNPGNHLKWKQIPDCENYKTCVFPQNVFQK 300
 Oy 241 NONTVLKMDYTYANMTFOYOMLHAFKRNPGNHLKWKQIPDCENYKTCVFPQNVFQK 300
 Db 301 GIYLLRVQASDGNNTSFWSSEIKFDTEIOAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360
 Oy 301 GIYLLRVQASDGNNTSFWSSEIKFDTEIOAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360
 Db 361 VIODYPLIYEIIFWENTSNAREKIIIEKTDVYVNLKPLTVYCVKRAHTMDKLNKSSV 420
 Oy 361 VIODYPLIYEIIFWENTSNAREKIIIEKTDVYVNLKPLTVYCVKRAHTMDKLNKSSV 420
 Db 421 FSDVCEKTRPGNTSK 436
 Oy 421 FSDVCEKTRPGNTSK 436

RESULT 5
 ID US-08-328-256-10 STANDARD; PRT: 557 AA.
 AC xxxxxx
 DE Sequence 10, Application US/08328256
 CC Sequence 10, Application US/08328256
 CC Patent No. 5643749
 CC GENERAL INFORMATION:
 CC APPLICANT: REVEL, Michel
 CC APPLICANT: ABRAMOVICH, Carolina
 CC APPLICANT: RATOVIETSKI, Edward
 CC TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
 CC NUMBER OF SEQUENCES: 12
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: BROWDY AND NEIMARK
 CC STREET: 419 Seventh Street, N.W., Suite 300
 CC CITY: Washington
 CC STATE: D.C.
 CC COUNTRY: USA
 CC ZIP: 20004
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/328,256
 CC FILING DATE: 24-OCT-1994
 CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: IL 107378
 CC FILING DATE: 24-OCT-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: BROWDY, Roger L.
 CC REGISTRATION NUMBER: REVEL-13
 CC REFERENCE/DOCKET NUMBER: 25,618
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-628-5197
 CC TELEFAX: 202-737-3528
 CC TELEX: 248633
 CC INFORMATION FOR SEQ ID NO: 10:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 557 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 SO SEQUENCE 557 AA; 63525 MW; 1718021 CN;

Query Match 100.0%; Score 3178; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 1,47e-277;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMVVLGATTLVAVAGPWLSAAGKNIKSPQKVEVDIIDNFTLRNRSDSEVGNVT 60
 Oy 1 MMVVLGATTLVAVAGPWLSAAGKNIKSPQKVEVDIIDNFTLRNRSDSEVGNVT 60
 Db 61 FSDYORTGDMNWKILSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120
 Oy 61 FSDYORTGDMNWKILSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120
 Db 121 TPRRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180
 Oy 121 TPRRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180
 Db 181 ENIYSRHKIKYKLSPEPTYCLKVAKAAITTSKIGVSPVHCIKTYVENELPPENIEVSQ 240
 Oy 181 ENIYSRHKIKYKLSPEPTYCLKVAKAAITTSKIGVSPVHCIKTYVENELPPENIEVSQ 240
 Db 241 NONTVLKMDYTYANMTFOYOMLHAFKRNPGNHLKWKQIPDCENYKTCVFPQNVFQK 300
 Oy 241 NONTVLKMDYTYANMTFOYOMLHAFKRNPGNHLKWKQIPDCENYKTCVFPQNVFQK 300
 Db 301 GIYLLRVQASDGNNTSFWSSEIKFDTEIOAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360
 Oy 301 GIYLLRVQASDGNNTSFWSSEIKFDTEIOAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360
 Db 361 VIODYPLIYEIIFWENTSNAREKIIIEKTDVYVNLKPLTVYCVKRAHTMDKLNKSSV 420
 Oy 361 VIODYPLIYEIIFWENTSNAREKIIIEKTDVYVNLKPLTVYCVKRAHTMDKLNKSSV 420
 Db 421 FSDVCEKTRPGNTSK 436
 Oy 421 FSDVCEKTRPGNTSK 436

RESULT 6
 ID US-08-307-588-4 STANDARD; PRT: 557 AA.
 AC xxxxxx
 DE Sequence 4, Application US/08307588
 CC Sequence 4, Application US/08307588
 CC Patent No. 5819453
 CC GENERAL INFORMATION:
 CC APPLICANT: BENOIT, Patrick
 CC APPLICANT: MEYER, Francois
 CC APPLICANT: MAGUIRE, Deborah
 CC APPLICANT: PLAVEC, Ivan
 CC APPLICANT: TOVEY, Michael G.

CC TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
CC TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Foley & Lardner
CC STREET: 3000 K Street, N.W., Suite 500
CC CITY: Washington
CC STATE: D.C.
CC ZIP: 20007
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/307,588
CC FILING DATE: 05-DEC-1994
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: PCT/EP93/00770
CC FILING DATE: 30-MAR-1993
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: EP 92400902.0
CC FILING DATE: 31-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Saxe, Bernhard D.
CC REGISTRATION NUMBER: 28,665
CC REFERENCE/DOCKET NUMBER: 17283/117/GUPL
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202)672-5300
CC TELEFAX: (202)672-5399
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 557 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 557 AA; 63525 MW; 1717510 CM;
Query Match 100.0%; Score 3178; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 1,47e-277;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MMYVLLGATTLVAVGPMVLSAAGGKNLSPQKVEVDIIDNFILRNRSDESVDGNT 60
Qy 1 MMYVLLGATTLVAVGPMVLSAAGGKNLSPQKVEVDIIDNFILRNRSDESVDGNT 60
Db 61 FSPDYOKTGMNMTKLSGCONITSTKCNFSSSLKLNVEETIKLRRAKENTSSMYEVSF 120
Qy 61 FSPDYOKTGMNMTKLSGCONITSTKCNFSSSLKLNVEETIKLRRAKENTSSMYEVSF 120
Db 121 TPRKAOIGPPEVHLEADAIVIHISPGTKDSVMMALDGLSFTYSLLIMKNSGVEERI 180
Qy 121 TPRKAOIGPPEVHLEADAIVIHISPGTKDSVMMALDGLSFTYSLLIMKNSGVEERI 180
Db 181 ENIYSRRIKIKLSPETTYCLKVKAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240
Qy 181 ENIYSRRIKIKLSPETTYCLKVKAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240
Db 241 NONVYLKMDTYANMTROYOMLAFLKRNPNHLYKKOIPDCNVYTCQVPPQNFQK 300
Qy 241 NONVYLKMDTYANMTROYOMLAFLKRNPNHLYKKOIPDCNVYTCQVPPQNFQK 300
Db 301 GYLLARVQASDGNNTSFESEIKFDTETQAFLLPPVNISSLSDSFHIIYGAPROSNT 360
Qy 301 GYLLARVQASDGNNTSFESEIKFDTETQAFLLPPVNISSLSDSFHIIYGAPROSNT 360
Db 361 VIDYDPLIYIITWENTSNARKITERTKTVYVNLKPLVYCVKAAHTMDEKLNSV 420
Qy 361 VIDYDPLIYIITWENTSNARKITERTKTVYVNLKPLVYCVKAAHTMDEKLNSV 420
Db 421 FSDAVCEKTRKGNSTK 436
Qy 421 FSDAVCEKTRKGNSTK 436

Qy 421 FSDAVCEKTRKGNSTK 436
RESULT 7
ID US-08-328-256-11 STANDARD; PRT; 434 AA.
XX XXXXXX
XX
XX
XX
XX
Sequence 11, Application US/08328256
XX
XX
Sequence 11, Application US/08328256
CC Patent No. 563749
CC GENERAL INFORMATION:
CC APPLICANT: REVEL, Michel
CC APPLICANT: ABRAMOVICH, Carolina
CC APPLICANT: RABOVITSKI, Edward
CC TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BROWDY AND NEIMARK
CC STREET: 419 Seventh Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20004
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/328,256
CC FILING DATE: 24-OCT-1994
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: IL 107378
CC FILING DATE: 24-OCT-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BROWDY, Roger L.
CC REGISTRATION NUMBER: REVEL-13
CC REFERENCE/DOCKET NUMBER: 25,618
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-628-5197
CC TELEFAX: 202-737-3528
CC TELEX: 248633
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 434 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 434 AA; 49546 MW; 1042221 CM;
Query Match 98.3%; Score 3124; DB 1; Length 434;
Best Local Similarity 99.8%; Pred. No. 1,43e-272;
Matches 427; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1 MMYVLLGATTLVAVGPMVLSAAGGKNLSPQKVEVDIIDNFILRNRSDESVDGNT 60
Qy 1 MMYVLLGATTLVAVGPMVLSAAGGKNLSPQKVEVDIIDNFILRNRSDESVDGNT 60
Db 61 FSPDYOKTGMNMTKLSGCONITSTKCNFSSSLKLNVEETIKLRRAKENTSSMYEVSF 120
Qy 61 FSPDYOKTGMNMTKLSGCONITSTKCNFSSSLKLNVEETIKLRRAKENTSSMYEVSF 120
Db 121 TPRKAOIGPPEVHLEADAIVIHISPGTKDSVMMALDGLSFTYSLLIMKNSGVEERI 180
Qy 121 TPRKAOIGPPEVHLEADAIVIHISPGTKDSVMMALDGLSFTYSLLIMKNSGVEERI 180
Db 181 ENIYSRRIKIKLSPETTYCLKVKAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240
Qy 181 ENIYSRRIKIKLSPETTYCLKVKAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240

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Query Match: 95.4%; Score 3032; DB 1; Length 496;
Best Local Similarity 98.1%; Pred. No. 4,556-264;
Matches 415; Conservative 1; Mismatches 7; Indels 0; Gaps 0

Dd 1 MMVVLGGATITVLVAVGFWVLSSAAGKRLKSPKVEVDIIDDFILKRNKSDSGVNT 60
Oy 1 MMVVLGGATITVLVAVGFWVLSSAAGKRLKSPKVEVDIIDDFILKRNKSDSGVNT 60
Dd 61 FSPDYQKGMNWKILSGCONITSTKCNFSSILKINVEEIKLRIRAEKENTSMYEVSF 120
Oy 61 FSPDYQKGMNWKILSGCONITSTKCNFSSILKINVEEIKLRIRAEKENTSMYEVSF 120
Dd 121 TPFRAQIGPPEVHLAEADKAIVIHISPGTDSYMMALDGLSFYSLIMNNSGVEERI 180
Oy 121 TPFRAQIGPPEVHLAEADKAIVIHISPGTDSYMMALDGLSFYSLIMNNSGVEERI 180
Dd 181 ENISRHHIYKLSPEPTYCLVKKALLSMKIGVSPHCKIKTVENELPPENIEVSQ 240
Oy 181 ENISRHHIYKLSPEPTYCLVKKALLSMKIGVSPHCKIKTVENELPPENIEVSQ 240
Dd 241 NONVYLKWDYIYANNTFQOVMLHAFLNKRNPNHLYKMKQIPDCENVAITYQCVFQNVFOK 300
Oy 241 NONVYLKWDYIYANNTFQOVMLHAFLNKRNPNHLYKMKQIPDCENVAITYQCVFQNVFOK 300
Dd 301 GIYLLRVAOSGNGNTSFSESEIKEDTEQOAPLLPPVPIRSLSSFHLYIGAPQSGNTP 360
Oy 301 GIYLLRVAOSGNGNTSFSESEIKEDTEQOAPLLPPVPIRSLSSFHLYIGAPQSGNTP 360
Dd 361 VIQDPLLYEIIIFEMENTSNAERKIIIEKTDVTYVNLKPLFYCYKARAHMTDESDANCEY 420
Oy 361 VIQDPLLYEIIIFEMENTSNAERKIIIEKTDVTYVNLKPLFYCYKARAHMTDEKLNRSV 420
Dd 421 FSE 423
Oy 421 FSD 423

RESULT 9
ID PCT-US94-14277-3 STANDARD; PRT; 202 AA.
AC xxxxxx
DT
XX
XX
XX
Sequence 3, Application PC/TUS9414277
CC Sequence 3, Application PC/TUS9414277
CC GENERAL INFORMATION:
CC APPLICANT: Agnet, Michel
CC APPLICANT: Bohml, Ruth
CC APPLICANT: Hemmi, Silvio
CC TITLE OF INVENTION: Receptor Subunit Polypeptides
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/14277
CC FILING DATE: 07-DEC-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/164596
CC FILING DATE: 09-DEC-1993
CC ATTORNEY/AGENT INFORMATION:
CC

```

CC NAME: Love, Richard B.
CC REGISTRATION NUMBER: 34,659
CC REFERENCE/DOCKET NUMBER: 866PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-5530
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 202 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE: 202 AA; 23375 MW; 241129 CN;

Query Match 22.2%; Score 705; DB 4; Length 202;
Best Local Similarity 49.0%; Pred. No. 6,64e-51;
Matches 99; Conservative 39; Mismatches 62; Indels 1; Gaps 1;

Db 2 NIKPPENIDYIIDNYILKSSHGSGSVTFSAEYTKDERKMLKAPCOHTTTTKE 61
Qy 29 NIKSPKVEVDIIDNFIKMRSDSEYGNVTFSPDYQKGMNLIKSGCONITSTCN 88
Db 62 FSLDLPNXYIKTFVRBEGNSTSMNEVDPIPEPYTAHMSPEVRLEREDKALVHTS 121
Qy 89 FSSLALNYEETIKLIRAEKEN-TSSWEVDSTPPRAQIGPPEVHLEAEKALVHTS 147
Db 122 PGQDGNMALEKPSFSYTIKMSKSDKINSTYYEYKIPPELLPETYCLEKKAHP 181
Qy 148 PGTKSYMMALDGLFTSLILKMKSSGYEERIENTYSHKIKLSPETTYCLAKYKALL 207
Db 182 SLKHSNSTXOCISTVAN 201
Qy 208 TSMKIGVYSPVHCIKTYVEN 227

RESULT 10 STANDARD: PRT: 200 AA.
ID PCT-US94-14277-4
AC xxxxxx
XX
XX
XX
XX

Sequence 4, Application PC/TUS9414277
CC GENERAL INFORMATION:
CC APPLICANT: Aguet, Michel
CC APPLICANT: Bonni, Ruth
CC APPLICANT: Hemmi, Silvio
CC TITLE OF INVENTION: Receptor Subunit Polypeptides
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/14277
CC FILING DATE: 07-DEC-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/164596
CC FILING DATE: 09-DEC-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Love, Richard B.
CC REGISTRATION NUMBER: 34,659

CC REFERENCE/DOCKET NUMBER: 866PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-5530
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 200 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE: 200 AA; 22525 MW; 227601 CN;

Query Match 20.1%; Score 640; DB 4; Length 200;
Best Local Similarity 47.6%; Pred. No. 4.26e-45;
Matches 99; Conservative 43; Mismatches 53; Indels 13; Gaps 11;

Db 1 MPVFNLOVDAQGSYVLMKMDYIASADYLFRRQMPGYSKSSGSHSDMKRIPICANYO 60
Qy 229 LPPENIEVSQNONIVLAKMDY-TYANMTFOVMHLAKRPNGLIKMKIIPCCENYK 287
Db 61 TTHCVFSDTXYTGFFLVQASBGNHTSFWSSE-KFIDSQKHLPPPVITVTAMSDTL 119
Qy 288 TLOCVFQVPOVFKGIYLLRVQASDGNNTSFMSEELKF-DTEIQAFLLPVPVFNIRSLSDSF 346
Db 120 LVYXNC-QDS-T-C-D-GLNYEIIEMENST-KISMEKGPFTLKNLOPLVYCYO 171
Qy 347 HIYIAPKSGCNTPIQDYPILYEIIIFEMENSNABRKIIERK-TDVTVPNLKPLVYCYK 405
Db 172 ARV-LFRALNKTNSFEKICEKTRPGS 198
Qy 406 ARAHTMDEKLNKSVSDVACEKTRPGN 433

RESULT 11 STANDARD: PRT: 325 AA.
ID US-08-683-743-4
AC xxxxxx
XX
XX
XX
XX
XX

Sequence 4, Application US/08683743
CC GENERAL INFORMATION:
CC PATENT NO. 5843697
CC APPLICANT: Pestka, Sidney
CC APPLICANT: Kotenko, Sergey
CC TITLE OF INVENTION: CITOKINE RECEPTOR SIGNAL TRANSDUCTION
CC CHAIN
CC NUMBER OF SEQUENCES: 25
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: David A. Jackson, Esq.
CC STREET: 411 Hackensack Ave, Continental Plaza, 4th
CC FLOOR
CC CITY: Hackensack
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07601
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/683,743
CC FILING DATE: 17-JUL-1996
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Jackson Esq., David A.
CC REGISTRATION NUMBER: 26,742
CC REFERENCE/DOCKET NUMBER: 601-1-050
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 201-487-5800

DE	Sequence 2, Application PC/TUS9414277		
XX			
CC	Sequence 2, Application PC/TUS9414277		
CC	GENERAL INFORMATION:		
CC			
CC	APPLICANT: Agnet, Michel		
CC	APPLICANT: Bonni, Ruth		
CC	TITLE OF INVENTION: Receptor Subunit Polypeptides		
CC	NUMBER OF SEQUENCES: 8		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Genentech, Inc.		
CC	STREET: 460 Point San Bruno Blvd		
CC	CITY: South San Francisco		
CC	STATE: California		
CC	COUNTRY: USA		
CC	ZIP: 94080		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: patin (genentech)		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: PCT/US94/14277		
CC	FILING DATE: 07-DEC-1994		
CC	CLASSIFICATION:		
CC	Prior Application DATA:		
CC	APPLICATION NUMBER: 08/164596		
CC	FILING DATE: 09-DEC-1993		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Love, Richard B.		
CC	REGISTRATION NUMBER: 34,659		
CC	REFERENCE/DOCKET NUMBER: 866PCT		
CC	TELECOMMUNICATION INFORMATION:		

	ID	RESULT	PRT;	553 AA
CC	DE	US-08-943-087-20	STANDARD;	
XX	DT	13		
XX	AC	xixxxx		
XX	xx			
CC	DE	Sequence 20, Application US/08943087		
CC	DE	Patent No. 5945511		
CC	CC	GENERAL INFORMATION:		
CC	CC	APPLICANT: Lok, Si		
CC	CC	APPLICANT: Kho, Chai		
CC	CC	APPLICANT: Jelmeberg, Anna C.		
CC	CC	APPLICANT: Adams, Robyn L.		
CC	CC	APPLICANT: Whitmore, Theodore E.		
CC	CC	TITLE OF INVENTION: CYTOKINE RECEPTOR		
CC	CC	NUMBER OF SEQUENCES: 60		
CC	CC	CORRESPONDENCE ADDRESS:		
CC	CC	ADDRESS: ZymoGenetics, Inc.		
CC	CC	STREET: 1201 Eastlake Avenue East		
CC	CC	CITY: Seattle		
CC	CC	STATE: WA		
CC	CC	COUNTRY: USA		
CC	CC	ZIP: 98102		
CC	CC	COMPUTER READABLE FORM:		
CC	CC	MEDIUM TYPE: Diskette		
CC	CC	COMPUTER: IBM Compatible		
CC	CC	OPERATING SYSTEM: DOS		
CC	CC	SOFTWARE: FASTSEQ for Windows Version 2.0		
CC	CC	CURRENT APPLICATION DATA:		
CC	CC	APPLICATION NUMBER: US/08/943,087		
CC	CC	FILING DATE:		
CC	CC	CLASSIFICATION: 536		
CC	CC	PRIOR APPLICATION DATA:		
CC	CC	APPLICATION NUMBER: 08/803,305		
CC	CC	FILING DATE: 20-FEB-1997		
CC	CC	ATTORNEY/AGENT INFORMATION:		
CC	CC	NAME: Luuu, Paul G		
CC	CC	REGISTRATION NUMBER: 32,743		

REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE 553 AA; 62533 MW; 1648042 CN;

Query Match 7.6%; YScore 243; DB 2; Length 553;
Best Local Similarity 30.3%; Pred. No. 1,31e-10;
Matches 43; Conservative 37; Mismatches 57; Indels 5; Gaps 5;

Db 18 LLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTQTPPEGLOGVRYVYVYFYTG 77
11 LVLAVGFWVLSAAGGNLKSPOKVEYDIIDNFIILMNSDESIG-NVTFSPDYQKTG 69
Db 78 QKKMLNSECNRINRTYCDLSAETS-D-YEQYAVKAIWGTCKSKMAESGRFYFLETQ 136
70 MDNNIKLSGCONITSTKCNFSSLKLNVE-EIKLIRAKENTSS-WYEVDSFTPFRAQ 127
Db 137 IGPEVALTTDEKISIVLTAP 158
128 IGPEVHLEADKAI-VIHISP 148

RESULT 14
ID US-08-943-087-22 STANDARD; PRT: 553 AA.

AC xxxxxx

Sequence 22, Application US/08943087

Sequence 22, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kho, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Robyn L.

APPLICANT: Farrah, Theodore E.

APPLICANT: Whitmore, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,087

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION NUMBER: 08/803,305

APPLICATION NUMBER: 08-FEB-1997

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE 553 AA; 62533 MW; 1648042 CN;

Query Match 7.6%; Score 243; DB 2; Length 553;
Best Local Similarity 30.3%; Pred. No. 1,31e-10;
Matches 43; Conservative 37; Mismatches 57; Indels 5; Gaps 5;

Db 18 LLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTQTPPEGLOGVRYVYVYFYTG 77
11 LVLAVGFWVLSAAGGNLKSPOKVEYDIIDNFIILMNSDESIG-NVTFSPDYQKTG 69
Db 78 QKKMLNSECNRINRTYCDLSAETS-D-YEQYAVKAIWGTCKSKMAESGRFYFLETQ 136
70 MDNNIKLSGCONITSTKCNFSSLKLNVE-EIKLIRAKENTSS-WYEVDSFTPFRAQ 127
Db 137 IGPEVALTTDEKISIVLTAP 158
128 IGPEVHLEADKAI-VIHISP 148

RESULT 15
ID US-08-943-087-30 STANDARD; PRT: 553 AA.

AC xxxxxx

Sequence 30, Application US/08943087

Sequence 30, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kho, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Robyn L.

APPLICANT: Farrah, Theodore E.

APPLICANT: Whitmore, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,087

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION NUMBER: 08/803,305

APPLICATION NUMBER: 08-FEB-1997

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

Tue Aug 22 08:32:01 2000

US-09-240-675-2.rai

Page 10

CC NAME: lunn, Paul G
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TEXT:
CC INFORMATION FOR SEQ ID NO: 30:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 553 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SEQUENCE 553 AA; 62553 MW; 1646042 CN

Query Match	7.68;	Score 243;	DB 2;	Length 553;
Best Local Similarity	30.38;	Pred. No. 1.31e-10;		
Matches	43;	Conservative	37;	Mismatches 57;
			Indels	5;
			Gaps	5;

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Db 18 LILLILAAPORAVCVSGGJPEKPNITFELSINKNVLOQWTPREGLOCVKTYTVQVQFIYG 77
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OY 11 LVLVAANGPMWLSAAAGGKNKNSPKQKVEVDITIDONEFILNRMSDSBYG-NYTFEFDYOKTG 69

Db 78 OKKWLKSECRNINRYTCDSLAESD-YEHQYAKVKAINGTRCSKAESGRYPFLEIQ 136
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 70 MDNWKISGCONITSTGNCNFSLEKLYE-EIKLRINAEKENTSS-WYEDSTPFRKAO 127

Db 137 IGPPEVALITDEKISIVLTAAP 158
    ||||| |:::|:::|:::|:::|
OY 128 IGPPEVHLEADKAI-VIHISP 148

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Search completed: Mon Aug 21 10:27:43 2000
Job time : 14 secs.

 W I L D E R N E S S
 (TM)

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MSrchLPP protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Aug 21 10:25:11 2000; MasPar time 23.63 Seconds
 Tabular output not generated. 870.350 Million cell updates/sec

Title: >US-09-240-675-2
 Description: (1-436) from US09240675.pep
 Perfect Score: 3178
 Sequence: 1 MMYVLGATTLVAVGPNV.....KSSVSDAVCEKTRPGNTSK 436

Scoring table: PAM 150
 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r64
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 48.543; Variance 89.320; scale 0.543

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	3178	100.0	557	2	A32694 Interferon alpha rece	0.00e+00
2	2949	92.8	545	2	S17112 Interferon alpha/beta	0.00e+00
3	2103	66.2	560	2	S27387 Interferon alpha rece	0.00e+00
4	1513	47.6	550	2	A45283 Interferon alpha/beta	0.00e+00
5	285	9.0	349	2	JC6311 Interferon receptor-c	6.40e-32
6	280	8.6	273	2	G01418 cytokine receptor fam	9.67e-31
7	274	8.6	325	2	A47003 Interferon gamma rece	2.35e-14
8	241	7.6	332	2	A49847 Interferon gamma rece	1.15e-13
9	183	5.8	337	2	I38500 Interferon gamma rece	2.01e-06
10	140	4.4	489	2	A31555 Interferon gamma rece	3.59e-05
11	138	4.2	575	2	A49667 Interleukin-10 recept	1.47e-04
12	122	4.0	918	2	A36337 membrane glycoprotein	8.27e-04
13	123	3.9	56	2	S41602 Interferon alpha rece	8.27e-04
14	123	3.9	26926	1	S16344 titin, cardiac muscle	8.65e-03
15	116	3.7	578	2	I56215 Interleukin-10 recept	4.48e-03
16	118	3.7	662	2	I37892 TL12 receptor compone	3.20e-03
17	119	3.7	918	2	A44257 Interleukin-6 signa	2.32e-02
18	113	3.6	6805	2	S20901 titin, rabbit (fragm	1.57e-01
19	107	3.4	817	2	A48721 titin, muscle - chick	1.57e-01
20	108	3.4	877	2	I48967 brain-specific kinase	1.57e-01
21	107	3.4	883	2	S51603 receptor-like tyrosin	1.57e-01
22	107	3.4	898	2	S47489 receptor tyrosine kin	1.57e-01
23	109	3.4	979	2	E72236 clostridium-related p	8.37e-02

24	107	3.4	981	2	S51604	receptor-like tyrosin	1.57e-01
25	107	3.4	1005	2	S49015	receptor tyrosine kin	1.57e-01
26	104	3.3	346	2	S66958	UPEI protein - yeast	3.98e-01
27	104	3.3	837	2	T03151	primase - alcelaphine	3.98e-01
28	104	3.3	917	2	I49699	glycoprotein 130 - mo	3.98e-01
29	101	3.2	132	2	S56573	hypothetical 14.6k pr	9.88e-01
30	101	3.2	215	2	I40299	variable outer membra	9.88e-01
31	103	3.2	897	1	A32555	cytokine receptor com	5.40e-01
32	101	3.2	2606	2	T03159	large tegument protei	9.88e-01
33	103	3.2	6839	2	S57242	twitclan - Caenorhabd	5.40e-01
34	100	3.1	306	2	F72287	esterase - Thermotoga	1.33e+00
35	99	3.1	356	2	S74766	hypothetical protein	1.79e+00
36	98	3.1	449	2	C69086	chitinase mutase - M	2.40e+00
37	100	3.1	466	2	S19685	dihydrolipamide dehy	1.33e+00
38	98	3.1	641	2	A71163	hypothetical protein	2.40e+00
39	98	3.1	686	2	B75061	alpha chain of format	2.40e+00
40	99	3.1	688	1	TVPPTJ	large T antigen - pol	1.79e+00
41	98	3.1	691	1	TVPPTS	large T antigen - pol	2.40e+00
42	98	3.1	695	1	TVPPTB	large T antigen - pol	2.40e+00
43	97	3.1	708	1	TVPPT4	large T antigen - rbe	3.22e+00
44	98	3.1	1013	2	I50615	receptor-type protein	2.40e+00
45	99	3.1	1897	1	TDHULK	leukocyte antigen-rel	1.79e+00

ALIGNMENTS

RESULT 1
 ENTRY A32694 #type complete
 TITLE Interferon alpha receptor precursor - human
 ORIGINISM #formal_name Homo sapiens #common_name man
 DATE 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 24-Sep-1998

ACCESSIONS
 REFERENCE A32694
 #authors Use, G.; Lutfalla, G.; Gresser, I.
 #journal Cell (1990) 60:225-234
 #title Genetic transfer of a functional human interferon alpha
 receptor into mouse cells: cloning and expression of its
 cDNA.

#cross-references MIM:90124632
 #accession A32694

#status preliminary
 #molecule_type mRNA
 #residues 1-557 #label UZE
 #cross-references GB:J03171; NID:g184645; PID:g306914

GENETICS
 #gene GDB:120078; IBC:120078
 #map_position 21q22.1-21q22.1

KEYWORDS
 SUMMARY #length 557 #molecular_weight 63525 #checksum 7035
 #keywords cytokine, receptor, transmembrane protein

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Best Local Similarity	100.0%	Pred. No.	0.00e+00						
Matches	436	Conservative	0	Mismatches	0	Indels	0	Gaps	0
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Qy	1	MMYVLGATTLVAVGPNVLSAAGGRKLPORVEVDIIDNFTLRNRNDSGAVNT	60						
Db	61	FSFDYOKTGMWIKISGONTSTKCNSSKLINVEIKIRIAEKENTSSWEVDSF	120						
Qy	61	FSFDYOKTGMWIKISGONTSTKCNSSKLINVEIKIRIAEKENTSSWEVDSF	120						
Db	121	TFPRKAOIPPEVHLAEKKAIVHISPTKSYVMALDGLSFTSLIMKSSGVEERI	180						
Qy	121	TFPRKAOIPPEVHLAEKKAIVHISPTKSYVMALDGLSFTSLIMKSSGVEERI	180						
Db	181	ENIYSRHKTYKISPEPTTYLAKKALITSMKIGVSPVCITTYENELPPENIEVSQ	240						
Qy	181	ENIYSRHKTYKISPEPTTYLAKKALITSMKIGVSPVCITTYENELPPENIEVSQ	240						
Db	241	NONYVLKMDYTYANMTFOVMHAFLKRNPGNHLKMKOIPDCENVKTTQCVFPONVK	300						

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OY 241 NONTVLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTQCVFQNTPOK 300
DB 301 GYLLRQVQASDGNNTSFWESEIKFDPTEIOAFLLPPEVINSLSDFHIYIGAPKQSGNT 360
OY 301 GYLLRQVQASDGNNTSFWESEIKFDPTEIOAFLLPPEVINSLSDFHIYIGAPKQSGNT 360
DB 361 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 420
OY 361 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 420
DB 421 FSDAVCEKTKPGNTSK 436
OY 421 FSDAVCEKTKPGNTSK 436

RESULT 2
ENTRY 2
TITLE S17112 #type complete
ORGANISM Interferon alpha/beta receptor - human
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
30-May-1997

ACCESSIONS
REFERENCE S17112
#authors Lutfalla, G.; Gardiner, X.Y.Z.; Proudhon, D.; Vleth, E.;
#submission submitted to the EMBL Data Library, July 1991
#description The structure of the human interferon alpha/beta receptor
gene.
#accession S17112
#status preliminary
#molecule_type DNA
#residues 1-545 #label LOT
#cross-references EMBL:X60459

GENETICS
#introns 26/3; 67/2; 126/1; 177/3; 225/1; 263/2; 330/1; 369/3; 420/1;
468/3
KEYWORDS cytokine receptor; transmembrane protein
SUMMARY #length 545 #molecular_weight 62169 #checksum 672
Query Match 92.8%; Score 2949; DB 2; Length 545;
Best Local Similarity 97.0%; Pred. No. 0.00e+00;
Matches 423; Conservative 1; Mismatches 0; Indels 12; Gaps 2;

DB 1 MNTVLLGATTLVLAAPVWLSAAGKKNLSPQKVEVDIIDDNFILRMNSDESIGNVT 60
OY 1 MNTVLLGATTLVLAAPVWLSAAGKKNLSPQKVEVDIIDDNFILRMNSDESIGNVT 60
DB 61 FSPDYOKTGMNWKISGCONITSTKCNFSSKLNTVEIKLRIRAKEMTSWYEVSF 120
OY 61 FSPDYOKTGMNWKISGCONITSTKCNFSSKLNTVEIKLRIRAKEMTSWYEVSF 120
DB 121 TPEKAOIGPPEVHLEADAIVHISPGTDSVMALDGLSFYSLLIMKNSGVEERI 180
OY 121 TPEKAOIGPPEVHLEADAIVHISPGTDSVMALDGLSFYSLLIMKNSGVEERI 180
DB 181 ENIYSRRIKIKSPETTYCLKVAALITSMKIGVSPVHCIKTVENELPPENIEVSQ 240
OY 181 ENIYSRRIKIKSPETTYCLKVAALITSMKIGVSPVHCIKTVENELPPENIEVSQ 240
DB 181 ENIYSRRIKIKSPETTYCLKVAALITSMKIGVSPVHCIKTVENELPPENIEVSQ 240
OY 181 ENIYSRRIKIKSPETTYCLKVAALITSMKIGVSPVHCIKTVENELPPENIEVSQ 240
DB 241 NONTVLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTQCVFQNTPOK 300
OY 241 NONTVLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTQCVFQNTPOK 300
DB 301 GYLLRQVQASDGNNTSFWESEIKFDPTEIOAFLLPPEVINSLSDFHIYIGAPKQSGNT 360
OY 301 GYLLRQVQASDGNNTSFWESEIKFDPTEIOAFLLPPEVINSLSDFHIYIGAPKQSGNT 360
DB 349 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 408
OY 349 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 408
DB 361 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 420
OY 361 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 420
DB 409 FSDAVCEKTKPGNTSK 424

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OY 421 FSDAVCEKTKPGNTSK 436

RESULT 3
ENTRY 3
TITLE S27387 #type complete
ORGANISM Interferon alpha receptor type 1 precursor - bovine
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Nov-1998

ACCESSIONS
REFERENCE S27387
#authors Mouchel-Vieilh, E.; Mogensen, K.E.; Uze, G.
#journal FEBS Lett. (1992) 313:255-259
#title Specific antiviral activities of the human alpha interferons
are determined at the level of receptor (IFNAR) structure.
#cross-references MIMD:93076908
#accession S27387
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-560 #label MOU
#cross-references EMBL:X68443; NID:9431; PID:9432
#experimental_source MDBK cells

REFERENCE
#authors Lim, J.K.; Langer, J.A.
#journal Biochim. Biophys. Acta (1993) 1173:314-319
#title Cloning and characterization of a bovine alpha interferon
receptor.
#cross-references MIMD:93305725
#accession S33770
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-421, 423-560 #label LIM
#cross-references EMBL:L06320; NID:9163187; PID:9163188
#experimental_source lung

KEYWORDS antiviral; cytokine receptor; transmembrane protein
FEATURE
1-24 #domain signal sequence #status predicted #label sig\
25-560 #product interferon alpha receptor type 1 #status
predicted #label MAT
SUMMARY #length 560 #molecular_weight 6818 #checksum 4991
Query Match 66.2%; Score 2103; DB 2; Length 560;
Best Local Similarity 65.2%; Pred. No. 0.00e+00;
Matches 287; Conservative 78; Mismatches 67; Indels 8; Gaps 8;

DB 1 MNTVLLGATTLVLAAPVWLSAAGKKNLSPQKVEVDIIDDNFILRMNSDESIGNVT 60
OY 1 MNTVLLGATTLVLAAPVWLSAAGKKNLSPQKVEVDIIDDNFILRMNSDESIGNVT 60
DB 59 SADYOLIGTDMNWKISGCOHITSTKCNFSSVELENYFERIKIRAEQNTSTYVEVP 118
OY 59 SADYOLIGTDMNWKISGCOHITSTKCNFSSVELENYFERIKIRAEQNTSTYVEVP 118
DB 62 SPDYOKTGMNWKISGCONITSTKCNFSSKLNTVEIKLRIRAKEMTSWYEVSF 119
OY 62 SPDYOKTGMNWKISGCONITSTKCNFSSKLNTVEIKLRIRAKEMTSWYEVSF 119
DB 119 FVPELENOIGPPEVHLEADAIVHISPGTDSVMALDGLSFYSLLIMKNSGVEERI 178
OY 119 FVPELENOIGPPEVHLEADAIVHISPGTDSVMALDGLSFYSLLIMKNSGVEERI 178
DB 120 FTFPRKAOIGPPEVHLEADAIVHISPGTDSVMALDGLSFYSLLIMKNSGVEERI 178
OY 120 FTFPRKAOIGPPEVHLEADAIVHISPGTDSVMALDGLSFYSLLIMKNSGVEERI 178
DB 179 KETFTVPEKIVTSLSEIYCYLKVAELLOS-RVCCISPVYCINTTEHKPSPENIOI 237
OY 179 KETFTVPEKIVTSLSEIYCYLKVAELLOS-RVCCISPVYCINTTEHKPSPENIOI 237
DB 179 KETFTVPEKIVTSLSEIYCYLKVAELLOS-RVCCISPVYCINTTEHKPSPENIOI 237
OY 179 KETFTVPEKIVTSLSEIYCYLKVAELLOS-RVCCISPVYCINTTEHKPSPENIOI 237
DB 238 NADNOIYVLKMDPYENAPYAFQAOMLAFKRIKGNHSDMKOIPNCENTSTHCVPEPV 297
OY 238 NADNOIYVLKMDPYENAPYAFQAOMLAFKRIKGNHSDMKOIPNCENTSTHCVPEPV 297
DB 238 SYONONTVLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTQCVFQNTPOK 297
OY 238 SYONONTVLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTQCVFQNTPOK 297
DB 298 SSGIGIYVRASNGSGISFWESEIKFDPTEIOAFLLPPEVINSLSDFHIYIGAPKQSG 357
OY 298 SSGIGIYVRASNGSGISFWESEIKFDPTEIOAFLLPPEVINSLSDFHIYIGAPKQSG 357
DB 298 FOKGIYLLRQVQASDGNNTSFWESEIKFDPTEIOAFLLPPEVINSLSDFHIYIGAPKQSG 356
OY 298 FOKGIYLLRQVQASDGNNTSFWESEIKFDPTEIOAFLLPPEVINSLSDFHIYIGAPKQSG 356
DB 358 ENMSVMOIPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 417
OY 358 ENMSVMOIPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 417
DB 357 GNTPVIODPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 416
OY 357 GNTPVIODPLIYEIIFEMENSNARKIIEKKTDTVTNPKPLPYCYKARAHNTDEKLNSV 416

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Db 418 KSSFSPTVCEKTRKPGNTSK 437
 OY 417 KSSVFSDAVCEKTRKPGNTSK 436

RESULT 4
 ENTRY 445283 #type complete
 TITLE Interferon alpha/beta receptor - mouse
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 25-Mar-1993 #sequence revision 18-Nov-1994 #text change

ACCESSIONS
 A45283; 148423; 148424; 148425; 148426; 148427; 148428;
 148429

REFERENCE
 #authors Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4774-4778
 #title Behavior of a cloned murine interferon alpha/beta receptor expressed in homospesific or heterospesific background.
 #cross-references MUID:92262522
 #accession A45283
 #status preliminary
 #molecule_type mRNA
 #residues 1-590 #label UZE
 #cross-references GB:M89641; NID:9194111; PID:9194112
 #note sequence extracted from NCBI backbone (NCBIN:102354, NCBIPI:102357)

REFERENCE
 #authors Lutfalla, G.; Uze, G.
 #journal Gene (1994) 148:343-346
 #title Structure of the murine interferon alpha/beta receptor-encoding gene: high-frequency rearrangements in the interferon-resistant L1210 cell line.
 #cross-references MUID:95047447
 #accession 148423
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 118-125 #label RES
 #cross-references EMBL:U06237; NID:9497103; PID:9755810
 #accession 148424
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 127-224 #label RE2
 #cross-references EMBL:U06238; NID:9497104; PID:9755811
 #accession 148425
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 243-264 #label RE3
 #cross-references EMBL:U06239; NID:9497106; PID:9755812
 #accession 148426
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 265-375 #label RE4
 #cross-references EMBL:U06240; NID:9497108; PID:9755813
 #accession 148427
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 397-424 #label RE5
 #cross-references EMBL:U06241; NID:9497110; PID:9755812
 #accession 148428
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 426-445 #label RE6
 #cross-references EMBL:U06242; NID:9497112; PID:9755813
 #accession 148429
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 473-590 #label RE7
 #cross-references EMBL:U06244; NID:9497114; PID:9755815

GENETICS
 #gene IFNAR
 #introns 177/3; 331/1

KEYWORDS
 SUMMARY cytokine receptor; transmembrane protein
 #length 590 #molecular weight 65776 #checksum 833

Query Match 47.6%; Score 1513; DB 2; Length 590;
 Best Local Similarity 50.1%; Pred. No. 0.00e+00;
 Matches 219; Conservative 93; Mismatches 109; Indels 16; Gaps 14;

Db 1 MAAVAGALAVLVGAPVLPVSAAGENIKRPNIDVYIIDNTLKSSHGSGSYTF 60
 OY 2 MVLIGATTVLVVANGPVLSAAGKRLKSPQAVYIIDNFKLRNRSDESGNTVF 61
 Db 61 SAETRTDANKLVKPECHTTTKCEFLDTNWTYIKTFORVRAEGNSSTSNWNEVDF 120
 OY 62 SEDYKTDMDWMKIKSGCNITSPKCNSSILKLVYEEKIKRIRAKEN-TSSWYEVDSF 120
 Db 121 IPFYAHMSPPVRLKADKALVHISPPGDKNNMALEKSPSTIRIRKSSSDKTI 180
 OY 121 TPFRAQIGPPEVHLKADKALVHISGTDVSMALDGLSFYSLLIMKNSGVEERI 180
 Db 181 NSTYVERKIPPELTCTEVKAIHPKLSHNSYVQISTVYANKMPYGNLOYDAQ 240
 OY 181 ENIYSRHKIYKLSPEITTCVAKKALTSKIGVSPHCITTYENLPPPENIEVSQ 240
 Db 241 GKSIVLKWYIASADVLFRQMLPGYSKSSGSHDKKPIPTCANYOTHCVSQDTYV 300
 OY 241 MONYVLKWDY-TYANMTPYOVMALHFLKRNPNHLYFKKQIPDCENVTQCVFPON-VF 298
 Db 301 TGTFFLAVQASGEGNHTSFNSE-KFIDSQHILPPPVITVYAMSGLLYVNC-QDS 356
 OY 299 OKGIYLLRVQASDGNSTSFNSEIKF-DTEIQALFLPVFVIRISDSFHYIGAPKOSG 357
 Db 357 T-C-D-GLVVEIIFMENTSNF-KISMEKGPETTLNLOPLVYVQOAVH-LFRALIN 409
 OY 358 NTPVYQDIPPLIYEIIFMENTSNNAEKITEK-TDVTYNALPLVYCYKAAAHMDEKLN 416
 Db 410 KTSNFESEKLCERTKPGS 426
 OY 417 KSSVFSDAVCEKTRKPGN 433

RESULT 5
 ENTRY JC6311 #type complete
 TITLE Interferon receptor-class II cytokine receptor - mouse
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 16-Jul-1999 #sequence revision 16-Jul-1999 #text change

ACCESSIONS
 JC6311
 #authors gibbs, V.C.; Pennica, D.
 #journal Gene (1997) 186:97-101
 #title CRF 4: Isolation of cDNA clones encoding the human and mouse proteins.
 #accession JC6311
 #status preliminary
 #molecule_type mRNA
 #residues 1-349 #label GIB
 #cross-references GB:U53696
 #length 349 #molecular weight 39766 #checksum 3090

SUMMARY
 Query Match 9.0%; Score 285; DB 2; Length 349;
 Best Local Similarity 28.5%; Pred. No. 6.60e-33;
 Matches 59; Conservative 60; Mismatches 73; Indels 15; Gaps 14;

Db 23 PPEVIRANSVNFKNLOVEVAFPTNLTFTAYEST-R-S-FO-DHCKRTASTQCDPSH 78
 OY 32 SPOKVEVDIIDNFKLRNRSDESGVNTFEDYKTDMDWMKIKSGCNITSPKCNSS 91
 Db 79 LS-K-YGDYTVRAVRLADESEVNV-TTPVEDTIIIGPEMGIESTASLEKRFAPQ 135
 OY 92 LKLVYETIKRIRAE-KENSSWYEVDSPTPFRAQIGPPEVHLKADKALVHIS-PG 149
 Db 136 IENPEWTLLKNIDSNVAVQYKNGNTEKRFQVSPDSSEVLNLEPMTYTCIOVGFL 195

OY 150 T-KDSVWALDGL--SFTYSLLIMKNSGVEERENIENISRHKIYKLSPTTYCLAKVAAAL 206
Db 196 LDNRKGESEPI-CEITG-NDERTPS 220
OY 207 LTSMKIGVYS-PVHCITKTYENELPP 232

RESULT 6
ENTRY G01418 #type complete
TITLE cytokine receptor family II, member 4 - human
ORANISM #formal_name Homo sapiens #common_name man
DATE 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998

ACCESSIONS G01418
REFERENCE G06935
#authors Lutfalla, G.
#submission submitted to the EMBL Data Library, April 1994
#accession G01418
#status preliminary; translated from GR/EMBL/DBJ
#molecule_type DNA
#residues 1-273 #label LUT
#cross-references EMBL:U08988; NID:9571295; PID:9571296

GENETICS
#gene GDB:CRFB4; CRF2-4
#map_position 21q22.1-21q22.2
#introns 17/1; 58/2; 111/1; 166/3; 216/1
SUMMARY #length 273 #molecular_weight 31546 #checksum 144

Query Match 8.8%; Score 280; DB 2; Length 273;
Best Local Similarity 30.6%; Pred. No. 6.40e-32;
Matches 63; Conservative 55; Mismatches 74; Indels 14; Gaps 10;

Db 23 PPNVNMNSVNFNIOWESPAPAKGNLTFTAOY---LSYRIFOKCMNTLTEDFSS 78
OY 32 SPQKVEVDIIDDIFILRMNSDESVCNVTFSEYQKTGMDNMKLSGCONITSTKCNFS 91
Db 79 LS-K-YGDHTLRARAEADSHDWNI-TCFVDDITIGPGQVEVLADSLMRPLAK 135
OY 92 LKINVEEIKLRIRAE-KENTSSMYEVDSTPPRKAQIGPEVHLAEADKAIYIH-ISP 149

Db 136 IENEYETWTKNKNYNSMTYVVOYKNGTDEKFOITPOYDEVLARNLEPMTTCVOYRGFL 195
OY 150 T-KDSVWALDGL--SFTYSLLIMKNSGVEERENIENISRHKIYKLSPTTYCLAKVAAAL 206
Db 196 LDNRKGESEPI-CEITG-NDERTPS 220
OY 207 LTSMKIGVYS-PVHCITKTYENELPP 232

RESULT 7
ENTRY A47003 #type complete
TITLE cytokine receptor family class II protein CRF2-4 precursor
ORANISM human
DATE 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997

ACCESSIONS A47003
REFERENCE A47003
#authors Lutfalla, G.; Gardiner, K.; Uze, G.
#journal Genomics (1993) 16:366-373
#title A new member of the cytokine receptor gene family maps on chromosome 21 at less than 35 kb from IFNAR.
#cross-references MUID:93300510
#accession A47003
#status preliminary;
#molecule_type mRNA
#residues 1-325 #label LUT
#cross-references GB:Z1727; NID:9393378; PID:9393379

GENETICS
#map_position 21q
KEYWORDS transmembrane protein
SUMMARY #length 325 #molecular_weight 37011 #checksum 9050

Query Match 8.6%; Score 274; DB 2; Length 325;
Best Local Similarity 30.1%; Pred. No. 9.67e-31;
Matches 62; Conservative 55; Mismatches 75; Indels 14; Gaps 10;

Db 23 PPNVNMNSVNFNIOWESPAPAKGNLTFTAOY---LSYRIFOKCMNTLTEDFSS 78
OY 32 SPQKVEVDIIDDIFILRMNSDESVCNVTFSEYQKTGMDNMKLSGCONITSTKCNFS 91
Db 79 LS-K-YGDHTLRARAEADSHDWNI-TCFVDDITIGPGQVEVLADSLMRPLAK 135
OY 92 LKINVEEIKLRIRAE-KENTSSMYEVDSTPPRKAQIGPEVHLAEADKAIYIH-ISP 149

Db 136 IENEYETWTKNKNYNSMTYVVOYKNGTDEKFOITPOYDEVLARNLEPMTTCVOYRGFL 195
OY 150 T-KDSVWALDGL--SFTYSLLIMKNSGVEERENIENISRHKIYKLSPTTYCLAKVAAAL 206
Db 196 LDNRKGESEPI-CEITG-NDERTPS 220
OY 207 LTSMKIGVYS-PVHCITKTYENELPP 232

RESULT 8
ENTRY A49947 #type complete
TITLE interferon gamma receptor beta subunit - mouse
ALTERNATE_NAMES IFN-gamma R beta chain; IFN-gamma R specific cofactor; type I transmembrane protein
ORANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999

ACCESSIONS A49947
REFERENCE A49947
#authors Hemmi, S.; Bohnl, R.; Stark, G.; Di Marco, F.; Agnet, M.
#journal Cell (1994) 76:803-810
#title A novel member of the interferon receptor family complements functionality of the murine interferon gamma receptor in human cells.
#cross-references MUID:94170381
#accession A49947
#status preliminary;
#molecule_type mRNA
#residues 1-332 #label HEM
#cross-references GB:S69336; NID:9545841; PID:9545842
#experimental_source early B-cell line Y16
#note sequence extracted from NCBI backbone (NCBI:145654, NCBI:145656)

KEYWORDS cytokine receptor
SUMMARY #length 332 #molecular_weight 37471 #checksum 3196

Query Match 7.6%; Score 241; DB 2; Length 332;
Best Local Similarity 27.8%; Pred. No. 2.35e-24;
Matches 60; Conservative 56; Mismatches 80; Indels 20; Gaps 16;

Db 10 SLLIGLGA-AASSPDSQSALAPINRLHLNDDOILTWEPSSNDPRPVYGVESF 68
OY 10 TLVLAVGVWVLSAAGCNILKSPQKVEVDIIDDIFILRMNSDSVSG-N-VTFSDFOK 67
Db 69 ID-GSMHRLBNCDDIETKCDLGGGRKLFPPHVFVFLVYRKRKGNLSKRWLEPF 127
OY 68 TQMDNMWIKL--SGCONITSTKCNFS--KLNYER-IR-LIRREKEN-TSSMYEVSF 120
Db 128 QHYEVNTGPPRNISVITGKSLVHSPF-D-V--FHGATFOYLVHYEKSSTQEO 182
OY 121 TPFRAAOIGP-EVHLAEADKAIYIHISPGTDSVWALDGLSFTYSLLIMKNSGVEER 179
Db 183 VEGPKSNSIYGNLKPVRVYCLQTEAQLILKNKI 218
OY 180 IENISRHKI-Y-KLSPTTYCLAKVAAAL-LTSMKI 212

RESULT 9
ENTRY I38500 #type complete
TITLE interferon gamma receptor accessory factor-1 precursor

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ORGANISM      human
DATE          16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
ACCESSIONS    138500; 138501
REFERENCE      A49946
AUTHORS       Sob, J.; Donnelly, R.J.; Kolenko, S.; Maritano, T.M.; Cook,
               J.R.; Wang, N.; Emanuel, S.L.; Schwartz, B.P.; Miki, T.;
               Pestka, S.
#journal      Cell (1994) 76:793-802
#title       Identification and sequence of an accessory factor required
               for activation of the human interferon gamma receptor.
#cross-references MUID:94170380
#accession    138500
#molecule_type mRNA
#residues     1-337 ##label RES
#cross-references EMBL:U05875; NID:9463549; PID:9463550
#experimental_source clone pSK1
#accession    138501
#molecule_type mRNA
#residues     1-63, Q; 65-337 ##label RE2
#cross-references EMBL:U05877; NID:9463551; PID:9463552
#experimental_source clone pUS3

GENETICS      #map_position 21
KEYWORDS      cytokine receptor
SUMMARY       #length 337 #molecular_weight 37834 #checksum 749

Query Match          5.8%; Score 183; DB 2; Length 337;
Best Local Similarity 23.7%; Pred. No. 1,156-13;
Matches 56; Conservative 60; Mismatches 93; Indels 25; Gaps 22;

Db 1 MRPILL-NSLLLLGVFAAAAAPPDPLSQLPAPQPKIRLYNAEVLSEPVALSSTR 59
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 1 MMVLLGATTLVAVAGPWLISAAGG-KNLKSPQKEVDIIDNDILMNR-S-DESG 57
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 60 PYYVQVQRYTDSKFTADINSGVNCITITTECDFTAASAGCPMDPNTLRRL 119
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 58 NVTFS--FDYQKTG-MDMNR-LS-GCONITSTKCNFSILKINV-Y--E-EIKLRIRAK 108
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 120 GALHSAMVMPFQHYRNVTPGPPENIEVTPGSGSLIRFSSPF-D-IA-DSTAFQCY 176
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 109 EMT-SSWYEVDSFTPRKQIGPPE-VHLEADKALVHIISGTDKDSVMALDGLSTYS 166
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 177 VHYWKG-GIQQ-VKGPFRNSISIDMLKPSRYCLOVQAOQL--WNKSNIRFVGH 228
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 167 LLIWNSGVEERIEIYSRHKI-Y-KLSPETTYGLKVAALLTSM-KIGVSPVH 219
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
ENTRY      A31555 #type complete
TITLE      Interferon gamma receptor precursor - human
ORGANISM   Homo sapiens #common_name man
DATE       28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
ACCESSIONS A31555
REFERENCE   Aguet, M.; Dembic, Z.; Meriin, G.
#journal    Cell (1988) 55:273-280
#title      Molecular cloning and expression of the human
               interferon gamma receptor.
#cross-references MUID:89003065
#accession   A31555
#molecule_type mRNA
#residues    1-489 ##label AGU
#cross-references GB:J03143; NID:9184650; PIDN:AAA52731.1; PID:9306915

GENETICS    #gene      GDB:IFNGR1; IFNGR
               #cross-references GDB:120688; OMIM:107470
#map_position 6q23-6q24
CLASSIFICATION #superfamily interferon gamma receptor
KEYWORDS      cytokine receptor; transmembrane protein
SUMMARY       #length 489 #molecular_weight 54404 #checksum 3842

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Query Match          4.4%; Score 140; DB 2; Length 489;
Best Local Similarity 25.3%; Pred. No. 2,016-06;
Matches 37; Conservative 38; Mismatches 68; Indels 3; Gaps 3;

Db 1 MALLFLPIVMGVSAEKNTADLGPSSVPTPRNVTIESNNMPYIWEIQIPQPV-F 59
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 3 VVLLGATTLVAVAGPWLISAAGG-GGKNLKSPQKEVDIIDDFILRMNSDSVGNVTF 61
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 60 TVEKRVKVNSEIMADINISHHYCNISHPVDDPNSILWVRKARVQKESAYAKSEEF 119
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 62 SPDYQKTGMDNWKILSGCONITSTKCNFSLKLVTEIKLRIRAKENTSSWYE-VDSF 120
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 120 AVCRDGIKGPPLDIRKEKQIMDI 145
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 121 TTPRKQIGPPEVHLEADKALVTHI 146
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
ENTRY      A49667 #type complete
TITLE      Interleukin-10 receptor - mouse
ORGANISM   Mus musculus #common_name house mouse
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS A49667
REFERENCE   A49667
AUTHORS     Ho, A.S.; Lau, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore,
               K.W.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1993) 90:11267-11271
#title      A receptor for Interleukin 10 is related to interferon
               receptors.
#cross-references MUID:94068585
#accession   A49667
#status      preliminary; translated from GB/EMBL/DBD
#molecule_type mRNA
#residues     1-575 ##label RES
#cross-references GB:L12120; NID:9437615; PID:9437616

GENETICS      #gene      cytokine receptor
KEYWORDS      cytokine receptor
SUMMARY       #length 575 #molecular_weight 64247 #checksum 311

Query Match          4.2%; Score 132; DB 2; Length 575;
Best Local Similarity 20.5%; Pred. No. 3,596-05;
Matches 33; Conservative 46; Mismatches 65; Indels 15; Gaps 13;

Db 69 WNDIHCKRAQLSCDLITFTLDLHRSYGYARARAVDANSQYSMTTETRPYVD-EVI 127
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 277 WKQIDPCENVKKTQC-V--FPQNVFOKGI-YLLRVQASDGNNTSFSE-EIKFDEIQAF 331
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 128 LVVDSVTLKAMGCIYGTIHPRPY-TTPAGDEYGVFDLAVYKISIRKFEELNATKR 186
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 332 LAPPVFNISLSDSHIYIGAPKQGNTPVODYPLTY-ET-IFENNTSN-AERRITTEK 388
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 187 VQOETFTLVPIGVKRFCKVLP-R-LESIRNKA-WSEECQ 225
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 389 TDVTVPNLK-PLTV--YCYKARAHMDKLNKSSVFSQAVC 426
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 12
ENTRY      A36337 #type complete
TITLE      membrane glycoprotein gp130 precursor - human
ORGANISM   Homo sapiens #common_name man
DATE       12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change
ACCESSIONS A36337
REFERENCE   A36337
AUTHORS     Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.;
               Kishimoto, T.
#journal    Cell (1990) 63:1149-1157
#title      Molecular cloning and expression of an IL-6 signal
               transducer, gp130.
#cross-references MUID:91084844

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#accession A36337
#status preliminary
#molecule_type mRNA
#residues 1-918 #label H1B
#cross-references GB:M57230; NID:g186353; PID:g186354
GENETICS
#gene GDB:1165T: GP130
#map_position 5q11-5q11
#map_position 5q11-5q11
#molecule_type mRNA
#residues 1-918 #label H1B
#cross-references GB:M57230; NID:g186353; PID:g186354
SUMMARY
#length 918 #molecular_weight 103522 #checksum 2664
Query Match 4.0% Score 128; DB 2; Length 918;
Best Local Similarity 22.9%; Pred. No. 1.47e-04;
Matches 19; Conservative: 25; Mismatches 36; Indels 3; Gaps 3;

Db 231 INSELSIIKLTWNTNSIKSVILIKYNIQRTDASTWQIIP-EDTASRSSFTYQDL 289
Oy 36 VEDDIIDNFIIR-NNSDESVGNTSFDTQKGMNWKLSGCONITSTKCFSSILKL 94
Db 290 KPTEYVRIKCKEDKGYMSD 312
Oy 95 NYEEIKIRIRAKERTSS-WYE 116

RESULT 13
ENTRY S41602 #type fragments
TITLE Interferon alpha receptor 2 - human (fragments)
ORANISM #formal name: Homo sapiens #common name: man
DATE 25-Dec-1994 #sequence_revision 01-Dec-1995 #text_change
30-May-1997
ACCESSIONS S41601
REFERENCE S41602
#authors Abramovich, C.; Ratovitski, E.; Lundgren, E.; Revel, M.
#journal FEBS Lett. (1994) 338:295-300.
#title Identification of mRNAs encoding two different soluble forms
of the human interferon alpha receptor.
#cross-references MUID:9413943
#accession S41602
#molecule_type mRNA
#residues 1-56 #label ABR
KEYWORDS cytokine receptor
SUMMARY #length 56 #checksum 845
Query Match 3.9% Score 123; DB 2; Length 56;
Best Local Similarity 69.2%; Pred. No. 8.27e-04;
Matches 18; Conservative: 1; Mismatches 7; Indels 0; Gaps 0;

Db 1 PLTVYCVKARHTMDESDAVCERFSE 26
Oy 398 PLTVYCVKARHTMDEKLNKSSVFSD 423

RESULT 14
ENTRY 138344 #type complete
TITLE titin, cardiac muscle - human
ALTERNATE_NAMES connectin
CONTAINS serine/threonine-specific protein kinase (EC 2.7.1.1)
ORANISM #formal name: Homo sapiens #common name: man
DATE 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
16-Jul-1999
ACCESSIONS 138344; 138345; S20898; S20899; S63665; S37393
REFERENCE A57430
#authors Labelt, S.; Kolmerer, B.
#journal Science (1995) 270:293-296
#title titins: giant proteins in charge of muscle ultrastructure and
elasticity.
#cross-references MUID:96026330
#accession 138344
#status nucleic acid sequence not shown; translation not shown;
#molecule_type mRNA translated from GB/EMBL/DBJ
#residues 1-26926 #label LAB1

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#cross-references EMBL:X90568; NID:g1017424; PID:g1017425
REFERENCE 138345
#authors Musco, G.; Tzatzalos, C.; Schuck, P.; Pastore, A.
#journal Biochemistry (1995) 34:553-561
#title Dissecting titin into its structural motifs: identification
of an alpha-helix motif near the titin N-terminus.
#cross-references MUID:95119041
#accession 138345
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1977-2014 #label MUS
#cross-references EMBL:X83270; NID:g602579; PIDN:CAA58243.1;
PID:g602580
#note conformation and properties are reported for a synthetic
peptide corresponding to the translated fragment shown

REFERENCE S20897
#authors Labelt, S.; Gaute, M.; Lakey, A.; Trinick, J.
#journal EMBO J. (1992) 11:1711-1716
#title Towards a molecular understanding of titin.
#cross-references MUID:92258380
#accession S20898
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 13597-14200; 'I', 14202-14696 #label LAB2
#cross-references EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
#accession S20899
#status nucleic acid sequence not shown; translation not shown
#molecule_type mRNA
#residues 16330-16382; 'S', 16384-16756; 'F', 16758-16860 #label LAB3
#cross-references EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191
#accession S20899
#status nucleic acid sequence not shown; translation not shown
#molecule_type mRNA
#residues 'P', 22278-22431; 'R', 22433-22448; 'G', 22450-22453; 'Q',
22455-22480; 'TR', 22483-22669; 'N', 22671-22696; 'SA',
22699-23323; 'L', 23325-25376 #label LAB4
#cross-references EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
REFERENCE S63665
#authors Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.;
Labelt, S.
#journal J. Mol. Biol. (1996) 256:556-563
#title Genomic organization of M line titin and its tissue-specific
expression in two distinct isoforms.
#cross-references MUID:96177761
#accession S63665
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 26729-26825 #label KOL
#cross-references EMBL:X92412; NID:g1236761
REFERENCE S37393
#authors Gaute, M.; Leonard, K.; Labelt, S.
#journal EMBO J. (1993) 12:3827-3834
#title Phosphorylation of KSP motifs in the C-terminal region of
titin in differentiating myoblasts.
#cross-references MUID:94008990
#accession S37393
#molecule_type mRNA
#residues 26831-26926 #label GAV
REFERENCE A66736
#authors Improtas, S.; Politou, A.S.; Pastore, A.
#submission submitted to the Brookhaven Protein Data Bank, February 1996
#cross-references PDB:1ITR
#contents annotation; conformation by (1)H-NMR, residues 5253-5341
REFERENCE A66201
#authors Pihl, M.; Pastore, A.
#submission submitted to the Brookhaven Protein Data Bank, August 1996
#cross-references PDB:1NCT
#contents annotation; conformation by (1)H-NMR, residues 'S',
26059-26155
GENETICS
#gene GDB:TTN
#cross-references GDB:127867; OMIM:188840
#map_position 2q31-2q32

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100

[illegible]

94	6	1.4	102 14	036140	HEPATITIS DELTA ANTIGE	1.96e+02	167	181 14	090109	LARGE T ANTIGEN (FRAG	1.96e+02
95	6	1.4	102 14	036103	HEPATITIS DELTA ANTIGE	1.96e+02	168	181 10	004147	CYCLOC PHOSPHODIESTRA	1.96e+02
96	6	1.4	102 14	036086	HEPATITIS DELTA ANTIGE	1.96e+02	169	181 6	P79389	ELAFIN FAMILY MEMBER P	1.96e+02
97	6	1.4	102 14	036062	HEPATITIS DELTA ANTIGE	1.96e+02	170	181 6	011356	SIMILAR TO VARIOLA N3L	1.96e+02
98	6	1.4	102 14	036121	HEPATITIS DELTA ANTIGE	1.96e+02	171	181 14	090124	T-ANTIGEN (FRAGMENT)	1.96e+02
99	6	1.4	102 14	036128	HEPATITIS DELTA ANTIGE	1.96e+02	172	182 2	052944	PLASMID PLS32 DNA FOR	1.96e+02
100	6	1.4	102 14	036152	HEPATITIS DELTA ANTIGE	1.96e+02	173	182 13	09W656	GLUTAMATE DECARBOXYLAS	1.96e+02
101	6	1.4	102 14	036122	HEPATITIS DELTA ANTIGE	1.96e+02	174	182 2	053569	PUTATIVE	1.96e+02
102	6	1.4	102 14	036131	HEPATITIS DELTA ANTIGE	1.96e+02	175	183 2	045054	PUTATIVE LIPOPROTEIN.	1.96e+02
103	6	1.4	102 14	036091	HEPATITIS DELTA ANTIGE	1.96e+02	176	184 1	09YCV0	HYPOHETICAL 21.3 KD P	1.96e+02
104	6	1.4	102 14	036088	HEPATITIS DELTA ANTIGE	1.96e+02	177	184 2	050894	184A LONG HYPOHETICAL	1.96e+02
105	6	1.4	102 14	036081	HEPATITIS DELTA ANTIGE	1.96e+02	178	184 1	050853	CONSERVED HYPOHETICAL	1.96e+02
106	6	1.4	102 14	036116	HEPATITIS DELTA ANTIGE	1.96e+02	179	185 2	053806	OUTER MEMBRANE PROTEIN	1.96e+02
107	6	1.4	102 14	036115	HEPATITIS DELTA ANTIGE	1.96e+02	180	185 2	018232	HYPOHETICAL 20.1 KD P	1.96e+02
108	6	1.4	102 14	036115	HEPATITIS DELTA ANTIGE	1.96e+02	181	186 5	056745	C2F1.3 PROTEIN.	1.96e+02
109	6	1.4	102 14	036101	HEPATITIS DELTA ANTIGE	1.96e+02	182	186 2	056745	DNA (FRAGMENT)	1.96e+02
110	6	1.4	102 14	036109	HEPATITIS DELTA ANTIGE	1.96e+02	183	187 3	007091	REGULATOR. PROTEIN.	1.96e+02
111	6	1.4	102 14	036085	HEPATITIS DELTA ANTIGE	1.96e+02	184	187 1	028824	TRANSCRIPTIONAL REGULA	1.96e+02
112	6	1.4	102 14	036094	HEPATITIS DELTA ANTIGE	1.96e+02	185	189 2	0928K3	BIOPOLYMER TRANSPORT P	1.96e+02
113	6	1.4	102 14	036158	HEPATITIS DELTA ANTIGE	1.96e+02	186	190 10	023413	HYPOHETICAL PROTEIN.	1.96e+02
114	6	1.4	105 1	03YFX2	105AA LONG HYPOHETICA	1.96e+02	187	191 6	029124	VIA-2 (FRAGMENT)	1.96e+02
115	6	1.4	105 5	03YXV6	F53F1.4 PROTEIN.	1.96e+02	188	191 2	054192	PUTATIVE TRANSCRIPTION	1.96e+02
116	6	1.4	108 1	03YGO0	108AA LONG HYPOHETICA	1.96e+02	189	191 1	P95300	PUTATIVE TRANSCRIPTION	1.96e+02
117	6	1.4	110 4	09YXV6	HYPOHETICAL 13.0 KD P	1.96e+02	190	192 2	066677	NIFH, GLNDA, GLNBB, AN	1.96e+02
118	6	1.4	111 9	092X37	GP41.	1.96e+02	191	192 2	064334	PEPTIDYL-TRNA HYDROLAS	1.96e+02
119	6	1.4	112 4	09YX3	CCL27 CHEMOKINE.	1.96e+02	192	194 10	09XFS2	GP20.	1.96e+02
120	6	1.4	114 1	09YX2	114AA LONG HYPOHETICA	1.96e+02	193	194 2	09ZES1	APETAL3 HOMOLOG RBP3	1.96e+02
121	6	1.4	115 2	09X107	50S RIBOSOMAL PROTEIN	1.96e+02	194	194 2	066404	ANTHRANILATE SYNTHASE	1.96e+02
122	6	1.4	115 6	092646	NONE.	1.96e+02	195	194 2	027791	HYPOHETICAL 23.4 KD P	1.96e+02
123	6	1.4	116 10	022485	SODIUM/POTASSIUM ATPAS	1.96e+02	196	195 5	002616	SUPEROXIDE DISMUTASE (1.96e+02
124	6	1.4	116 10	022485	LIPID TRANSFER PROTEIN	1.96e+02	197	195 14	P87885	DELTA ANTIGEN.	1.96e+02
125	6	1.4	119 10	040810	S-BNASE (FRAGMENT)	1.96e+02	198	195 14	081834	DELTA ANTIGEN.	1.96e+02
126	6	1.4	121 2	048305	DNA ORF1-ORF5.	1.96e+02	199	196 4	093062	DELTA ANTIGEN.	1.96e+02
127	6	1.4	122 2	092749	CTF16 HYPOHETICAL PRO	1.96e+02	200	197 14	081847	WS-1/TYPER4.	1.96e+02
128	6	1.4	123 6	095277	PROTEIN KINASE (FRAGME	1.96e+02	201	197 11	09WVB0	DELTA ANTIGEN (FRAGMEN	1.96e+02
129	6	1.4	125 2	P95271	HYPOHETICAL 13.6 KD P	1.96e+02	202	199 10	000318	HEMES.	1.96e+02
130	6	1.4	128 1	026723	HYPOHETICAL 13.1 KD P	1.96e+02	203	200 5	094933	22 KD GAMMA-COIXIN PRE	1.96e+02
131	6	1.4	131 13	057446	INSULIN-LIKE GROWTH FA	1.96e+02	204	202 13	090675	40S RIBOSOMAL PROTEIN	1.96e+02
132	6	1.4	133 2	P94342	CHEV.	1.96e+02	205	203 10	P93450	TISSUE-TYPE PLASMINOGE	1.96e+02
133	6	1.4	133 2	066170	TRBC.	1.96e+02	206	204 2	P94431	LIGHT-HARVESTING COMPL	1.96e+02
134	6	1.4	135 8	036742	ATPASE 8 PROTEIN (FRAG	1.96e+02	207	204 4	092516	DNA FOR 25-36 DEGREE R	1.96e+02
135	6	1.4	140 14	P89914	16 KDA PROTEIN (FRAGME	1.96e+02	208	207 2	050259	RBP-MS/TYPER 2.	1.96e+02
136	6	1.4	141 11	062237	SEX-LIMITED PROTEIN SL	1.96e+02	209	208 8	021530	LEUCYL/PHENILALANYL-TR	1.96e+02
137	6	1.4	144 1	09WV29	INNER MEMBRANE HG(II)	1.96e+02	210	211 2	09X819	NADH DEHYDROGENASE SUB	1.96e+02
138	6	1.4	145 8	099994	RIBOSOMAL PROTEIN L16.	1.96e+02	211	211 2	09X819	HYPOHETICAL 21.1 KD P	1.96e+02
139	6	1.4	154 1	030100	TRANSPOSASE. PUTATIVE.	1.96e+02	212	214 2	09YBC4	213AA LONG HYPOHETICA	1.96e+02
140	6	1.4	157 6	058919	INTERLEUKIN 2 PRECURSO	1.96e+02	213	215 5	09XCD0	PUTATIVE PARTITION PRO	1.96e+02
141	6	1.4	157 1	026990	157AA LONG HYPOHETICA	1.96e+02	214	215 10	039946	LARGE DELTA ANTIGEN.	1.96e+02
142	6	1.4	158 14	09YVY8	CONSERVED PROTEIN.	1.96e+02	215	216 9	P92003	F53F1.5 PROTEIN.	1.96e+02
143	6	1.4	162 2	050527	ORF MSV134 HYPOHETICA	1.96e+02	216	216 14	084523	APETAL3 HOMOLOG PBP3	1.96e+02
144	6	1.4	163 1	050828	A2 MATING TYPE LOCUS,	1.96e+02	217	216 5	017526	HYPOHETICAL 25.3 KD P	1.96e+02
145	6	1.4	163 1	050828	(ATCC 19859).	1.96e+02	218	217 1	093659	GENOME, PARTIAL SEQUEN	1.96e+02
146	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	219	218 2	092517	W02D1.5. PROTEIN.	1.96e+02
147	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	220	219 8	003361	TRIMETHYLAMINE CORRINO	1.96e+02
148	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	221	219 8	003361	RBP-MS/TYPER 3.	1.96e+02
149	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	222	221 4	092517	ATP SYNTHASE A CHAIN (1.96e+02
150	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	223	222 2	003361	ZINC INDUCIBLE PROTEIN	1.96e+02
151	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	224	223 6	006076	CYTOTOXIC T-LYMPHOCYTE	1.96e+02
152	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	225	224 2	062824	HYPOHETICAL 24.1 KD P	1.96e+02
153	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	226	225 2	005248	BETA-CASEIN.	1.96e+02
154	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	227	225 5	001604	HYPOHETICAL 24.7 KD P	1.96e+02
155	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	228	225 5	001604	COSMID 110E9.	1.96e+02
156	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	229	225 5	001604	NIFH CLASS. IV PROTEIN	1.96e+02
157	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	230	225 5	001604	HYPOHETICAL 25.9 KD P	1.96e+02
158	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	231	225 5	001604	REPLICATION-ASSOCIATED	1.96e+02
159	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	232	225 5	001604	W03B1.3 PROTEIN.	1.96e+02
160	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	233	225 5	001604	243AA LONG HYPOHETICA	1.96e+02
161	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	234	225 5	001604	F13A7.4 PROTEIN.	1.96e+02
162	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	235	225 5	001604	252AA LONG HYPOHETICA	1.96e+02
163	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	236	225 5	001604	CHROMOSOME XVI COSMID	1.96e+02
164	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	237	225 5	001604	CHROMOSOME COMPONENT.	1.96e+02
165	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	238	225 5	001604	PSEUDOURIDYLATE SYNTHA	1.96e+02
166	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	239	225 5	001604		

240	6	1.4	254	4	Q9YK2	KALLIREIN 4.	1.966+02	313	316	2	P95164	HYPOHETICAL 32.7 KD P	1.966+02
241	6	1.4	254	6	Q9XSN6	ENAMEL MATRIX SERINE P	1.966+02	314	316	2	P95114	L-LACTATE DEHYDROGENAS	1.966+02
242	6	1.4	255	1	Q9Z0M1	ENAMEL MATRIX SERINE P	1.966+02	315	319	2	P96845	HYPOHETICAL 33.5 KD P	1.966+02
243	6	1.4	256	1	Q26605	POTASSIUM CHANNEL RELA	1.966+02	316	319	2	P96850	P67 ANTIGEN	1.966+02
244	6	1.4	257	14	Q98624	MATRIX PROTEIN	1.966+02	317	321	2	P92820	HYPOHETICAL 33.8 KD P	1.966+02
245	6	1.4	257	13	Q13069	KN-B2 PRECURSOR	1.966+02	318	322	1	P95895	322A LONG HYPOHETICA	1.966+02
246	6	1.4	258	2	Q85382	EXTRACELLULAR ENTEROTO	1.966+02	319	323	5	Q15557	GLYCERALDEHYDE-3-PHOS	1.966+02
247	6	1.4	259	5	Q23406	SIMILARITY TO ONOSOPHI	1.966+02	320	323	5	Q36002	LAMBDAL CII STABILITY-G	1.966+02
248	6	1.4	260	13	Q13057	SERINE PROTEASE PRECUR	1.966+02	321	324	2	Q12222	HYPOHETICAL 37.8 KD P	1.966+02
249	6	1.4	260	13	Q13060	SERINE PROTEASE PRECUR	1.966+02	322	324	2	Q92636	HYPOHETICAL 37.8 KD P	1.966+02
250	6	1.4	261	5	Q19431	FL3E9-6 PROTEIN	1.966+02	323	324	13	Q90320	CANDIDAL HOMOLOG CDX1	1.966+02
251	6	1.4	261	5	Q62052	C08F11.10 PROTEIN	1.966+02	324	324	5	Q45806	T3D5.7 PROTEIN	1.966+02
252	6	1.4	261	2	Q34627	HYPOHETICAL 29.2 KD P	1.966+02	325	324	5	Q45806	HEAT SHOCK PROTEIN	1.966+02
253	6	1.4	262	1	Q9YF28	262AA LONG HYPOHETICA	1.966+02	326	327	5	Q9XW66	X379A.2 PROTEIN	1.966+02
254	6	1.4	265	1	Q58351	265AA LONG HYPOHETICA	1.966+02	327	327	5	Q17032	MULTISE PRECURSOR (FRA	1.966+02
255	6	1.4	267	6	Q02764	OX40 PRECURSOR (FRAGME	1.966+02	328	327	5	Q16979	TBP	1.966+02
256	6	1.4	268	14	Q65117	MULTIGENE FAMILY 300 P	1.966+02	329	327	10	Q92835	327AA LONG HYPOHETICA	1.966+02
257	6	1.4	268	5	Q26561	NE-YA SUBUNIT	1.966+02	330	328	13	Q93550	POTASSIUM CHANNEL RECP	1.966+02
258	6	1.4	269	2	Q85135	FLAGELLAR PROTEIN FLIR	1.966+02	331	328	5	Q17706	C54C8.1 PROTEIN	1.966+02
259	6	1.4	269	2	Q92E14	NORO PROTEIN	1.966+02	332	328	5	Q56126	OUTER MEMBRANE PROTEIN	1.966+02
260	6	1.4	272	2	Q9ZHH1	DIHYDRODIOL DEHYDROGEN	1.966+02	333	329	5	Q44829	F54D12.5 PROTEIN	1.966+02
261	6	1.4	273	6	Q9XSP9	VOLTAGE-GATED POTASSIU	1.966+02	334	329	10	Q92835	CYTIDINE DEAMINASE 7 (1.966+02
262	6	1.4	273	10	Q23571	HYPOHETICAL 28.8 KD P	1.966+02	335	330	8	Q92835	NADH-UBIQUINONE OXIDOR	1.966+02
263	6	1.4	273	5	Q68480	ACCESSORY PROTEIN NOSY	1.966+02	336	330	11	Q62353	COMPLEMENT COMPONENT 1	1.966+02
264	6	1.4	274	5	Q44071	MEROZOITE ANTIGEN 2	1.966+02	337	331	1	Q00893	PECTATE LYASE (FRAGMEN	1.966+02
265	6	1.4	274	6	Q09078	POTASSIUM CHANNEL PROT	1.966+02	338	331	14	Q98337	SPIKE PROTEIN (FRAGMEN	1.966+02
266	6	1.4	276	2	Q9ZNS2	PANTOATE--BETA-ALANINE	1.966+02	339	334	5	Q25121	SPERM-ACTIVATING PEPTI	1.966+02
267	6	1.4	277	5	Q19291	SIMILAR TO D. MELANOCA	1.966+02	340	335	2	Q83811	HYPOHETICAL 37.4 KD P	1.966+02
268	6	1.4	279	14	Q84944	COAT PROTEIN (FRAGMEN	1.966+02	341	336	5	Q93642	F30A10.2 PROTEIN	1.966+02
269	6	1.4	280	1	Q26743	HYPOHETICAL 31.7 KD P	1.966+02	342	337	2	Q92KJ6	POTASSIUM CHANNEL RECP	1.966+02
270	6	1.4	281	14	Q98601	MOVEMENT PROTEIN	1.966+02	343	340	5	Q48759	C1PC ATPASE (MEC)	1.966+02
271	6	1.4	282	4	Q9Y390	CGI-81 PROTEIN	1.966+02	344	340	5	P91232	COSMID F08D12	1.966+02
272	6	1.4	283	14	Q71132	PUTATIVE MOVEMENT PROT	1.966+02	345	343	5	Q001758	SIMILARITY TO INSECT-T	1.966+02
273	6	1.4	283	14	Q70914	PUTATIVE MOVEMENT PROT	1.966+02	346	344	5	Q045761	TG6E6.7 PROTEIN	1.966+02
274	6	1.4	283	14	Q70916	PUTATIVE MOVEMENT PROT	1.966+02	347	347	14	Q55649	T05D4.3 PROTEIN	1.966+02
275	6	1.4	283	14	Q71130	MOVEMENT PROTEIN	1.966+02	348	347	2	Q9XK69	NBP-HEXOSE 4-KETOREDDC	1.966+02
276	6	1.4	284	14	Q98599	MOVEMENT PROTEIN	1.966+02	349	348	10	Q92K34	ACYLOXENIN	1.966+02
277	6	1.4	284	14	Q85205	PUTATIVE MOVEMENT PROT	1.966+02	350	348	5	Q27281	TC1-LIKE TRANSPOSASE	1.966+02
278	6	1.4	285	14	Q71140	MOVEMENT PROTEIN	1.966+02	351	349	9	P87249	HAPD PROTEIN	1.966+02
279	6	1.4	288	7	Q46707	MAJOR HISTOCOMPATIBILI	1.966+02	352	349	10	Q80912	PEROXIDASE	1.966+02
280	6	1.4	289	5	P91392	CODED FOR BY C. ELEGAN	1.966+02	353	351	1	Q9YV98	351AA LONG HYPOHETICA	1.966+02
281	6	1.4	290	14	Q9YNA2	REVERSE TRANSCRIPTASE	1.966+02	354	352	10	Q9XG26	TIN24.5 PROTEIN	1.966+02
282	6	1.4	290	14	Q9YU1	TUMOR SUPPRESSING STP	1.966+02	355	352	2	Q096599	HYPOHETICAL 37.5 KD P	1.966+02
283	6	1.4	293	2	Q53855	HYPOHETICAL 34.5 KD P	1.966+02	356	353	2	Q066894	HYDROGENASE SMALL SUBU	1.966+02
284	6	1.4	290	2	Q67210	REVERSE TRANSCRIPTASE	1.966+02	357	353	14	Q85447	PROTEIN 10.	1.966+02
285	6	1.4	291	14	Q9YMN9	HYPOHETICAL 31.0 KD P	1.966+02	358	353	14	Q84642	GENOME, PARTIAL SEQUEN	1.966+02
286	6	1.4	291	2	Q86678	HYPOHETICAL 31.0 KD P	1.966+02	359	356	4	Q9XEA7	BAV4	1.966+02
287	6	1.4	293	2	Q53855	RECA-LIKE PROTEIN (REC	1.966+02	360	357	10	Q9XEA7	CYSTEINE SYNTHASE (EC	1.966+02
288	6	1.4	293	14	Q89458	POLY(A) POLYMERASE REG	1.966+02	361	357	10	Q9XEA7	MELANOCORTIN 2-RECEPT	1.966+02
289	6	1.4	293	2	Q9ZMC6	CONSERVED HYPOHETICAL	1.966+02	362	357	13	Q57317	MHC CLASS I ALPHA CHAI	1.966+02
290	6	1.4	293	2	Q25080	PUTATIVE HYPOHETICAL	1.966+02	363	358	1	Q9YK29	358AA LONG HYPOHETICA	1.966+02
291	6	1.4	294	5	Q19891	F28H7.3 PROTEIN	1.966+02	364	358	1	Q9YK29	HYPOHETICAL 42.2 KD P	1.966+02
292	6	1.4	295	3	Q04947	HYPOHETICAL 32.9 KD P	1.966+02	365	359	5	Q14045	CHLOROPLAST CYCLOIS	1.966+02
293	6	1.4	296	2	Q56953	YFEB	1.966+02	366	361	7	Q062896	GLYCULATE OXIDASE (EC	1.966+02
294	6	1.4	299	2	Q04816	OREF PROTEIN PRECURSOR	1.966+02	367	363	10	Q9X190	IRON UPTAKE PROTEIN	1.966+02
295	6	1.4	299	2	Q9XK98	HYPOHETICAL 34.4-KDA	1.966+02	368	368	2	Q9X190	(CPSE)	1.966+02
296	6	1.4	300	5	Q87534	FTMH	1.966+02	369	370	2	Q9XK98	POLYPROTEIN (FRAGMENT)	1.966+02
297	6	1.4	300	5	Q9XK22	L291.1.3 PROTEIN	1.966+02	370	370	11	Q9XK98	POLYPROTEIN (FRAGMENT)	1.966+02
298	6	1.4	300	13	Q9XK22	ZE-CAD1 PROTEIN	1.966+02	371	370	2	Q9XK98	ENVELOPE PROTEIN (FRAG	1.966+02
299	6	1.4	301	10	Q9XK24	POLLEN ALLERGEN IOL P	1.966+02	372	370	1	Q34182	TESTICULAR 3-BETA HYDR	1.966+02
300	6	1.4	301	8	Q02681	HYPOHETICAL 35.3 KD P	1.966+02	373	371	14	Q9XK98	ATP SYNTHASE BETA-SUBU	1.966+02
301	6	1.4	301	10	Q9XK24	HYPOHETICAL 35.3 KD P	1.966+02	374	371	14	Q9XK98	HYPOHETICAL 41.9 KD P	1.966+02
302	6	1.4	302	2	Q9XK24	HYPOHETICAL 33.2 KD P	1.966+02	375	371	14	Q9XK98	HYPOHETICAL 40.4 KD P	1.966+02
303	6	1.4	303	5	Q93792	ESB12.2 PROTEIN	1.966+02	376	371	14	Q9XK98	HYPOHETICAL 40.8 KD P	1.966+02
304	6	1.4	304	5	Q93792	ESB12.2 PROTEIN	1.966+02	377	371	14	Q9XK98	GLYCOPROTEIN (FRAGMENT	1.966+02
305	6	1.4	305	1	Q9YK95	305AA LONG HYPOHETICA	1.966+02	378	371	14	Q9XK98		
306	6	1.4	310	10	Q9XK95	310AA LONG HYPOHETICA	1.966+02	379	376	8	Q9XK98		
307	6	1.4	310	11	Q9XK95	310AA LONG HYPOHETICA	1.966+02	380	376	8	Q9XK98		
308	6	1.4	312	2	Q52060	ACETALDEHYDE DEHYDROGE	1.966+02	381	376	8	Q9XK98		
309	6	1.4	312	2	Q50821	DNA SEQUENCE COMPLETE	1.966+02	382	379	3	Q00751		
310	6	1.4	312	13	Q57338	SULFOTRANSFERASE	1.966+02	383	379	3	Q00751		
311	6	1.4	312	13	Q9M625	XIMPACT	1.966+02	384	380	2	Q005875		
312	6	1.4	313	10	Q39089	PALE CRESS GENE	1.966+02	385	381	14	P87762		

386	6	1.4	381 14	P87763	GLYCOPROTEIN (FRAGMENT	1.96e+02	459	6	1.4	452 1	029889	DNA REPAIR PROTEIN RAD	1.96e+02
387	6	1.4	382 2	005825	DNAJ2	1.96e+02	460	6	1.4	452 2	09X019	NADH DEHYDROGENASE, PU	1.96e+02
388	6	1.4	383 11	09WVM2	DEMATIN 48 KDA SUBUNIT	1.96e+02	461	6	1.4	458 1	026298	CONSERVED PROTEIN	1.96e+02
389	6	1.4	385 8	098475	NADH DEHYDROGENASE SUB	1.96e+02	462	6	1.4	458 2	084822	PHOSPHOLIPIDOMITASE	1.96e+02
390	6	1.4	387 2	055304	ORF GENES, COMPLETE CD	1.96e+02	463	6	1.4	459 8	035376	MTDNA FOR LARGE SUBUNIT	1.96e+02
391	6	1.4	389 2	046816	HELC AND ORF2 PROTEIN	1.96e+02	464	6	1.4	460 14	089222	ORF1L (FRAGMENT)	1.96e+02
392	6	1.4	390 8	098481	NADH DEHYDROGENASE SUB	1.96e+02	465	6	1.4	461 5	021419	K1003.5 PROTEIN	1.96e+02
393	6	1.4	391 2	P72824	HYPOTHETICAL 42.2 KD P	1.96e+02	466	6	1.4	461 11	061706	RNA FOR TYPE IIB INTRA	1.96e+02
394	6	1.4	391 1	09Y238	HYPOTHETICAL 39.1A LONG	1.96e+02	467	6	1.4	463 2	P74236	HYPOTHETICAL 52.5 KD P	1.96e+02
395	6	1.4	391 2	P95247	HYPOTHETICAL 37.4 KD P	1.96e+02	468	6	1.4	463 3	05X109	TNF-RECEPTOR-ASSOCIATE	1.96e+02
396	6	1.4	392 5	019858	SIMILAR TO DOMAINS OF	1.96e+02	469	6	1.4	464 5	002068	METHYLASPARTATE MUTASE	1.96e+02
397	6	1.4	392 2	09X245	CONSERVED HYPOTHETICAL	1.96e+02	470	6	1.4	466 5	046125	SIMILARITY TO XENOPUS	1.96e+02
398	6	1.4	393 2	005099	RUBREDOXIN OXIDOREDUCT	1.96e+02	471	6	1.4	470 2	092887	HGM1 PROTEIN PRECURSOR	1.96e+02
399	6	1.4	393 3	057920	393AA LONG HYPOTHETICA	1.96e+02	472	6	1.4	473 3	P78719	DICARBOXYLASE TRANSLOC	1.96e+02
400	6	1.4	394 11	09W554	ACID CERAMIDASE (EC 3.	1.96e+02	473	6	1.4	477 5	001597	CELSUJL	1.96e+02
401	6	1.4	395 8	098473	NADH DEHYDROGENASE SUB	1.96e+02	474	6	1.4	479 1	029072	OSMID T05E8	1.96e+02
402	6	1.4	397 2	069639	SERINE PROTEINASE	1.96e+02	475	6	1.4	480 2	056817	ACTIVATOR 1, REPLICATI	1.96e+02
403	6	1.4	397 2	006670	POTATIVE SERINE PROTEA	1.96e+02	476	6	1.4	480 2	056817	FATTY ACID REDUCTASE	1.96e+02
404	6	1.4	398 2	084701	HYPOTHETICAL 44.3 KD P	1.96e+02	477	6	1.4	482 5	096267	CHROMATIN-BINDING PROT	1.96e+02
405	6	1.4	398 8	098478	NADH DEHYDROGENASE SUB	1.96e+02	478	6	1.4	484 2	053466	ORF2 PROTEIN (FRAGMENT	1.96e+02
406	6	1.4	398 5	018884	CODED FOR BY C. ELEGAN	1.96e+02	479	6	1.4	485 2	P77811	RIBULOSE BIPHOSPHATE	1.96e+02
407	6	1.4	399 2	056257	HEMOLYSIN	1.96e+02	480	6	1.4	485 11	0921M4	S6 KINASE 2	1.96e+02
408	6	1.4	400 4	014183	DOC2	1.96e+02	481	6	1.4	485 5	09XW17	Y54E2A.8 PROTEIN	1.96e+02
409	6	1.4	401 2	047476	ORF401	1.96e+02	482	6	1.4	487 5	09XW17	Y51A2D.13 PROTEIN	1.96e+02
410	6	1.4	403 8	098479	NADH DEHYDROGENASE SUB	1.96e+02	483	6	1.4	489 13	091781	PORASSIUM CHANNEL	1.96e+02
411	6	1.4	403 11	P70611	DOC2B	1.96e+02	484	6	1.4	490 3	060028	ALPHA-GALACTOSIDASE	1.96e+02
412	6	1.4	405 4	013215	DEMATIN 52 KDA SUBUNIT	1.96e+02	485	6	1.4	491 2	044465	AGSPL1 PROTEIN	1.96e+02
413	6	1.4	405 5	015921	AP-ENONUCLEASE	1.96e+02	486	6	1.4	493 14	083444	DINITROGENASE ALPHA SU	1.96e+02
414	6	1.4	405 2	046465	HYPOTHETICAL 45.9 KD P	1.96e+02	487	6	1.4	493 14	083444	NSP1	1.96e+02
415	6	1.4	405 11	035527	DOUBLE C2, ALPHA (DOC2	1.96e+02	488	6	1.4	493 14	093184	HYPOTHETICAL 54.5 KD P	1.96e+02
416	6	1.4	406 2	09WV69	DEMATIN 52 KDA SUBUNIT	1.96e+02	489	6	1.4	494 11	092188	CYCROCHROME P-450 2A14	1.96e+02
417	6	1.4	406 2	059723	CYCROCHROME P450 LIN (E	1.96e+02	490	6	1.4	495 4	094809	P70 RIBOSOMAL S6 KINAS	1.96e+02
418	6	1.4	407 10	022028	ORF407	1.96e+02	491	6	1.4	495 4	094809	RIBOSE ABC TRANSPORTER	1.96e+02
419	6	1.4	408 2	048658	407AA LONG HYPOTHETICA	1.96e+02	492	6	1.4	495 4	094809	ZIC-RELATED-2	1.96e+02
420	6	1.4	408 2	048658	LMR INTEGRAL MEMBRANE	1.96e+02	493	6	1.4	497 13	09Y1A7	MINDICS	1.96e+02
421	6	1.4	409 14	041629	ENVELOPE GLYCOPROTEIN	1.96e+02	494	6	1.4	499 5	045364	FLH3.10-PROTEIN	1.96e+02
422	6	1.4	409 14	09YAC7	409AA LONG HYPOTHETICA	1.96e+02	495	6	1.4	499 5	045364	ZINC FINGER PROTEIN ZI	1.96e+02
423	6	1.4	411 2	P95146	HYPOTHETICAL 43.6 KD P	1.96e+02	496	6	1.4	501 13	093487	ZINC TRANSPORTER 1 (ZN	1.96e+02
424	6	1.4	412 11	070450	HMG BOX TRANSCRIPTION	1.96e+02	497	6	1.4	501 13	093487	RIBOSOMAL MATURASE (FR	1.96e+02
425	6	1.4	412 8	098472	NADH DEHYDROGENASE SUB	1.96e+02	498	6	1.4	503 11	093487	KIA0020 PROTEIN	1.96e+02
426	6	1.4	413 8	098476	NADH DEHYDROGENASE SUB	1.96e+02	499	6	1.4	507 8	047119	HYPOTHETICAL 56.7 KD P	1.96e+02
427	6	1.4	415 4	095906	DJ1039K5.1 (SIMILAR TO	1.96e+02	500	6	1.4	508 4	015397	HYPOHETICAL 54.6 KD P	1.96e+02
428	6	1.4	415 14	041523	CUS4	1.96e+02	501	6	1.4	509 2	P74537	HYPOHETICAL 56.7 KD P	1.96e+02
429	6	1.4	416 5	09XV64	Y102ASD.1-PROTEIN	1.96e+02	502	6	1.4	509 2	P74537	HYPOHETICAL 56.7 KD P	1.96e+02
430	6	1.4	416 11	062083	PROTEIN THAT INTERACTS	1.96e+02	503	6	1.4	510 5	024425	TROPOMOSIN 1 (ISOFORM	1.96e+02
431	6	1.4	417 8	098480	NADH DEHYDROGENASE SUB	1.96e+02	504	6	1.4	510 5	075926	PUTATIVE SUGAR TRANSPO	1.96e+02
432	6	1.4	417 2	059260	TRIACTYLGLYCEROL LIPASE	1.96e+02	505	6	1.4	511 10	09X1H7	PUTATIVE SUGAR TRANSPO	1.96e+02
433	6	1.4	417 8	095683	NADH DEHYDROGENASE SUB	1.96e+02	506	6	1.4	515 5	016968	FISH HOMOLOG	1.96e+02
434	6	1.4	419 11	066015	LIPASE (EC 3.1.1.3) (T	1.96e+02	507	6	1.4	517 4	09Y202	SIGMA-LIKE FACTOR PREC	1.96e+02
435	6	1.4	425 2	P74524	ATAXIN-2 (FRAGMENT)	1.96e+02	508	6	1.4	519 10	09XN9	VENTRAL NEURAL CADHERI	1.96e+02
436	6	1.4	425 2	P74524	HYPOHETICAL 46.3 KD P	1.96e+02	509	6	1.4	519 10	09XN9	HYPOHETICAL PROTEIN	1.96e+02
437	6	1.4	426 2	020569	SIMILAR TO ACETYLCHOLIN	1.96e+02	510	6	1.4	520 8	032477	NADH DEHYDROGENASE SUB	1.96e+02
438	6	1.4	426 2	P71006	SNF1 RELATED PROTEIN K	1.96e+02	511	6	1.4	521 10	082507	F2P5.14 PROTEIN	1.96e+02
439	6	1.4	429 10	09X1W0	COSMID M03A8	1.96e+02	512	6	1.4	524 5	09XU74	Y49E10.17 PROTEIN	1.96e+02
440	6	1.4	432 5	021482	HOMOSERINE DEHYDROGENA	1.96e+02	513	6	1.4	525 5	044079	CHITINASE	1.96e+02
441	6	1.4	433 10	065516	ALDEHYDE DEHYDROGENASE	1.96e+02	514	6	1.4	527 2	051259	GLUCANOL-3-PHOSPHATE D	1.96e+02
442	6	1.4	433 10	065516	DNA FOR TYPE IIB INTRA	1.96e+02	515	6	1.4	527 2	097492	CAVALASE (EC 1.11.1.6)	1.96e+02
443	6	1.4	434 11	061709	EYES ABSENT HOMOLOG (F	1.96e+02	516	6	1.4	527 2	068018	HYPOHETICAL 56.2 KD P	1.96e+02
444	6	1.4	434 11	061709	MAL3P8.11 PROTEIN	1.96e+02	517	6	1.4	529 4	015680	TYROSINASE PRECURSOR (1.96e+02
445	6	1.4	437 5	060647	AL3P8.11 PROTEIN	1.96e+02	518	6	1.4	529 4	034355	TYROSINASE PRECURSOR (1.96e+02
446	6	1.4	437 5	060647	SIMILAR TO ESTERASE ANS	1.96e+02	519	6	1.4	530 10	024372	GLUTATHIONE SYNTHETASE	1.96e+02
447	6	1.4	437 5	022993	VP2 PROTEIN (FRAGMENT)	1.96e+02	520	6	1.4	531 5	024372	TROPOMOSIN ISOFORM 33	1.96e+02
448	6	1.4	439 5	018384	MG-PROTOPHILIN IX M	1.96e+02	521	6	1.4	531 5	015675	PUTATIVE TYROSINASE PR	1.96e+02
449	6	1.4	441 14	065744	HYPOTHETICAL 49.8 KD P	1.96e+02	522	6	1.4	533 2	0929N5	TNBB3PROTEIN	1.96e+02
450	6	1.4	442 3	041431	NADH DEHYDROGENASE 1 C	1.96e+02	523	6	1.4	534 4	015675	TYROSINASE	1.96e+02
451	6	1.4	444 5	019296	SIMILAR TO REPEAT OF C	1.96e+02	524	6	1.4	534 10	080953	TRANSPOSASE	1.96e+02
452	6	1.4	445 2	052782	449AA LONG HYPOTHETICA	1.96e+02	525	6	1.4	535 3	001165	356AA LONG HYPOTHETICA	1.96e+02
453	6	1.4	445 5	019296	PUTATIVE LIPROTEIN	1.96e+02	526	6	1.4	536 1	09YBMS	HYPOHETICAL 58.7 KD P	1.96e+02
454	6	1.4	448 8	058175	HYPOTHETICAL 45.8 KD P	1.96e+02	527	6	1.4	538 2	085801	REPLICATION PROTEIN A.	1.96e+02
455	6	1.4	449 1	058175		1.96e+02	528	6	1.4	538 2	085801		1.96e+02
456	6	1.4	450 1	09YC69		1.96e+02	529	6	1.4	538 2	085801		1.96e+02
457	6	1.4	451 2	058588		1.96e+02	530	6	1.4	538 2	085801		1.96e+02
458	6	1.4	451 2	058588		1.96e+02	531	6	1.4	538 2	09YX00		1.96e+02

678	6	1.4	695	8	032700	NADH DEHYDROGENASE SUB	1.96e+02	751	6	1.4	736	10	023362	HYPOTHETICAL 80.8 KD P	1.96e+02
679	6	1.4	695	8	032339	NADH DEHYDROGENASE SUB	1.96e+02	752	6	1.4	737	8	019932	NADH DEHYDROGENASE (FR	1.96e+02
680	6	1.4	695	8	P92308	NADH DEHYDROGENASE SUB	1.96e+02	753	6	1.4	738	8	098709	NADH DEHYDROGENASE (FR	1.96e+02
681	6	1.4	695	8	095679	NADH DEHYDROGENASE SUB	1.96e+02	754	6	1.4	738	8	019931	NADH DEHYDROGENASE (FR	1.96e+02
682	6	1.4	695	8	095687	NADH DEHYDROGENASE SUB	1.96e+02	755	6	1.4	739	8	091188	NADH DEHYDROGENASE (FR	1.96e+02
683	6	1.4	695	8	095686	NADH DEHYDROGENASE SUB	1.96e+02	756	6	1.4	740	8	032055	NADH DEHYDROGENASE (FR	1.96e+02
684	6	1.4	695	8	095682	NADH DEHYDROGENASE SUB	1.96e+02	757	6	1.4	740	8	019944	NADH DEHYDROGENASE (FR	1.96e+02
685	6	1.4	695	8	032058	NADH DEHYDROGENASE SUB	1.96e+02	758	6	1.4	741	8	098703	NADH DEHYDROGENASE (FR	1.96e+02
686	6	1.4	697	8	031877	NADH DEHYDROGENASE SUB	1.96e+02	759	6	1.4	742	14	089713	NADH DEHYDROGENASE (FR	1.96e+02
687	6	1.4	697	8	030659	NADH DEHYDROGENASE (FR	1.96e+02	760	6	1.4	742	14	069156	ENVELOPE GLYCOPROTEIN	1.96e+02
688	6	1.4	697	8	031860	NADH DEHYDROGENASE SUB	1.96e+02	761	6	1.4	743	14	069158	ENVELOPE GLYCOPROTEIN	1.96e+02
689	6	1.4	698	8	032447	NADH DEHYDROGENASE SUB	1.96e+02	762	6	1.4	743	14	069161	ENVELOPE GLYCOPROTEIN	1.96e+02
690	6	1.4	698	8	098653	NADH DEHYDROGENASE SUB	1.96e+02	763	6	1.4	743	14	069162	ENVELOPE GLYCOPROTEIN	1.96e+02
691	6	1.4	698	8	098647	NADH DEHYDROGENASE SUB	1.96e+02	764	6	1.4	743	14	069155	ENVELOPE GLYCOPROTEIN	1.96e+02
692	6	1.4	698	8	098644	NADH DEHYDROGENASE SUB	1.96e+02	765	6	1.4	743	14	069157	ENVELOPE GLYCOPROTEIN	1.96e+02
693	6	1.4	698	8	098645	NADH DEHYDROGENASE SUB	1.96e+02	766	6	1.4	744	14	035673	ENVELOPE GLYCOPROTEIN	1.96e+02
694	6	1.4	698	8	098641	NADH DEHYDROGENASE SUB	1.96e+02	767	6	1.4	745	14	068415	ENVELOPE GLYCOPROTEIN	1.96e+02
695	6	1.4	698	8	098648	NADH DEHYDROGENASE SUB	1.96e+02	768	6	1.4	745	14	068414	ENVELOPE GLYCOPROTEIN	1.96e+02
696	6	1.4	698	8	098642	NADH DEHYDROGENASE SUB	1.96e+02	769	6	1.4	746	14	068413	ENVELOPE GLYCOPROTEIN	1.96e+02
697	6	1.4	698	8	098651	NADH DEHYDROGENASE SUB	1.96e+02	770	6	1.4	746	14	068412	ENVELOPE GLYCOPROTEIN	1.96e+02
698	6	1.4	698	8	032665	NADH DEHYDROGENASE SUB	1.96e+02	771	6	1.4	753	4	075117	ENVELOPE GLYCOPROTEIN	1.96e+02
699	6	1.4	698	8	098646	NADH DEHYDROGENASE SUB	1.96e+02	772	6	1.4	753	2	092711	ENVELOPE GLYCOPROTEIN	1.96e+02
700	6	1.4	699	8	051319	DNA HELICASE (VWR)	1.96e+02	773	6	1.4	753	13	091651	ENVELOPE GLYCOPROTEIN	1.96e+02
701	6	1.4	699	8	033257	NADH DEHYDROGENASE SUB	1.96e+02	774	6	1.4	759	3	P87244	ENVELOPE GLYCOPROTEIN	1.96e+02
702	6	1.4	700	8	033281	NADH DEHYDROGENASE SUB	1.96e+02	775	6	1.4	759	2	033613	ENVELOPE GLYCOPROTEIN	1.96e+02
703	6	1.4	700	8	033181	NADH DEHYDROGENASE SUB	1.96e+02	776	6	1.4	762	4	014965	ENVELOPE GLYCOPROTEIN	1.96e+02
704	6	1.4	700	8	031815	NADH DEHYDROGENASE SUB	1.96e+02	777	6	1.4	765	11	070445	ENVELOPE GLYCOPROTEIN	1.96e+02
705	6	1.4	700	8	032598	NADH DEHYDROGENASE SUB	1.96e+02	778	6	1.4	771	3	014100	ENVELOPE GLYCOPROTEIN	1.96e+02
706	6	1.4	700	8	033046	NADH DEHYDROGENASE SUB	1.96e+02	779	6	1.4	773	2	051099	ENVELOPE GLYCOPROTEIN	1.96e+02
707	6	1.4	700	8	033143	NADH DEHYDROGENASE SUB	1.96e+02	780	6	1.4	790	2	084481	ENVELOPE GLYCOPROTEIN	1.96e+02
708	6	1.4	700	8	032922	NADH DEHYDROGENASE SUB	1.96e+02	781	6	1.4	791	2	P72084	ENVELOPE GLYCOPROTEIN	1.96e+02
709	6	1.4	700	8	095662	NADH DEHYDROGENASE SUB	1.96e+02	782	6	1.4	792	11	092132	ENVELOPE GLYCOPROTEIN	1.96e+02
710	6	1.4	702	5	017968	NADH DEHYDROGENASE SUB	1.96e+02	783	6	1.4	793	14	091186	ENVELOPE GLYCOPROTEIN	1.96e+02
711	6	1.4	702	5	033150	NADH DEHYDROGENASE SUB	1.96e+02	784	6	1.4	794	2	092913	ENVELOPE GLYCOPROTEIN	1.96e+02
712	6	1.4	704	5	092856	EG-23E12.5 PROTEIN	1.96e+02	785	6	1.4	803	13	013080	ENVELOPE GLYCOPROTEIN	1.96e+02
713	6	1.4	704	5	032852	NADH DEHYDROGENASE SUB	1.96e+02	786	6	1.4	814	2	P71283	ENVELOPE GLYCOPROTEIN	1.96e+02
714	6	1.4	705	8	033170	NADH DEHYDROGENASE SUB	1.96e+02	787	6	1.4	815	2	P66644	ENVELOPE GLYCOPROTEIN	1.96e+02
715	6	1.4	705	8	019832	NADH DEHYDROGENASE (FR	1.96e+02	788	6	1.4	830	14	09W725	ENVELOPE GLYCOPROTEIN	1.96e+02
716	6	1.4	705	8	032650	NADH DEHYDROGENASE SUB	1.96e+02	789	6	1.4	840	10	058419	ENVELOPE GLYCOPROTEIN	1.96e+02
717	6	1.4	706	8	093690	NADH DEHYDROGENASE SUB	1.96e+02	790	6	1.4	842	10	049363	ENVELOPE GLYCOPROTEIN	1.96e+02
718	6	1.4	706	8	092854	NADH DEHYDROGENASE SUB	1.96e+02	791	6	1.4	844	13	090579	ENVELOPE GLYCOPROTEIN	1.96e+02
719	6	1.4	712	13	000531	TENASCIN-R (RESTRICTIN	1.96e+02	792	6	1.4	854	13	093244	ENVELOPE GLYCOPROTEIN	1.96e+02
720	6	1.4	712	13	042443	TAP2	1.96e+02	793	6	1.4	855	13	093244	ENVELOPE GLYCOPROTEIN	1.96e+02
721	6	1.4	715	11	088967	ATP-DEPENDENT METALLOP	1.96e+02	794	6	1.4	855	5	092610	ENVELOPE GLYCOPROTEIN	1.96e+02
722	6	1.4	719	2	045751	INSECTICIDAL PROTEIN	1.96e+02	795	6	1.4	859	5	094174	ENVELOPE GLYCOPROTEIN	1.96e+02
723	6	1.4	719	2	045756	CCCRV	1.96e+02	796	6	1.4	874	14	09W723	ENVELOPE GLYCOPROTEIN	1.96e+02
724	6	1.4	719	2	085796	INSECTICIDAL PROTEIN	1.96e+02	797	6	1.4	885	13	09W723	ENVELOPE GLYCOPROTEIN	1.96e+02
725	6	1.4	719	2	092852	INSECTICIDAL CRYSTAL P	1.96e+02	798	6	1.4	885	4	012791	ENVELOPE GLYCOPROTEIN	1.96e+02
726	6	1.4	719	2	045709	CRYSTAL. PROTEIN	1.96e+02	799	6	1.4	892	2	084098	ENVELOPE GLYCOPROTEIN	1.96e+02
727	6	1.4	719	2	087404	CRYSTAL. PROTEIN TOXIN	1.96e+02	800	6	1.4	892	2	050747	ENVELOPE GLYCOPROTEIN	1.96e+02
728	6	1.4	719	8	098659	NADH DEHYDROGENASE (FR	1.96e+02	801	6	1.4	899	5	044872	ENVELOPE GLYCOPROTEIN	1.96e+02
729	6	1.4	719	2	045752	INSECTICIDAL PROTEIN	1.96e+02	802	6	1.4	904	5	045544	ENVELOPE GLYCOPROTEIN	1.96e+02
730	6	1.4	721	8	019934	NADH DEHYDROGENASE (FR	1.96e+02	803	6	1.4	909	4	014820	ENVELOPE GLYCOPROTEIN	1.96e+02
731	6	1.4	722	10	004514	HYPOTHETICAL 81.3 KD P	1.96e+02	804	6	1.4	914	11	035378	ENVELOPE GLYCOPROTEIN	1.96e+02
732	6	1.4	724	5	017856	C1A11.1 PROTEIN	1.96e+02	805	6	1.4	918	11	035378	ENVELOPE GLYCOPROTEIN	1.96e+02
733	6	1.4	724	2	005748	PRPB	1.96e+02	806	6	1.4	918	11	035378	ENVELOPE GLYCOPROTEIN	1.96e+02
734	6	1.4	726	8	019938	NADH DEHYDROGENASE (FR	1.96e+02	807	6	1.4	918	11	035378	ENVELOPE GLYCOPROTEIN	1.96e+02
735	6	1.4	726	8	019937	NADH DEHYDROGENASE (FR	1.96e+02	808	6	1.4	925	11	064702	ENVELOPE GLYCOPROTEIN	1.96e+02
736	6	1.4	727	8	019942	NADH DEHYDROGENASE (FR	1.96e+02	809	6	1.4	925	11	035276	ENVELOPE GLYCOPROTEIN	1.96e+02
737	6	1.4	728	8	098702	NADH DEHYDROGENASE (FR	1.96e+02	810	6	1.4	926	11	035374	ENVELOPE GLYCOPROTEIN	1.96e+02
738	6	1.4	728	8	019948	NADH DEHYDROGENASE (FR	1.96e+02	811	6	1.4	930	5	017339	ENVELOPE GLYCOPROTEIN	1.96e+02
739	6	1.4	730	8	019945	NADH DEHYDROGENASE (FR	1.96e+02	812	6	1.4	931	4	060462	ENVELOPE GLYCOPROTEIN	1.96e+02
740	6	1.4	731	8	019947	NADH DEHYDROGENASE (FR	1.96e+02	813	6	1.4	931	11	035375	ENVELOPE GLYCOPROTEIN	1.96e+02
741	6	1.4	731	8	098700	NADH DEHYDROGENASE (FR	1.96e+02	814	6	1.4	937	5	017469	ENVELOPE GLYCOPROTEIN	1.96e+02
742	6	1.4	732	8	019933	NADH DEHYDROGENASE (FR	1.96e+02	815	6	1.4	943	4	094960	ENVELOPE GLYCOPROTEIN	1.96e+02
743	6	1.4	732	8	098711	NADH DEHYDROGENASE (FR	1.96e+02	816	6	1.4	944	3	060043	ENVELOPE GLYCOPROTEIN	1.96e+02
744	6	1.4	732	8	098710	NADH DEHYDROGENASE (FR	1.96e+02	817	6	1.4	946	4	014517	ENVELOPE GLYCOPROTEIN	1.96e+02
745	6	1.4	732	8	098707	NADH DEHYDROGENASE (FR	1.96e+02	818	6	1.4	947	2	086487	ENVELOPE GLYCOPROTEIN	1.96e+02
746	6	1.4	733	8	098706	NADH DEHYDROGENASE (FR	1.96e+02	819	6	1.4	949	3	014093	ENVELOPE GLYCOPROTEIN	1.96e+02
747	6	1.4	735	1	026409	HYPOTHETICAL 83.5 KD P	1.96e+02	820	6	1.4	954	14	066704	ENVELOPE GLYCOPROTEIN	1.96e+02
748	6	1.4	736	8	019936	NADH DEHYDROGENASE (FR	1.96e+02	821	6	1.4	955	2	045574	ENVELOPE GLYCOPROTEIN	1.96e+02
749	6	1.4	736	8	019946	NADH DEHYDROGENASE (FR	1.96e+02	822	6	1.4	955	2	045574	ENVELOPE GLYCOPROTEIN	1.96e+02
750	6	1.4	736	8	019939	NADH DEHYDROGENASE (FR	1.96e+02	823	6	1.4	971	11	086659	ENVELOPE GLYCOPROTEIN	1.96e+02

824	6	1.4	973	2	092836	POLYMORPHIC OUTER MEMB	1.96e+02	897	6	1.4	1304	5	015765	CYTOPLASMIC DYNEIN HEA	1.96e+02
825	6	1.4	986	10	064429	ALDEHYDE OXIDASE (FRAG	1.96e+02	898	6	1.4	1323	3	013686	HYDROTHERMAL 149.1 KD	1.96e+02
826	6	1.4	987	8	003684	PROBABLY DNA POLYMERAS	1.96e+02	899	6	1.4	1324	3	059328	ENO-1.3(4)-BETA-GLUCA	1.96e+02
827	6	1.4	988	14	087041	SPVCPZ, COMPLETE GENOM	1.96e+02	900	6	1.4	1348	2	060043	ENDOXILANASE PRECURSOR	1.96e+02
828	6	1.4	992	14	069119	NUCLEAR ANTIGEN PRECUR	1.96e+02	901	6	1.4	1358	4	092752	TEANASCIN-R.	1.96e+02
829	6	1.4	1002	2	000037	TRANSPOSON GAMMA-DELTA	1.96e+02	902	6	1.4	1375	4	099461	ASR1	1.96e+02
830	6	1.4	1002	3	074674	VARIANT REGION OF MAJO	1.96e+02	903	6	1.4	1375	11	035099	MER KINASE 5 (APOPTOSI	1.96e+02
831	6	1.4	1005	13	013075	NUCLEAR FACTOR NF-KB1	1.96e+02	904	6	1.4	1385	5	091389	SIMILARITY TO SEVERAL	1.96e+02
832	6	1.4	1009	3	074378	2-OXOGUTARATE DEHYDRO	1.96e+02	905	6	1.4	1388	3	014139	HYDROTHERMAL 159.4 KD	1.96e+02
833	6	1.4	1018	3	094068	CONSERVED HYDROTHERMAL	1.96e+02	906	6	1.4	1394	4	000512	BC19 PROTEIN.	1.96e+02
834	6	1.4	1019	3	094267	PURATIVE YEAST CELL DI	1.96e+02	907	6	1.4	1398	1	092186	BI22 PROTEIN.	1.96e+02
835	6	1.4	1020	5	025415	GLUTAMATE DEHYDROGENAS	1.96e+02	908	6	1.4	1408	5	092438	RETROFT.	1.96e+02
836	6	1.4	1026	5	094071	PURATIVE LIPRIN BETA (1.96e+02	909	6	1.4	1445	5	010463	T24H7.5 PROTEIN.	1.96e+02
837	6	1.4	1035	10	093812	F19p19.7	1.96e+02	910	6	1.4	1454	5	010463	T24H7.5 PROTEIN.	1.96e+02
838	6	1.4	1039	10	022792	F49.19 PROTEIN.	1.96e+02	911	6	1.4	1477	5	076931	TUMOR-SUPPRESSOR PROTEI	1.96e+02
839	6	1.4	1039	2	074552	HELICASE OF THE SNE2/R	1.96e+02	912	6	1.4	1518	5	021442	LAMININ A (FRAGMENT).	1.96e+02
840	6	1.4	1045	3	093796	TRANSLATION ELONGATION	1.96e+02	913	6	1.4	1551	4	075445	USHER SYNDROME TYPE II	1.96e+02
841	6	1.4	1049	14	088099	(CLONE 2) (ENV).	1.96e+02	914	6	1.4	1556	3	006554	SIMILAR TO S.-CEREVISI	1.96e+02
842	6	1.4	1051	14	066108	CITRUS-LEAF RUGOSE ILA	1.96e+02	915	6	1.4	1556	10	092VW3	T22H22.1 PROTEIN.	1.96e+02
843	6	1.4	1054	5	096077	EPFDE3.	1.96e+02	916	6	1.4	1575	4	013576	RASAP-RELATED PROTEIN	1.96e+02
844	6	1.4	1054	4	094887	KIA0793 PROTEIN.	1.96e+02	917	6	1.4	1590	5	091152	SIMILAR TO DROSOPHILA	1.96e+02
845	6	1.4	1055	14	065146	HELICASE.	1.96e+02	918	6	1.4	1602	2	065933	HYDROTHERMAL 167.1 KD	1.96e+02
846	6	1.4	1055	2	053348	HYDROTHERMAL 123.6 KD	1.96e+02	919	6	1.4	1611	10	049311	PURATIVE MYOSIN HEAVY	1.96e+02
847	6	1.4	1062	5	076657	F25E5.1 PROTEIN.	1.96e+02	920	6	1.4	1633	5	001510	COMPLEMENT C3-H2.	1.96e+02
848	6	1.4	1064	2	073770	HYDROTHERMAL 123.6 KD	1.96e+02	921	6	1.4	1663	5	001510	SIMILARITY TO THW P13/	1.96e+02
849	6	1.4	1080	3	043134	P-TYPE TRANSPORTING AT	1.96e+02	922	6	1.4	1696	11	09WTR8	SCOP.	1.96e+02
850	6	1.4	1083	5	019336	FLA10.3 PROTEIN.	1.96e+02	923	6	1.4	1701	5	061164	ERYTHROCYTE BINDING PR	1.96e+02
851	6	1.4	1102	2	095684	SUBTILISIN-LIKE PROTEA	1.96e+02	924	6	1.4	1721	4	095216	INTERSCITIN LONG FORM.	1.96e+02
852	6	1.4	1108	2	092568	PURATIVE MEMBRANE ASSO	1.96e+02	925	6	1.4	1738	11	070346	COMPLEMENT C4.	1.96e+02
853	6	1.4	1108	10	09XIE1	F23H11.20 PROTEIN.	1.96e+02	926	6	1.4	1740	5	097019	ASC3 PROTEIN.	1.96e+02
854	6	1.4	1113	4	012917	CALCIUM DEPENDENT POTA	1.96e+02	927	6	1.4	1751	5	017143	TRANSCRIPTIONAL CO-REP	1.96e+02
855	6	1.4	1120	10	024515	UNCONVENTIONAL MYOSIN	1.96e+02	928	6	1.4	1762	2	030480	PKS MODULE 2.	1.96e+02
856	6	1.4	1132	4	014636	RECEPTOR-ASSOCIATED TY	1.96e+02	929	6	1.4	1763	14	066914	POLYPROTEIN.	1.96e+02
857	6	1.4	1132	4	075297	JAK2 KINASE.	1.96e+02	930	6	1.4	1763	14	066914	NON-STRUCTURAL PROTEIN	1.96e+02
858	6	1.4	1134	6	028204	LARGE CONDUCTANCE CALC	1.96e+02	931	6	1.4	1773	5	066913	TRANSCRIPTIONAL CO-REP	1.96e+02
859	6	1.4	1146	5	09Y0Y9	BCDMA.LD24702.	1.96e+02	932	6	1.4	1774	11	017142	PROCOLLAGEN, TYPE XVII	1.96e+02
860	6	1.4	1146	11	061372	C4 COMPLEMENT PROTEIN	1.96e+02	933	6	1.4	1795	4	014674	KIA0165 PROTEIN.	1.96e+02
861	6	1.4	1151	6	018867	CALCIUM-ACTIVATED POTA	1.96e+02	934	6	1.4	1807	3	013661	HYDROTHERMAL 229.9KD P	1.96e+02
862	6	1.4	1152	6	018866	CALCIUM-ACTIVATED POTA	1.96e+02	935	6	1.4	1847	2	09X992	POLYKETIDE SYNTHASE.	1.96e+02
863	6	1.4	1153	5	093598	F29D11.2 PROTEIN.	1.96e+02	936	6	1.4	1860	3	09Y878	GLUCAN SYNTHASE (FRAGM	1.96e+02
864	6	1.4	1154	4	012921	CALCIUM-ACTIVATED POTA	1.96e+02	937	6	1.4	1893	11	072026	PLEKXIN 1.	1.96e+02
865	6	1.4	1156	6	028265	CALCIUM-ACTIVATED POTA	1.96e+02	938	6	1.4	1903	3	087204	FKBP PROTEIN INVOLVED	1.96e+02
866	6	1.4	1156	6	064371	LARGE CONDUCTANCE CALC	1.96e+02	939	6	1.4	1905	3	092225	1,3-BETA-D-GLUCAN SYNT	1.96e+02
867	6	1.4	1156	6	093209	POL. PROTEIN.	1.96e+02	940	6	1.4	1919	3	042998	HYDROTHERMAL 217.7 KD	1.96e+02
868	6	1.4	1162	5	093139	ORF2.	1.96e+02	941	6	1.4	1928	4	099736	HSGCN1 (FRAGMENT).	1.96e+02
869	6	1.4	1163	11	008626	CALCIUM-ACTIVATED POTA	1.96e+02	942	6	1.4	1976	2	09WX18	ALPHA-1,2-MANNOSIDASE	1.96e+02
870	6	1.4	1167	4	075578	INTEGRIN SUBUNIT ALPHA	1.96e+02	943	6	1.4	2061	5	077025	PURATIVE FATY ACID SY	1.96e+02
871	6	1.4	1172	14	006526	STRUCTURAL PROTEIN.	1.96e+02	944	6	1.4	2080	3	092215	SIMILAR TO MYOSIN.	1.96e+02
872	6	1.4	1176	14	098587	HYDROTHERMAL 119.0 KD	1.96e+02	945	6	1.4	2098	5	091443	PKS MODULE 3.	1.96e+02
873	6	1.4	1178	4	031350	CALCIUM-ACTIVATED POTA	1.96e+02	946	6	1.4	2100	2	030481	PKS MODULE 3.	1.96e+02
874	6	1.4	1178	4	012960	LARGE-CONDUCTANCE CALC	1.96e+02	947	6	1.4	2109	5	076416	H05009.1 PROTEIN (FRAG	1.96e+02
875	6	1.4	1178	11	062976	CALCIUM-ACTIVATED POTA	1.96e+02	948	6	1.4	2126	2	094996	HYDROTHERMAL 221.0 KD	1.96e+02
876	6	1.4	1179	2	092618	DNA POLYMERASE III ALP	1.96e+02	949	6	1.4	2157	3	091724	RNA-DEPENDENT RNA POLY	1.96e+02
877	6	1.4	1183	5	094447	TRP PROTEIN.	1.96e+02	950	6	1.4	2161	14	009705	TRANS-GOLGI P230. (256	1.96e+02
878	6	1.4	1194	2	053645	PURATIVE ABC TRANSPORT	1.96e+02	951	6	1.4	2230	14	009705	COMPLETE VIRAL PROTEIN	1.96e+02
879	6	1.4	1196	11	008460	SLOWMOLOG, POTA	1.96e+02	952	6	1.4	2230	4	013439	TOXIN B.	1.96e+02
880	6	1.4	1198	2	053730	POLYKETIDE SYNTHASE (F	1.96e+02	953	6	1.4	2292	14	099272	ZONDHESIN (FRAGMENT).	1.96e+02
881	6	1.4	1203	4	09Y3Q4	HYPERPOLARIZATION-ACTI	1.96e+02	954	6	1.4	2353	2	046034	MYELOBLAST KIA0219 (F	1.96e+02
882	6	1.4	1208	14	039273	COUNTERPART OF HSV-1 G	1.96e+02	955	6	1.4	2367	2	094993	WGCSC.L267D11.3 PROTE	1.96e+02
883	6	1.4	1210	11	09WUT3	LARGE-CONDUCTANCE CALC	1.96e+02	956	6	1.4	2379	4	09Y519	GIANTIN (GOLGI COMPLEX	1.96e+02
884	6	1.4	1219	4	015242	NRD2 CONVERTASE (EC 3.	1.96e+02	957	6	1.4	2392	4	095001	GIANTIN (GOLGI COMPLEX	1.96e+02
885	6	1.4	1221	5	045796	TR19C.7 PROTEIN.	1.96e+02	958	6	1.4	2412	4	092616	PKS MODULE 1.	1.96e+02
886	6	1.4	1221	4	09Y2K9	KIA1006 PROTEIN (FRAG	1.96e+02	959	6	1.4	2589	14	066776	PURATIVE VACUOLATING C	1.96e+02
887	6	1.4	1229	11	035836	NRD2 CONVERTASE (EC 3.	1.96e+02	960	6	1.4	2723	2	030479	TRANSCRIPTIONAL ACTIVA	1.96e+02
888	6	1.4	1230	5	020626	F49E2.5A PROTEIN.	1.96e+02	961	6	1.4	2902	2	09ZME6	DB063.3 PROTEIN.	1.96e+02
889	6	1.4	1234	2	060046	XYNA PRECURSOR (EC 3.2	1.96e+02	962	6	1.4	2971	4	09Y519	DB063.3 PROTEIN.	1.96e+02
890	6	1.4	1264	5	091767	NEUROGLIAN.	1.96e+02	963	6	1.4	3187	11	063714	DB063.3 PROTEIN.	1.96e+02
891	6	1.4	1265	5	09X0E3	F52G2.2 PROTEIN.	1.96e+02	964	6	1.4	3228	5	093593	DB063.3 PROTEIN.	1.96e+02
892	6	1.4	1278	11	035604	NPC1.	1.96e+02	965	6	1.4	3268	5	093280	DB063.3 PROTEIN.	1.96e+02
893	6	1.4	1278	4	015118	NIEHANN-PICK C DISEASE	1.96e+02	966	6	1.4	3410	14	089278	POLYPROTEIN.	1.96e+02
894	6	1.4	1285	11	070305	SPINOCEREBELLAR ATAXIA	1.96e+02	967	6	1.4	3410	14	089278	POLYPROTEIN.	1.96e+02
895	6	1.4	1286	10	093R72	P-GLYCOPROTEIN.	1.96e+02	968	6	1.4	3410	14	089278	POLYPROTEIN PRECURSOR	1.96e+02
896	6	1.4	1288	11	061437	PROCOLLAGEN, TYPE XVII	1.96e+02	969	6	1.4	3411	14	09W878	POLYPROTEIN.	1.96e+02

ID	Q9YHMO	PRELIMINARY	PRT	569 AA
970	6	1.4	3411 14	Q9YHMO
971	6	1.4	3411 14	Q9YHMO
972	6	1.4	3411 14	Q9YHMO
973	6	1.4	3411 14	Q9YHMO
974	6	1.4	3411 14	Q9YHMO
975	6	1.4	3411 14	Q9YHMO
976	6	1.4	3411 14	Q9YHMO
977	6	1.4	3411 14	Q9YHMO
978	6	1.4	3411 14	Q9YHMO
979	6	1.4	3411 14	Q9YHMO
980	6	1.4	3411 14	Q9YHMO
981	6	1.4	3411 14	Q9YHMO
982	6	1.4	3411 14	Q9YHMO
983	6	1.4	3411 14	Q9YHMO
984	6	1.4	3411 14	Q9YHMO
985	6	1.4	3411 14	Q9YHMO
986	6	1.4	3411 14	Q9YHMO
987	6	1.4	3411 14	Q9YHMO
988	6	1.4	3411 14	Q9YHMO
989	6	1.4	3411 14	Q9YHMO
990	6	1.4	3411 14	Q9YHMO
991	6	1.4	3411 14	Q9YHMO
992	6	1.4	3411 14	Q9YHMO
993	6	1.4	3411 14	Q9YHMO
994	6	1.4	3411 14	Q9YHMO
995	6	1.4	3411 14	Q9YHMO
996	6	1.4	3411 14	Q9YHMO
997	6	1.4	3411 14	Q9YHMO
998	6	1.4	3411 14	Q9YHMO
999	6	1.4	3411 14	Q9YHMO
1000	6	1.4	3411 14	Q9YHMO

ALIGNMENTS

ID	Q9YHMO	PRELIMINARY	PRT	569 AA
AC	Q9YHMO			
DT	01-MAY-1999 (TREMELREL. 10, Created)			
DT	01-MAY-1999 (TREMELREL. 10, Last sequence update)			
DT	01-MAY-1999 (TREMELREL. 10, Last annotation update)			
DE	INTERFERON ALPHA/BETA RECEPTOR 1.			
GN	IFNARI.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;			
OC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER:			
RA	REBOUL J., GARDINER K., MONNERON D., UZE G., LUTPALLA G.,			
RA	"Comparative genomic analysis of the interferon/interleukin-10			
RA	receptor gene cluster."			
RA	Genome Res. 0:0-0(1999).			
DR	EMBL: AF082664; AAD13669.1.			
RT	Receptor.			
RV	SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;			
SO	SEQUENCE			
Query Match	2.1%; Score 9; DB 13; Length 569;			
Best Local Similarity	100.0%; Pred. No. 1.18e-04;			
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DB	201 PRTYCLAY 209			
QY	194 PRTYCLAY 202			
RESULT	2			
ID	080566	PRELIMINARY;	PRT; 421 AA.	
AC	080566;			
DT	01-NOV-1998 (TREMELREL. 08, Created)			
DT	01-NOV-1998 (TREMELREL. 08, Last sequence update)			
DT	01-NOV-1998 (TREMELREL. 08, Last annotation update)			
DE	F6E13.9 PROTEIN.			

ID	Q9YHMO	PRELIMINARY	PRT	571 AA
AC	Q9YHMO			
DT	01-JAN-1998 (TREMELREL. 05, Created)			
DT	01-JAN-1998 (TREMELREL. 05, Last sequence update)			
DT	01-JAN-1999 (TREMELREL. 09, Last annotation update)			
DE	Y57G11C.7 PROTEIN.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;			
OC	Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RA	MCWURRAY A.			
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 94150718.			
RA	WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERRS M.,			
RA	BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,			
RA	CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,			
RA	GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,			
RA	JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,			
RA	LIGHTNING J., LLOYD C., MCWURRAY A., MORTIMORE B., O'CALLAGHAN M.,			
RA	PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,			
RA	SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,			
RA	THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,			
RA	WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLMAN P.,			
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.			
RT	elegans."			
RL	Nature 368:32-38(1994).			
DR	EMBL: Z99281; CAB16509.1.			
SO	SEQUENCE 571 AA; 66883 MW; 2A34A731 CRC32;			
Query Match	1.8%; Score 8; DB 5; Length 571;			
Best Local Similarity	100.0%; Pred. No. 2.34e-02;			
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
DB	164 VEEIKLR 171			
QY	96 VEEIKLR 103			
RESULT	4			
ID	024315	PRELIMINARY;	PRT; 1235 AA.	
AC	024315;			
DT	01-NOV-1996 (TREMELREL. 01, Created)			

DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLER. 12, Last annotation update)
 DE TYROSINE KINASE (FRAGMENT)
 OS Drosophila melanogaster (Fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ITO M., MATSUI T., TANGUCHI T., CHIHARA K.;
 RT "Alternative splicing generates two distinct transcripts for the
 RT Drosophila melanogaster fibroblast growth factor receptor homolog."
 RL Gene 0:0-0(1994)
 DR EMBL: D17550; BAA04488.1;
 DR HSSP: P08631; 2HCK.
 DR FLYBASE: FBgn0014073; Tle.
 DR PFAM: PF00069; pkinase.2.
 FT NON_TER 1 1
 SQ SEQUENCE 1235 AA; 135257 MW; 86277084 CRC32;

Query Match 1.6%; Score 7; DB 5; Length 1235;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 731 TLVLVAVG 738
 1111111111
 QY 10 TLVLVAVG 17

RESULT 5
 ID 054100; PRELIMINARY; PRT; 93 AA.
 AC 054100;
 DT 01-NOV-1996 (TREMBLER. 01, Created)
 DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLER. 08, Last annotation update)
 DE ORF1, 5 END; NADH-FERREDOXIN OXIDOREDUCTASE (FORA) (FRAGMENT).
 OS Saccharopolyspora erythraea (Streptomyces erythraeus).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
 OC Actinomycetales; Pseudonocardiales; Pseudonocardaceae;
 OC Saccharopolyspora.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-MNH22;
 RC MEDLINE: 95255650.
 RA ZOTCHEV S.B., HUTCHINSON C.R.;
 RT "Cloning and heterologous expression of the genes encoding nonspecific
 RT electron transport components for a cytochrome P450 system of
 RT Saccharopolyspora erythraea involved in erythromycin production."
 RL Gene 156:101-106(1995).
 DR EMBL: L38646; AAA4472.1;
 DR NON_TER 93 93
 SQ SEQUENCE 93 AA; 10784 MW; E8184524 CRC32;

Query Match 1.6%; Score 7; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 48 TLVLVAVG 54
 1111111111
 QY 9 TLVLVAVG 15

RESULT 6
 ID 09YRD2; PRELIMINARY; PRT; 101 AA.
 AC 09YRD2;
 DT 01-MAY-1999 (TREMBLER. 10, Created)
 DT 01-MAY-1999 (TREMBLER. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLER. 10, Last annotation update)
 DE DNA METHYLTRANSFERASE (FRAGMENT).
 OS European catfish virus.
 OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.
 RN [1]
 RP SEQUENCE FROM N.A.

RA MAO J., WANG J., CHINCHAR G.D., CHINCHAR V.G.;
 RT "Molecular characterization of a Ranavirus isolated from Largemouth
 RT bass (Micropterus salmoides)."
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF100201; AAC79866.1;
 KW Transferase; Methyltransferase.
 FT NON_TER 1 1
 SQ SEQUENCE 101 AA; 11970 MW; 16425730 CRC32;

Query Match 1.6%; Score 7; DB 14; Length 101;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 VLKWDYT 8
 1111111111
 QY 245 VLKWDYT 251

RESULT 7
 ID 061696; PRELIMINARY; PRT; 141 AA.
 AC 061696;
 DT 01-AUG-1998 (TREMBLER. 07, Created)
 DT 01-AUG-1998 (TREMBLER. 07, Last sequence update)
 DT 01-MAY-1999 (TREMBLER. 10, Last annotation update)
 DE PUTATIVE MULTIFUNCTIONAL PROTEIN ADE2 (FRAGMENT).
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-FATBODY.
 RC SCHOLZ F.R., TRENCEK T., KANOST M.R.;
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF060796; AAC15763.1;
 DR PFAM: PF01259; SAICAR synt. 1.
 FT NON_TER 141 141
 SQ SEQUENCE 141 AA; 15515 MW; 97657734 CRC32;

Query Match 1.6%; Score 7; DB 5; Length 141;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 111 FLKRNPG 117
 1111111111
 QY 265 FLKRNPG 271

RESULT 8
 ID 076631; PRELIMINARY; PRT; 150 AA.
 AC 076631;
 DT 01-NOV-1996 (TREMBLER. 01, Created)
 DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLER. 08, Last annotation update)
 DE REV PROTEIN.
 GN REV.
 OS Human immunodeficiency virus type 2.
 OC Viruses; Retrovirus; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 93124535.
 RA BARNETT S.W., QUIROGA M., WERNER A., DINA D., LEVY J.A.;
 RT "Distinguishing features of an infectious molecular clone of the
 RT highly divergent and noncytopathic human immunodeficiency virus type 2
 RT UCI strain."
 RL J. Virol. 67:1006-1014(1993).
 DR EMBL: L07625; AAA3939.1;
 DR PFAM: PF00424; REV.1.
 SQ SEQUENCE 150 AA; 17186 MW; 2825384E CRC32;

Query Match 1.6%; Score 7; DB 14; Length 150;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 55 IRSIDS 61
OY 339 IRSIDS 345

RESULT 9

ID 050273 PRELIMINARY; PRT: 163 AA.

AC 050273; 050272;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).

GN MCR1.
OS Methanohalophilus portuacensis.

OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;

CC Methanohalophilus.

RP STRAIN-VARIOUS STRAINS;

RA SPRINGER E., SACHS M.S., MOESE C.R., BOONE D.R.;

RT "Partial gene sequences for the A subunit of methyl-coenzyme M

reductase (mcrI) as a phylogenetic tool for the family

Methanosarcinaceae."

RL Int. J. Syst. Bacteriol. 45:554-559(1995).

DR EMBL; U22238; AAC43416.1;

DR HSSP; P11558; IMRO.

FT NON_TER 1 163

SEQUENCE 163 AA; 17603 MW; BA95C61C CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;

Best Local Similarity 100.0%; Pred. No. 2.89e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97

OY 20 VLSAAG 26

RESULT 10 PRELIMINARY; PRT: 163 AA.

ID 050908; 050908;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).

GN MCR1.

OS Methanohalophilus zhilinae.

OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;

CC Methanohalophilus.

RP STRAIN-VARIOUS STRAINS;

RA SPRINGER E., SACHS M.S., MOESE C.R., BOONE D.R.;

RT "Partial gene sequences for the A subunit of methyl-coenzyme M

reductase (mcrI) as a phylogenetic tool for the family

Methanosarcinaceae."

RL Int. J. Syst. Bacteriol. 45:554-559(1995).

DR EMBL; U22252; AAC43429.1;

DR HSSP; P11558; IMRO.

FT NON_TER 1 163

SEQUENCE 163 AA; 17573 MW; 5EBF170F CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;

Best Local Similarity 100.0%; Pred. No. 2.89e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97

OY 20 VLSAAG 26

RESULT 11 PRELIMINARY; PRT: 163 AA.

ID 048921; 048921;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).

GN MCR1.

OS Methanococcus burtonii.

OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;

CC Methanococcus.

RP STRAIN-DSM 6242, OREGON COLLECTION OF METHANOGENS ACCESSION #OCM 468;

RA SPRINGER E., SACHS M.S., MOESE C.R., BOONE D.R.;

RT "Partial gene sequences for the A subunit of methyl-coenzyme M

reductase (mcrI) as a phylogenetic tool for the family

Methanosarcinaceae."

RL Int. J. Syst. Bacteriol. 45:554-559(1995).

DR EMBL; U22234; AAC43406.1;

DR HSSP; P11558; IMRO.

FT NON_TER 1 163

SEQUENCE 163 AA; 17494 MW; 5826284D CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;

Best Local Similarity 100.0%; Pred. No. 2.89e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97

OY 20 VLSAAG 26

RESULT 12 PRELIMINARY; PRT: 163 AA.

ID 057067; 057067;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).

GN MCR1.

OS Methanohalophilus sp. (strain Cas-1),

OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;

CC Methanohalophilus sp. (strain SF-1).

RP STRAIN-CAS-1 / OCM 135, REF-1 / OCM 57, SF-1 / OCM 13;

RA SPRINGER E., SACHS M.S., MOESE C.R., BOONE D.R.;

RT "Partial gene sequences for the A subunit of methyl-coenzyme M

reductase (mcrI) as a phylogenetic tool for the family

Methanosarcinaceae."

RL Int. J. Syst. Bacteriol. 45:554-559(1995).

DR EMBL; U22240; AAC43417.1;

DR HSSP; P11558; IMRO.

FT NON_TER 1 163

SEQUENCE 163 AA; 17565 MW; 1DCCF1D5 CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;

Best Local Similarity 100.0%; Pred. No. 2.89e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97

OY 20 VLSAAG 26

Db 91 VLSAAG 97
 OY 20 VLSAAG 26

RESULT 13
 ID 049114 PRELIMINARY; PRT; 163 AA.

AC 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT)
 GN MCRI
 OS Methanohalobium evestigatum
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
 CC Methanohalobium
 RN [1]
 RP SEQUENCE FROM N.A.
 RX SPRINGER E., SACHS M.S., WOESE C.R., BOONE D.R.;
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M
 RT reductase (mcrI) as a phylogenetic tool for the family
 RT Methanosarcinaceae."
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).
 DR EMBL: U22335; AAC43408.1;
 DR HSSP: P11558; IMRO.
 FT NON_TER 1 1
 FT 163 163
 SQ SEQUENCE 163 AA; 17559 MW; 56892275 CRC32;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 1; Length 163;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 VLSAAG 97
 OY 20 VLSAAG 26

RESULT 14
 ID 050215 PRELIMINARY; PRT; 163 AA.

AC 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT)
 GN MCRI
 OS Methanohalophilus mahl.
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
 CC Methanohalophilus
 RN [1]
 RP SEQUENCE FROM N.A.
 RX SPRINGER E., SACHS M.S., WOESE C.R., BOONE D.R.;
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M
 RT reductase (mcrI) as a phylogenetic tool for the family
 RT Methanosarcinaceae."
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).
 DR EMBL: U22337; AAC43411.1;
 DR HSSP: P11558; IMRO.
 FT NON_TER 1 1
 FT 163 163
 SQ SEQUENCE 163 AA; 17617 MW; 56673AD4 CRC32;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 1; Length 163;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 VLSAAG 97
 OY 20 VLSAAG 26

RESULT 15
 ID 050387 PRELIMINARY; PRT; 163 AA.

AC 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT)
 GN MCRI
 OS Methanohalobium sp. (strain SD-1)
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
 CC [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-SD-1 / OCM 134;
 RX SPRINGER E., SACHS M.S., WOESE C.R., BOONE D.R.;
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M
 RT reductase (mcrI) as a phylogenetic tool for the family
 RT Methanosarcinaceae."
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).
 DR EMBL: U22356; AAC43423.1;
 DR HSSP: P11558; IMRO.
 FT NON_TER 1 1
 FT 163 163
 SQ SEQUENCE 163 AA; 17606 MW; 90801B67 CRC32;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 1; Length 163;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 VLSAAG 97
 OY 20 VLSAAG 26

RESULT 16
 ID 050214 PRELIMINARY; PRT; 163 AA.

AC 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT)
 GN MCRI
 OS Methanococcus methylophilus
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
 CC Methanococcus
 RN [1]
 RP SEQUENCE FROM N.A.
 RX SPRINGER E., SACHS M.S., WOESE C.R., BOONE D.R.;
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M
 RT reductase (mcrI) as a phylogenetic tool for the family
 RT Methanosarcinaceae."
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).
 DR EMBL: U22335; AAC43410.1;
 DR HSSP: P11558; IMRO.
 FT NON_TER 1 1
 FT 163 163
 SQ SEQUENCE 163 AA; 17548 MW; 1F36B74 CRC32;

Query Match
 Best Local Similarity 100.0%; Score 7; DB 1; Length 163;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 VLSAAG 97
 OY 20 VLSAAG 26

RESULT 17
 ID 049535 PRELIMINARY; PRT; 163 AA.
 AC 049535;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).
 GN MCRI.
 OS Methanohalophilus halophilus.
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
 OC Methanohalophilus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-2-7982, OREGON COLLECTION OF METHANOGENS ACCESSION #OCM 160;
 RX MEDLINE; 96174929.
 RA SPRINGER E.; SACHS M.S.; MOESE C.R.; BOONE D.R.;
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M
 reductase (mcrl) as a phylogenetic tool for the family
 Methanosarcinaceae".
 RT Methanosarcinaceae.
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).
 DR EMBL; U22259; AAC3409.1;
 DR HSSP; P11558; IMRO.
 FT NON_TER 1 163
 FT NON_TER 1 163
 SQ SEQUENCE 163 AA; 17603 MW; BA95C61C CRC32;
 Query Match 1.6%; Score 7; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97
 OY 20 VLSAAG 26

RESULT 18
 ID 050386 PRELIMINARY; PRT; 163 AA.
 AC 050386;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).
 GN MCRI.
 OS Methanohalophilus sp. (strain HCM6).
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HCM6, OREGON COLLECTION OF METHANOGENS ACCESSION #OCM 152;
 RX MEDLINE; 96174929.
 RA SPRINGER E.; SACHS M.S.; MOESE C.R.; BOONE D.R.;
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M
 reductase (mcrl) as a phylogenetic tool for the family
 Methanosarcinaceae".
 RT Methanosarcinaceae.
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).
 DR EMBL; U22259; AAC3442.1;
 DR HSSP; P11558; IMRO.
 FT NON_TER 1 163
 FT NON_TER 1 163
 SQ SEQUENCE 163 AA; 17595 MW; 4C706148 CRC32;
 Query Match 1.6%; Score 7; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97
 OY 20 VLSAAG 26

RESULT 19
 ID 035576 PRELIMINARY; PRT; 239 AA.
 AC 035576;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE TROPONIN T3, SKELETAL, FAST.
 GN TNN3.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamm
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RX MEDLINE; 97390134.
 RA WANG J.; JIN J.P.;
 RT "Primary structure and developmental acidic to basic transition of 13
 RT alternatively spliced mouse fast skeletal muscle troponin T
 RT isoforms".
 RL Gene 193:105-114(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RA GSDB;
 RL Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; L48989; AAB67284.1;
 DR MGI; MGI:109550; Tnn3.
 DR PFAM; PF00992; Troponin; 1.
 SQ SEQUENCE 239 AA; 28337 MW; D29A2E63 CRC32;
 Query Match 1.6%; Score 7; DB 11; Length 239;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 89 RIRAEK 95
 OY 103 RIRAEK 109

RESULT 20
 ID 035575 PRELIMINARY; PRT; 239 AA.
 AC 035575;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
 DE TROPONIN T3, SKELETAL, FAST.
 GN TNN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RX MEDLINE; 97390134.
 RA WANG J.; JIN J.P.;
 RT "Primary structure and developmental acidic to basic transition of 13
 RT alternatively spliced mouse fast skeletal muscle troponin T
 RT isoforms".
 RL Gene 193:105-114(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RA GSDB;
 RL Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; L48989; AAB67283.1;
 DR MGI; MGI:109550; Tnn3.
 DR PFAM; PF00992; Troponin; 1.
 SQ SEQUENCE 239 AA; 28335 MW; 16C16AE3 CRC32;
 Query Match 1.6%; Score 7; DB 11; Length 239;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 89 RIRAEK 95
 OY 103 RIRAEK 109

RESULT 21
 ID 035581 PRELIMINARY; PRT; 248 AA.
 AC 035581;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE TROPONIN T3, SKELETAL, FAST
 GN TNN3
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129; TISSUE-FAST SKELETAL MUSCLE;
 RX MEDLINE; 97390134.
 RA WANG J., JIN J.P.;
 RT "Primary structure and developmental acidic to basic transition of 13
 RT alternatively spliced mouse fast skeletal muscle troponin T
 RT isoforms."
 RL Gene 193:105-114(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129; TISSUE-FAST SKELETAL MUSCLE;
 RA GSD; Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RL EMBL; L48918; AAB67289.1;
 DR MGD; MGI:109550; Tnn3.
 DR PFAM; PF00992; Troponin; 1.
 SO SEQUENCE 248 AA; 29346 MW; 740C8991 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 248;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 RIRAKE 104
 |||||
 OY 103 RIRAKE 109

RESULT 22 PRELIMINARY; PRT; 248 AA.
 AC P97456;
 DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE TROPONIN T3, SKELETAL, FAST
 DE (FAST SKELETAL MUSCLE TROPONIN T ISOFORM PROPT).
 GN TNN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC KOGH A., JUAN T.S.C., JENKINS N.A., GILBERT D.J., COPELAND N.G.,
 RA MCNIECE I.K., FLETCHER F.A.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U77779; AAB39743.1;
 DR MGD; MGI:109550; Tnn3.
 DR PFAM; PF00992; Troponin; 1.
 SO SEQUENCE 248 AA; 29376 MW; B2CB1C58 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 248;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 RIRAKE 104
 |||||
 OY 103 RIRAKE 109

RESULT 23 PRELIMINARY; PRT; 248 AA.
 ID 035578;
 AC 035578;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE TROPONIN T3, SKELETAL, FAST

GN TNN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ma
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RX MEDLINE; 97390134.
 RA WANG J., JIN J.P.;
 RT "Primary structure and developmental acidic to basic transition of 13
 RT alternatively spliced mouse fast skeletal muscle troponin T
 RT isoforms."
 RL Gene 193:105-114(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RA GSD; Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RL EMBL; L48991; AAB67286.1;
 DR MGD; MGI:109550; Tnn3.
 DR PFAM; PF00992; Troponin; 1.
 SO SEQUENCE 248 AA; 29344 MW; B057CD11 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 248;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 RIRAKE 104
 |||||
 OY 103 RIRAKE 109

RESULT 24 PRELIMINARY; PRT; 250 AA.
 ID 035579;
 AC 035579;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE TROPONIN T3, SKELETAL, FAST
 GN TNN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RX MEDLINE; 97390134.
 RA WANG J., JIN J.P.;
 RT "Primary structure and developmental acidic to basic transition of 13
 RT alternatively spliced mouse fast skeletal muscle troponin T
 RT isoforms."
 RL Gene 193:105-114(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RA GSD; Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RL EMBL; L48992; AAB67287.1;
 DR MGD; MGI:109550; Tnn3.
 DR PFAM; PF00992; Troponin; 1.
 SO SEQUENCE 250 AA; 29757 MW; DCD2DBE7 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 100 RIRAKE 106
 |||||
 OY 103 RIRAKE 109

RESULT 25 PRELIMINARY; PRT; 250 AA.
 ID 035580;
 AC 035580;

US-09-240-675-2.rsp

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Query Match      1.6% score 7; DB 11; length 250;
Best Local Similarity 100.0%
Pred. No. 2.89e+00;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Db      100-RIRAEKE 106      .      .      .
      1111111
Oy      103 RIRAEKE 109

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Query Match	1.68;	Score 7;	DB 11;	Length 254;
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Db 104 RIRAEKE 110

RESULT 27
ID 035585
PRELIMINARY;
PRT; 255 AA

Query Match	1.6%;	Score 7;	DB 11;	length 255;
Best local Similarity	100.0%;	Pred. No.	2.89e+00;	
Matches	7;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0

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Db      105 RIRAEKE 111
        |||||
OY      103 RIRAEKE 109

RESULT  28
ID      09ZWZ8      PRELIMINARY;      PRT;      259 AA.
AC      09ZWZ8;
DT      01-MAY-1999 (TREMBLrel, 10, Created)
DT      01-MAY-1999 (TREMBLrel, 10, Last sequence update)
DT      01-MAY-1999 (TREMBLrel, 10, Last annotation update)
DE      GP82.
OS      Mycobacteriophage TM4.
OC      Viruses.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      FORN M.E., STENSTROM C., HENDRIX R.W., HATPUILL G.F.;
DR      "Mycobacteriophage TM4: genome structure and gene expression.";
RL      Tuberc. Lung Dis. 79:63-73(1998).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      FORN M.E., STENSTROM C., HENDRIX R.W., HATPUILL G.F.;
DR      Submitted (May-1998) to the EMBL/Genbank/DBDj databases.
RL      EMBL, AF068845; AAd17647.1;
OS      SEQUENCE 239 AA; 26662 MW; 4B4C5D92 CRC32;

```

Query Match 1.68; Score 7; DB 9; Length 259;

Best Local Similarity 100.0%; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	59	WVLGAT	65
QY	3	WVLGAT	9

RESULT 29 PRELIMINARY; PRT; 259 AA.
 ID 035583
 AC 035583
 DT 01-JAN-1998 (TREMBLERL. 05, Created)
 DT 01-JAN-1998 (TREMBLERL. 05, Last sequence update)
 DE TROPONIN T3, SKELETAL, FAST
 DE (TROPONIN T FAST SKELETAL MUSCLE ISOFORM)
 GN TNN3
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RX MEDLINE; 97390134.
 RA WANG J., JIN J.P.;
 RT Primary structure and developmental acidic to basic transition of 13
 RT alternatively spliced mouse fast skeletal muscle troponin T
 RT isoforms.
 RT Gene 193:105-114(1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L49470; AAB67291.1;
 DR MGD; MGI:109550; Tnn3.
 DR PFAM; PF00992; Troponin; 1.
 SO SEQUENCE 259 AA; 30709 MW; 4631E971 CRC32;
 Query Match 1.68; Score 7; DB 11; Length 259;
 Best Local Similarity 100.08; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 109 RIRAKE 115
 QY 103 RIRAKE 109
 RESULT 30 PRELIMINARY; PRT; 262 AA.
 ID 035584
 AC 035584
 DT 01-JAN-1998 (TREMBLERL. 05, Created)
 DT 01-JAN-1998 (TREMBLERL. 05, Last sequence update)
 DE TROPONIN T3, SKELETAL, FAST
 DE (TROPONIN T FAST SKELETAL MUSCLE ISOFORM)
 GN TNN3
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RX MEDLINE; 97390134.
 RA WANG J., JIN J.P.;
 RT Primary structure and developmental acidic to basic transition of 13
 RT alternatively spliced mouse fast skeletal muscle troponin T
 RT isoforms.
 RT Gene 193:105-114(1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L49471; AAB67292.1;
 DR MGD; MGI:109550; Tnn3.
 DR PFAM; PF00992; Troponin; 1.
 SO SEQUENCE 262 AA; 31038 MW; 0D965DEF CRC32;
 Query Match 1.68; Score 7; DB 11; Length 262;
 Best Local Similarity 100.08; Pred. No. 2.89e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 112 RIRAKE 118
 QY 103 RIRAKE 109
 RESULT 31 PRELIMINARY; PRT; 268 AA.
 ID 035582
 AC 035582
 DT 01-JAN-1998 (TREMBLERL. 05, Created)
 DT 01-JAN-1998 (TREMBLERL. 05, Last sequence update)
 DE TROPONIN T3, SKELETAL, FAST
 DE (TROPONIN T FAST SKELETAL MUSCLE ISOFORM)
 GN TNN3
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RX MEDLINE; 97390134.
 RA WANG J., JIN J.P.;
 RT Primary structure and developmental acidic to basic transition of 13
 RT alternatively spliced mouse fast skeletal muscle troponin T
 RT isoforms.
 RT Gene 193:105-114(1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SV129;
 RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L49466; AAB67290.1;
 DR MGD; MGI:109550; Tnn3.
 DR PFAM; PF00992; Troponin; 1.
 SO SEQUENCE 268 AA; 31846 MW; 2AB79748 CRC32;
 Query Match 1.68; Score 7; DB 11; Length 268;
 Best Local Similarity 100.08; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 118 RIRAKE 124
 QY 103 RIRAKE 109
 RESULT 32 PRELIMINARY; PRT; 287 AA.
 ID 057559
 AC 057559
 DT 01-JUN-1998 (TREMBLERL. 06, Created)
 DT 01-JUN-1998 (TREMBLERL. 06, Last sequence update)
 DE TROPONIN T VARIANT TNNX7-E16.
 DE TROPONIN T VARIANT TNNX7-E16.
 OS Gallus gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LEGHORN;
 RA JIN J.-P., HUANG Q.Q., WANG J., OGUT O.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF044922; AAC70917.1;
 DR PFAM; PF00992; Troponin; 1.
 SO SEQUENCE 287 AA; 33799 MW; 05C1E0A1 CRC32;
 Query Match 1.68; Score 7; DB 13; Length 287;
 Best Local Similarity 100.08; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 139 RIRAKE 145
 QY 103 RIRAKE 109

RESULT 33
ID 020382 PRELIMINARY; PRT: 298 AA.
AC P73049.
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-JAN-1999 (TREMblrel. 09, Last annotation update)
DE HYPOTHEICAL 32.8 KD PROTEIN
OS Synchocystis sp. (strain PCC 6803)
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RA TABATA S.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RX MEDLINE; 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROKAWA M., SUGIURA M., SASAKOTO S., KITURA T.,
RA SHIMOTO T., MATSUO A., MORI A., NAKAZAKI N., NARO R., OKUMURA S.,
RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA TABATA S.;
RT *Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.*;
RL DNA Res. 3:109-136(1996).
DR EMBL; D90903; BAA17070.1; -
DR PFM; PF01145; Baa1707.1;
KW Hypothetical protein.
SQ SEQUENCE 298 AA; 32828 MW; 0BBBC7E0 CRC32;

Query Match 1.6%; Score 7; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 AERKIE 242
OY 380 AERKIE 386
RESULT 34
ID 069606 PRELIMINARY; PRT: 336 AA.
AC 069606;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE TAI44 PLASMID PTA144 UP, COMPLETE SEQUENCE.
OS Moraxella sp.
OC Moraxellaceae; Moraxella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TAI44;
RA MORETTI M.A., TUTTINO L., DUTILLO A., SANNA G., MARINO G.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
KW Plasmid.
SQ SEQUENCE 336 AA; 38277 MW; 48794102 CRC32;

Query Match 1.6%; Score 7; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 IRSLSOS 57
OY 339 IRSLSOS 345

RESULT 35
ID 020382 PRELIMINARY; PRT: 344 AA.
AC 020382;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMblrel. 01, Last annotation update)
DE COSMID F44A2.
GN F44A2.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditidae; Rhabditidae; Pelodietinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HARKINS T., HILLER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATELLE P.,
RA LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WINTSTOCK L., WILKINSON-SPROUT J., WOHIDMAN P.,
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.*;
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA DU Z., LE T.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA WATERSTON R.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41993; AAA83448.1; -
SQ SEQUENCE 344 AA; 39963 MW; 3CFDDF08 CRC32;

Query Match 1.6%; Score 7; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 EVDIIDD 9
OY 37 EVDIIDD 43
RESULT 36
ID 09XS14 PRELIMINARY; PRT: 364 AA.
AC 09XS14;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE MHC CLASS I ANTIGEN (FRAGMENT).
OS Aulonocara hansbaenschli.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Perciformes; Labroidae; Cichlidae; Aulonocara.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97293242.
RA SATO A., KLEIN D., SULTMANN H., FIGUEROA F., O'HUIGIN C., KLEIN J.;
RT *Class I mhc genes of cichlid fishes: Identification, expression, and
RT polymorphism.*;
RL Immunogenetics 46:63-72(1997).
DR EMBL; AF038551; AAD37814.1; -
FT NON-TER
SQ SEQUENCE 364 AA; 41428 MW; 0A580653 CRC32;

Query Match 1.6%; Score 7; DB 7; Length 364;
Best Local Similarity 100.0%; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Aug 22 08:32:30 2000

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DB 326 LVLVAVG 332
11 LVLVAVG 17
Query Match 1.68; Score 7; DB 11; Length 394;
Best Local Similarity 100.08; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 37
ID 09W7A2 PRELIMINARY; PRT; 380 AA.
AC 09W7A2
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE FAST TROPONIN T ISOFORM.
GN TROPONIN
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 99292729.
RA BUCHER E.A., DHOOF G.K., EMERSON M.M., OBER M., EMERSON C.P. JR.;
RT Structure and evolution of the alternatively spliced fast troponin T
isoform gene.
RT J. Biol. Chem. 274:17661-17670(1999).
RL EMBL: AF139128; AAD42799.1;
DR EMBL: 380 AA; 43814 MW; 1FD2A7AF CRC32;
SQ SEQUENCE 380 AA; 43814 MW; 1FD2A7AF CRC32;

Query Match 1.68; Score 7; DB 13; Length 380;
Best Local Similarity 100.08; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 111 RIRAKE 117
103 RIRAKE 109
Query Match 1.68; Score 7; DB 13; Length 380;
Best Local Similarity 100.08; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 38
ID 062156 PRELIMINARY; PRT; 394 AA.
AC 062156; 061486;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE DIHYDROLYATE REDUCTASE (REP-3).
GN MSH3 OR REP-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95011610.
RA LIT K., NIT L., LINTON J.P., CROUSE G.F.;
RT Characterization of the mouse Rep-3 gene: sequence similarities to
bacterial and yeast mismatch-repair proteins.*
RT Gene 147:169-177(1994).
RL [2]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE: 89384567.
RA LINTON J.P., YEN J.Y.J., SELBY E., CHEN Z., CHINSKY J.M., LIT K.,
RA KELLEMS R.E., CROUSE G.F.;
RT Dual bidirectional promoters at the mouse thfr locus: cloning and
RT characterization of two mRNA classes of the divergently transcribed
RT Rep-1 gene.*
RL Mol. Cell. Biol. 9:3058-3072(1989).
DR EMBL: L10303; AAB60710.1;
DR EMBL: L10295; AAB60710.1; JOINED.
DR EMBL: L10296; AAB60710.1; JOINED.
DR EMBL: L10297; AAB60710.1; JOINED.
DR EMBL: L10298; AAB60710.1; JOINED.
DR EMBL: L10299; AAB60710.1; JOINED.
DR EMBL: L10300; AAB60710.1; JOINED.
DR EMBL: L10301; AAB60710.1; JOINED.
DR MGD: MGI:109519; Msh3.
DR PRAW: PF01624; Muts; 1.
SO SEQUENCE 394 AA; 44599 MW; E9E7F821 CRC32;

DB 247 NKSSVES 253
416 NKSSVES 422
Query Match 1.68; Score 7; DB 11; Length 394;
Best Local Similarity 100.08; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 39
ID 063994 PRELIMINARY; PRT; 403 AA.
AC 063994; 063997;
DT 01-NOV-1998 (TREMREL. 08, Created)
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE MELOID CELL SURFACE ANTIGEN CD33 PRECURSOR.
GN CD33.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C; TISSUE-BONE MARROW;
RX MEDLINE: 94250900.
RA TCHILIAN E.Z., BEVERLEY P.C., YOUNG B.D., WATT S.M.;
RT Molecular cloning of two isoforms of the murine homolog of the
myeloid CD33 antigen.*
RT Blood 83:3188-3198(1994).
RL [1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN, 33-A AND 33-B, ARE
PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE
SHOWN HERE IS THAT OF 33-B.
-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND ONE C2-LIKE DOMAIN.
CC CC
CC -1- SIMILARITY: TO MYELIN-ASSOCIATED GLYCOPROTEIN AND SIALOADHESIN.
CC CC
CC EMBL: S71345; AAB30842.1;
DR EMBL: S71403; AAB30843.1;
DR MGD: MGI:99440; Cd33.
KW Glycoprotein; Transmembrane; Antigen; Signal; Immunoglobulin domain;
FT Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 403
FT DOMAIN 17 120
FT DOMAIN 18 240
FT DOMAIN 18 240
FT TRANSMEM 241 267
FT DOMAIN 268 403
FT CARBOHYD 110 110
FT CARBOHYD 160 160
FT CARBOHYD 230 230
FT VARSPLIC 287 403
POTENTIAL.
MYELOID CELL SURFACE ANTIGEN CD33.
IG-LIKE V-TYPE DOMAIN.
EXTRACELLULAR (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
ROEATSYNHCSPYASDAVTPCCSYHRLISRPCTALIR
IDDPYRTHLRNVAVSTLRPMVSWGSLRSTGRSCTKIC
SPVKNLCPLMLPYDNCSICPLIPEMVMLCVSTLS -> AH
OODSKVSNPNENRPLKOPKOPSOSSVHRTSIDFNGCKPO
EYSEI (IN ISOFORM 33-A).

Query Match 1.68; Score 7; DB 11; Length 403;
Best Local Similarity 100.08; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 LVLVAVG 247
11 LVLVAVG 17
Query Match 1.68; Score 7; DB 11; Length 412 AA.
Best Local Similarity 100.08; Pred. No. 2.89e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 40
ID 09ZORS PRELIMINARY; PRT; 412 AA.
AC 09ZORS;
DT 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DT 01-MAY-1999 (TREMREL. 10, Last annotation update)

DE T13P21.9 PROTEIN.
 GN T13P21.9
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC eudicotyledons; Magnoliophyta; Eudicotyledons;
 CC core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae;
 CC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA.
 RA LIN X., KAUL S., SHEA T.P., FUJII C.T., SHEN M., VANAKEN S.E.,
 RA BANSHEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,
 RA CARREIRA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,
 RA FRASER C.M., VENTER J.C.;
 RT "Arabidopsis thaliana chromosome II BAC T13P21 genomic sequence."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AC006067; AAD15463.1;
 SQ SEQUENCE 412 AA; 46462 MW; D27623A2 CRC32;

Query Match 1.6%; Score 7; DB 10; Length 412;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 376 AAAGKN 382
 OY 23 AAAGKN 29

RESULT 41
 ID 029121 PRELIMINARY; PRT; 451 AA.
 AC 029121;
 DT 01-JAN-1998 (TRENDEL. 05, Created)
 DT 01-JAN-1998 (TRENDEL. 05, Last sequence update)
 DT 01-NOV-1998 (TRENDEL. 08, Last annotation update)
 DE MULTIDRUG RESISTANCE PROTEIN.
 GN AF1144.
 OS Archaeoglobus fulgidus.
 CC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
 CC Archaeoglobus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE; 98049343.
 RA KLEIN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
 RA KETCHUM K.A., DODSON R.J., GRINN M., HICKER E.K., PETERSON J.D.,
 RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
 RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
 RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
 RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
 RA OVERBERG R., GOCAVNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
 RA COTTON M.D., SPRIGGS T., ARTACH P., KAINE B.P., STRES S.M.,
 RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
 RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., MORSE C.R.,
 RA VENTER J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulfate-
 reducing archaeon Archaeoglobus fulgidus."
 RL Nature 390:364-370(1997).
 DR EMBL; AEO01025; AAB90102.1;
 DR TIGR; AF1144;
 DR PFAM; PF00083; sugar_tr; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 451 AA; 47918 MW; D803BD5B CRC32;

Query Match 1.6%; Score 7; DB 1; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 5 KAAITTS 11
 OY 203 KAAITTS 209

RESULT 42

ID 080668 PRELIMINARY; PRT; 454 AA.
 AC 080668;
 DT 01-NOV-1998 (TRENDEL. 08, Created)
 DT 01-NOV-1998 (TRENDEL. 08, Last sequence update)
 DT 01-NOV-1998 (TRENDEL. 08, Last annotation update)
 DE T3K9.4 PROTEIN.
 GN T3K9.4
 OS Arabidopsis thaliana (Mouse-ear cress)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC eudicotyledons; Magnoliophyta; Eudicotyledons;
 CC core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae;
 CC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA.
 RA BRANDON R.C., SYKES S.M., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
 RA SORVITILE C.R., VENTER J.C.;
 RT "Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AC004261; AAD11993.1;
 SQ SEQUENCE 454 AA; 50448 MW; 57898FF5 CRC32;

Query Match 1.6%; Score 7; DB 10; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 9 EKKTDVT 15
 OY 386 EKKTDVT 392

RESULT 43
 ID P11753 PRELIMINARY; PRT; 563 AA.
 AC P11753;
 DT 01-FEB-1997 (TRENDEL. 02, Created)
 DT 01-FEB-1997 (TRENDEL. 02, Last sequence update)
 DT 01-NOV-1999 (TRENDEL. 12, Last annotation update)
 DE HYPOHETICAL 63.0 KD PROTEIN.
 GN MTCY253.30C.
 OS Mycobacterium tuberculosis.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE; 96181548.
 RA PHILLIP W.J., POULET S., EIGLMEIER K., PASCOBELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RT "An integrated map of the genome of the tubercle bacillus,
 Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium
 leprae."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
 DR EMBL; Z81368; CAB03734.1;
 DR PFAM; PF01077; NIT_STR; 1.
 DR PRINTS; PR00397; STROHAEM.
 KW Hypothetical protein.
 SQ SEQUENCE 563 AA; 62997 MW; 688877C5 CRC32;

Query Match 1.6%; Score 7; DB 2; Length 563;
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: Mon Aug 21 10:34:20 2000
 Job time : 74 secs.

Db 48 ERIENIT 54
 OY 178 ERIENIT 184

RESULT 44
 ID 070681 PRELIMINARY; PRT; 588 AA.
 AC 070681;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE COAT PROTEIN (FRAGMENT).
 OS Sugarcane streak mosaic virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HALL J.S., ADAMS B., PARSONS T.J., FRENCH R., LANE L., JENSEN S.C.;
 RL Mol. Phylogenet. Evol. 0:0-0(1998).
 DR EMBL; U75456; AAC16271.1;
 DR PFAM; PF00767; Poly-coat; 1.
 KW Coat protein.
 FT NON_TER 1
 SQ SEQUENCE 588 AA; 66336 MW; 529F3579 CRC32;

Query Match 1.68; Score 7; DB 14; Length 588;
 Best Local Similarity 100.08; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 214 ILMNRS 220
 OY 46 ILMNRS 52

RESULT 45
 ID 092CY6 PRELIMINARY; PRT; 594 AA.
 AC 092CY6;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE PENICILLIN-BINDING PROTEIN (PBP1).
 GN RP565.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MADRID E;
 RX MEDLINE; 99039499.
 RA ANDERSSON S.G.E., ZONORODIPOUR A., ANDERSSON J.O.,
 RA SICHERITZ-PONTEN T., ALSMARK U.C.M., PODOMSKI R.M., NAEGLUND A.K.,
 RA ERIKSSON A.S., WINKLER H.H., KURLAND C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria."
 RL Nature 396:133-140(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MADRID E;
 RA ANDERSSON S.G.E.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ235272; CA15013.1;
 SQ SEQUENCE 594 AA; 67195 MW; C492617E CRC32;

Query Match 1.68; Score 7; DB 2; Length 594;
 Best Local Similarity 100.08; Pred. No. 2.89e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 186 NIRSLS 192
 OY 338 NIRSLS 344

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 10:30:38 2000; Maspar time 21.79 Seconds

Tabular output not generated. 944.075 Million cell updates/sec

Title: >US-09-240-675-2
Description: (1-436) from US09240675.pep
Sequence: 1 MGVVLLGATTLVAVGPMV.....KSSVPSDVCCKTKPCNTSK 436

Scoring table: TABLE uniprottable
Gap 60

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database: plr64
1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 3.711; Variance 0.436; scale 8.515

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description	Pred. No.
1	436	100.0	557 2 A32694	Interferon alpha rece	0.00e+00
2	312	71.6	545 2 S17112	Interferon alpha/beta	0.00e+00
3	16	3.7	56 2 S41602	Interferon alpha rece	1.22e-22
4	13	3.0	560 2 S27387	Interferon alpha rece	2.82e-14
5	11	2.5	590 2 A45283	Interferon alpha/beta	4.53e-09
6	8	1.8	421 2 T00676	hypothetical protein	3.98e-02
7	8	1.8	1235 2 T13710	protein-tyrosine kina	3.98e-02
8	7	1.6	11 2 B26744	megascollaklinin - gar	3.73e+00
9	7	1.6	93 2 PC4027	hypothetical protein	3.73e+00
10	7	1.6	195 1 SAVLDM	delta large antigen -	3.73e+00
11	7	1.6	234 2 B44459	troponin T, fast skel	3.73e+00
12	7	1.6	249 2 A44459	troponin T, fast skel	3.73e+00
13	7	1.6	249 2 A44327	troponin T, fast skel	3.73e+00
14	7	1.6	251 2 D31957	troponin T, skeletal	3.73e+00
15	7	1.6	257 2 B34327	troponin T, fast skel	3.73e+00
16	7	1.6	257 2 B31957	troponin T, skeletal	3.73e+00
17	7	1.6	258 2 I53021	troponin T, human	3.73e+00
18	7	1.6	263 2 C13957	troponin T, skeletal	3.73e+00
19	7	1.6	266 1 TPRBMS	troponin T, fast skel	3.73e+00
20	7	1.6	272 2 A44824	troponin T, fast skel	3.73e+00
21	7	1.6	274 2 A31957	troponin T, skeletal	3.73e+00
22	7	1.6	298 2 S75156	hypothetical protein	3.73e+00
23	7	1.6	337 2 I38500	Interferon gamma rece	3.73e+00

24	7	1.6	353 1 B26952	electron transfer fla	3.73e+00
25	7	1.6	369 1 S14071	electron transfer fla	3.73e+00
26	7	1.6	394 2 B32495	Rep-1 protein B - mou	3.73e+00
27	7	1.6	403 2 I52590	m3-B isoform - mouse	3.73e+00
28	7	1.6	423 2 T15309	hypothetical protein	3.73e+00
29	7	1.6	425 2 S14147	multifunctional purin	3.73e+00
30	7	1.6	425 2 S55684	aminimidazole ribonu	3.73e+00
31	7	1.6	426 2 A35641	5-aminimidazole ribo	3.73e+00
32	7	1.6	442 2 S74801	ammonium transport pr	3.73e+00
33	7	1.6	450 1 W2BEB4	49.2K membrane protei	3.73e+00
34	7	1.6	451 1 G63932	multidrug resistance	3.73e+00
35	7	1.6	454 2 T02100	hypothetical protein	3.73e+00
36	7	1.6	530 2 B75080	hypothetical protein	3.73e+00
37	7	1.6	563 2 B70682	probable nitrite redu	3.73e+00
38	7	1.6	594 2 C71661	penicillin-binding pr	3.73e+00
39	7	1.6	681 2 F64889	membrane protein maco	3.73e+00
40	7	1.6	698 2 G70559	probable uvrB protein	3.73e+00
41	7	1.6	929 2 A32495	Rep-1 protein, form A	3.73e+00
42	7	1.6	1051 2 A40021	Integrin VLA-3 alpha-	3.73e+00
43	7	1.6	1053 2 I55534	VLA-3 alpha subunit -	3.73e+00
44	7	1.6	1126 2 JC4019	DNA mismatch repair p	3.73e+00
45	7	1.6	1184 2 G70600	hypothetical protein	3.73e+00
46	7	1.6	1201 2 T00444	hypothetical protein	3.73e+00
47	7	1.6	1205 1 GNNY2W	genome polypotein -	3.73e+00
48	7	1.6	2205 1 GNNY27	genome polypotein -	3.73e+00
49	7	1.6	2206 2 S03822	genome polypotein -	3.73e+00
50	7	1.6	2206 2 GNNY4P	genome polypotein -	3.73e+00
51	7	1.6	2207 1 S09553	genome polypotein -	3.73e+00
52	7	1.6	2207 1 GNNY5P	genome polypotein -	3.73e+00
53	7	1.6	2214 1 A48548	genome polypotein -	3.73e+00
54	7	1.6	3744 2 S46715	hypothetical protein	3.73e+00
55	6	1.4	16 2 C49655	T-cell-receptor beta	1.97e+02
56	6	1.4	28 2 A60359	pollen allergen DG3 -	1.97e+02
57	6	1.4	30 2 S55674	cerastoxin - horn v	1.97e+02
58	6	1.4	53 2 E75136	rubredoxin (rd) PAB2	1.97e+02
59	6	1.4	53 1 RUPE	rubredoxin - Pyrococc	1.97e+02
60	6	1.4	75 2 S73297	hypothetical protein	1.97e+02
61	6	1.4	79 2 H64643	hypothetical protein	1.97e+02
62	6	1.4	80 2 T10326	lef-10 protein - Orgy	1.97e+02
63	6	1.4	84 2 S44989	dmp protein - phage T	1.97e+02
64	6	1.4	85 1 CCPB6	cytochrome c6 - Plec	1.97e+02
65	6	1.4	88 1 CCA16	cytochrome c6 - Anaba	1.97e+02
66	6	1.4	89 2 T13546	hypothetical protein	1.97e+02
67	6	1.4	93 2 A71207	hypothetical protein	1.97e+02
68	6	1.4	93 2 B27590	T-cell receptor beta	1.97e+02
69	6	1.4	103 2 E72767	hypothetical protein	1.97e+02
70	6	1.4	105 2 B30554	Ig lambda chain C reg	1.97e+02
71	6	1.4	106 2 S28239	NADH dehydrogenase (u	1.97e+02
72	6	1.4	106 2 S25416	T-cell receptor beta	1.97e+02
73	6	1.4	108 2 A72764	hypothetical protein	1.97e+02
74	6	1.4	110 2 T12499	hypothetical protein	1.97e+02
75	6	1.4	110 2 A24444	hypothetical protein	1.97e+02
76	6	1.4	111 1 CCA153	cytochrome c6, precus	1.97e+02
77	6	1.4	111 2 I39601	Cytochrome c6 - Anaba	1.97e+02
78	6	1.4	112 2 S10918	hypothetical 12K prot	1.97e+02
79	6	1.4	114 2 C72566	hypothetical protein	1.97e+02
80	6	1.4	114 2 I38313	T-cell receptor beta	1.97e+02
81	6	1.4	114 2 S17379	T-cell receptor beta	1.97e+02
82	6	1.4	115 2 D72237	lipid transfer protei	1.97e+02
83	6	1.4	116 2 T02044	hypothetical protein	1.97e+02
84	6	1.4	121 2 C71480	hypothetical protein	1.97e+02
85	6	1.4	122 2 A72025	ctf16, hypothetical pr	1.97e+02
86	6	1.4	125 2 C70637	hypothetical protein	1.97e+02
87	6	1.4	128 2 C69183	hypothetical protein	1.97e+02
88	6	1.4	129 2 G22845	hypothetical protein	1.97e+02
89	6	1.4	129 2 CCR6P	cytochrome c556 - Rio	1.97e+02
90	6	1.4	133 2 I51914	glutaryl aminopeptida	1.97e+02
91	6	1.4	134 2 D56915	fumarate hydratase, c	1.97e+02
92	6	1.4	134 2 G43868	lactate dehydrogenase	1.97e+02
93	6	1.4	136 2 I49013	thymic shared antigen	1.97e+02
94	6	1.4	137 2 B64208	hypothetical protein	1.97e+02
95	6	1.4	140 2 S36942	T-cell receptor beta	1.97e+02
96	6	1.4	141 2 I48769	Slp(w) alpha-chain -	1.97e+02

97	1.4	141	2	B41543	integrin alpha-3A cha	1.97e+02	170	6	1.4	220	2	E34012	H+-transporting ATP s	1.97e+02
98	1.4	142	2	D68891	yeak protein - Bacilli	1.97e+02	171	6	1.4	220	2	B34012	H+-transporting ATP s	1.97e+02
99	1.4	145	2	T11243	ribosomal protein L16	1.97e+02	172	6	1.4	220	2	C34012	H+-transporting ATP s	1.97e+02
100	1.4	145	2	C41543	integrin alpha-3B cha	1.97e+02	173	6	1.4	220	2	F34012	H+-transporting ATP s	1.97e+02
101	1.4	154	2	A69267	transposase homolog -	1.97e+02	174	6	1.4	221	2	JC1250	ependymin-Om-1-precu	1.97e+02
102	1.4	155	2	A42437	gastrin-releasing pep	1.97e+02	175	6	1.4	221	2	I50538	ependymin - northern	1.97e+02
103	1.4	156	2	T10140	moda.3 protein - phag	1.97e+02	176	6	1.4	221	2	T02086	zinc inducible protel	1.97e+02
104	1.4	157	2	C71060	hypothetical protein	1.97e+02	177	6	1.4	222	2	H64983	GTP:cytohydrolase I	1.97e+02
105	1.4	157	2	B69221	conserved hypothetical	1.97e+02	178	6	1.4	222	2	JC1384	beta-casein precursor	1.97e+02
106	1.4	157	2	G02355	tumor-associated memb	1.97e+02	179	6	1.4	222	2	A32979	beta-casein precursor	1.97e+02
107	1.4	158	2	S64691	a2-mating type protei	1.97e+02	180	6	1.4	223	2	T03662	H+-transporting ATP s	1.97e+02
108	1.4	159	1	CYP279	heat shock protein (c	1.97e+02	181	6	1.4	223	2	B64396	hypothetical protein	1.97e+02
109	1.4	161	2	G43255	hoxo - Alcaligenes eu	1.97e+02	182	6	1.4	223	2	I46696	CitA-4 precursor - ra	1.97e+02
110	1.4	162	1	CFRKA	C-phycocyanin alpha c	1.97e+02	183	6	1.4	223	2	S29895	GTP:cytohydrolase I	1.97e+02
111	1.4	164	2	F70894	probable transcripcto	1.97e+02	184	6	1.4	224	1	KBBOA2	beta-casein precursor	1.97e+02
112	1.4	165	2	T02833	Mov34 protein, homolog	1.97e+02	185	6	1.4	225	2	F70011	hypothetical protein	1.97e+02
113	1.4	166	2	S69527	hypothetical protein	1.97e+02	186	6	1.4	229	1	BVECTJ	trna protein - Escher	1.97e+02
114	1.4	167	1	RMSHD3	T-cell surface glycop	1.97e+02	187	6	1.4	231	2	A75103	phosphoglycolate phos	1.97e+02
115	1.4	168	2	S64830	hypothetical protein	1.97e+02	188	6	1.4	231	2	B64920	cuticlin 2 - Caenorha	1.97e+02
116	1.4	175	2	G72692	probable methylated-D	1.97e+02	189	6	1.4	231	2	S37108	ovalbumin-related x p	1.97e+02
117	1.4	176	2	C70602	hypothetical protein	1.97e+02	190	6	1.4	232	1	DXCH	hypothetical protein	1.97e+02
118	1.4	176	2	S67150	hypothetical protein	1.97e+02	191	6	1.4	234	2	S76694	H+-transporting ATP s	1.97e+02
119	1.4	177	2	B55517	hypothetical protein	1.97e+02	192	6	1.4	237	2	J01754	H+-transporting ATP s	1.97e+02
120	1.4	178	1	S73447	uracil phosphoribosyl	1.97e+02	193	6	1.4	238	2	S28758	ribosomal protein S6	1.97e+02
121	1.4	179	2	S74360	hypothetical protein	1.97e+02	194	6	1.4	239	1	R32P6E	probable glutaredoxin	1.97e+02
122	1.4	180	2	C71869	hypothetical protein	1.97e+02	195	6	1.4	243	2	A72669	complement factor D (1.97e+02
123	1.4	181	2	JE0253	trappin-7 - pig	1.97e+02	196	6	1.4	246	1	DBHU	trypsin (EC 3.4.21.4)	1.97e+02
124	1.4	181	2	T05030	cyclic lipopeptidester	1.97e+02	197	6	1.4	246	2	JQ1472	trypsin (EC 3.4.21.4)	1.97e+02
125	1.4	182	2	A70804	probable ipge protein	1.97e+02	198	6	1.4	246	2	B69311	proteasome, subunit a	1.97e+02
126	1.4	182	2	A71861	hypothetical protein	1.97e+02	199	6	1.4	246	2	J01471	trypsin (EC 3.4.21.4)	1.97e+02
127	1.4	184	2	E72586	hypothetical protein	1.97e+02	200	6	1.4	247	2	S05494	trypsin (EC 3.4.21.4)	1.97e+02
128	1.4	184	2	A70245	outer membrane protel	1.97e+02	201	6	1.4	247	1	BVECFE	mcbe protein - Escher	1.97e+02
129	1.4	184	2	D70257	outer membrane protel	1.97e+02	202	6	1.4	248	2	S55065	trypsin (EC 3.4.21.4)	1.97e+02
130	1.4	185	2	S39318	replication initiatio	1.97e+02	203	6	1.4	248	2	S55067	trypsin (EC 3.4.21.4)	1.97e+02
131	1.4	185	2	S39317	replication initiatio	1.97e+02	204	6	1.4	248	2	S55066	trypsin (EC 3.4.21.4)	1.97e+02
132	1.4	185	2	B70824	hypothetical protein	1.97e+02	205	6	1.4	249	2	H64368	trypsin (EC 3.4.21.4)	1.97e+02
133	1.4	186	2	T15643	hypothetical protein	1.97e+02	206	6	1.4	251	2	A64363	hypothetical protein	1.97e+02
134	1.4	187	2	I46650	ATPase inhibitor SPAL	1.97e+02	207	6	1.4	252	2	F73560	hypothetical protein	1.97e+02
135	1.4	187	2	G69430	transcription regulat	1.97e+02	208	6	1.4	252	2	S61142	hypothetical protein	1.97e+02
136	1.4	187	2	A70153	hypothetical protein	1.97e+02	209	6	1.4	253	2	A71648	hypothetical protein	1.97e+02
137	1.4	187	2	S50615	U6 snRNA-associated p	1.97e+02	210	6	1.4	256	2	A35340	pseudouridylyl synth	1.97e+02
138	1.4	187	2	S08418	heat shock protein gr	1.97e+02	211	6	1.4	256	2	J01144	H+-transporting ATP s	1.97e+02
139	1.4	189	2	B71855	biopolymer transport	1.97e+02	212	6	1.4	256	2	E69166	conserved hypothetical	1.97e+02
140	1.4	189	2	B64661	biopolymer transport	1.97e+02	213	6	1.4	256	2	B26720	cAMP-regulated M3L pr	1.97e+02
141	1.4	190	2	B71421	hypothetical protein	1.97e+02	214	6	1.4	259	1	S73911	protein phosphatase 2C	1.97e+02
142	1.4	191	2	A72301	VLA-2 protein - pig (1.97e+02	215	6	1.4	259	1	MMMS28	adipin (EC 3.4.21.-)	1.97e+02
143	1.4	192	2	T13106	minor tail protein gp	1.97e+02	216	6	1.4	261	2	A70002	protein kinase homo	1.97e+02
144	1.4	192	2	A70331	peptidyl-RNA hydroly	1.97e+02	217	6	1.4	262	2	C72764	hypothetical protein	1.97e+02
145	1.4	194	2	D69486	probable ribosomal pr	1.97e+02	218	6	1.4	262	2	T06600	acetyl-CoA carboxylas	1.97e+02
146	1.4	195	2	T04161	trypsin inhibitor (Bo	1.97e+02	219	6	1.4	263	2	I55608	endogenous vascular e	1.97e+02
147	1.4	195	1	R30C7	ribosomal protein S7	1.97e+02	220	6	1.4	264	2	B72462	probable lipase-prot	1.97e+02
148	1.4	195	1	SAVLI1	delta large antigen -	1.97e+02	221	6	1.4	265	2	H71105	hypothetical protein	1.97e+02
149	1.4	196	1	JC6127	RNA-binding protein t	1.97e+02	222	6	1.4	266	2	E64314	translation initiatio	1.97e+02
150	1.4	197	2	S23381	hypothetical protein	1.97e+02	223	6	1.4	266	1	IPGCA1	aggliprotein A-I pr	1.97e+02
151	1.4	199	1	S50398	ribosomal protein L13	1.97e+02	224	6	1.4	269	2	S22781	transcription factor	1.97e+02
152	1.4	199	2	S23635	gamma-coixin, 22k, pr	1.97e+02	225	6	1.4	270	2	S16579	chitinase (EC 3.2.1.1	1.97e+02
153	1.4	199	2	H70736	hypothetical protein	1.97e+02	226	6	1.4	270	2	S77191	hypothetical protein	1.97e+02
154	1.4	199	2	S67618	ribosomal protein L13	1.97e+02	227	6	1.4	273	2	H71441	hypothetical protein	1.97e+02
155	1.4	201	2	A41899	hyperosmically indu	1.97e+02	228	6	1.4	276	2	B25345	tioponin T, cardiac m	1.97e+02
156	1.4	204	2	E69764	hypothetical protein	1.97e+02	229	6	1.4	276	2	A25345	tioponin T, cardiac m	1.97e+02
157	1.4	205	1	SAVIMC	delta large antigen -	1.97e+02	230	6	1.4	276	2	H71985	panoate-beta-alanin	1.97e+02
158	1.4	207	2	JQ2167	delta large antigen -	1.97e+02	231	6	1.4	280	2	T16020	hypothetical protein	1.97e+02
159	1.4	209	2	A59068	beta-casein variant C	1.97e+02	232	6	1.4	287	2	A69186	hypothetical protein	1.97e+02
160	1.4	213	2	E72548	hypothetical protein	1.97e+02	233	6	1.4	285	2	D64448	hypothetical protein	1.97e+02
161	1.4	213	2	JC4928	histone H1x - human	1.97e+02	234	6	1.4	285	2	A25561	tiopomyosin II, muscl	1.97e+02
162	1.4	214	1	SAVIDV	delta large antigen -	1.97e+02	235	6	1.4	285	2	C25242	tiopomyosin, exon 9D	1.97e+02
163	1.4	214	1	SAVIDV	delta large antigen -	1.97e+02	236	6	1.4	286	2	B25242	tiopomyosin, exon 9C	1.97e+02
164	1.4	216	2	T12727	hypothetical protein	1.97e+02	237	6	1.4	286	2	A25242	tiopomyosin, exon 9B	1.97e+02
165	1.4	218	2	G71722	probable glutamine tr	1.97e+02	238	6	1.4	290	2	G70397	hypothetical protein	1.97e+02
166	1.4	218	1	A43522	23K integral membrane	1.97e+02	239	6	1.4	292	2	C65070	hypothetical protein	1.97e+02
167	1.4	218	1	A40181	23K integral membrane	1.97e+02	240	6	1.4	293	2	H71949	hypothetical protein	1.97e+02
168	1.4	218	1	B70645	probable fuculose-1-	1.97e+02	241	6	1.4	293	2	F64558	conserved hypothetical	1.97e+02
169	1.4	220	2	D34012	H+-transporting ATP s	1.97e+02	242	6	1.4	295	2	S59439	probable membrane pro	1.97e+02

243	6	1.4	298	2	S75972	hypothetical protein	1.97e+02	316	6	1.4	379	2	S14885	hypothetical protein	1.97e+02
244	6	1.4	299	1	G64143	hypothetical protein	1.97e+02	317	6	1.4	380	2	H70590	hypothetical protein	1.97e+02
245	6	1.4	299	1	S32896	hypothetical protein	1.97e+02	318	6	1.4	382	2	D70587	hypothetical protein	1.97e+02
246	6	1.4	300	2	S56545	hypothetical protein	1.97e+02	319	6	1.4	383	1	A48222	hypothetical protein	1.97e+02
247	6	1.4	300	2	S25706	hypothetical protein	1.97e+02	320	6	1.4	384	1	S17957	hypothetical protein	1.97e+02
248	6	1.4	301	2	D48326	hypothetical protein	1.97e+02	321	6	1.4	384	1	S00516	hypothetical protein	1.97e+02
249	6	1.4	302	1	S60777	hypothetical protein	1.97e+02	322	6	1.4	384	2	S20303	hypothetical protein	1.97e+02
250	6	1.4	302	1	ORBP15	hypothetical protein	1.97e+02	323	6	1.4	388	2	S51671	hypothetical protein	1.97e+02
251	6	1.4	303	2	JC2410	hypothetical protein	1.97e+02	324	6	1.4	390	2	S18202	hypothetical protein	1.97e+02
252	6	1.4	304	2	S02284	hypothetical protein	1.97e+02	325	6	1.4	390	2	A36737	hypothetical protein	1.97e+02
253	6	1.4	304	2	I49586	hypothetical protein	1.97e+02	326	6	1.4	390	2	S18201	hypothetical protein	1.97e+02
254	6	1.4	305	2	F72574	hypothetical protein	1.97e+02	327	6	1.4	391	2	D72653	hypothetical protein	1.97e+02
255	6	1.4	305	2	D69199	hypothetical protein	1.97e+02	328	6	1.4	391	2	S74688	hypothetical protein	1.97e+02
256	6	1.4	306	2	I46903	hypothetical protein	1.97e+02	329	6	1.4	391	2	A70663	hypothetical protein	1.97e+02
257	6	1.4	307	2	T09923	hypothetical protein	1.97e+02	330	6	1.4	392	2	I39521	hypothetical protein	1.97e+02
258	6	1.4	308	2	E64340	hypothetical protein	1.97e+02	331	6	1.4	392	2	E72219	hypothetical protein	1.97e+02
259	6	1.4	308	2	S11151	hypothetical protein	1.97e+02	332	6	1.4	393	2	T08203	hypothetical protein	1.97e+02
260	6	1.4	312	2	S24419	hypothetical protein	1.97e+02	333	6	1.4	393	2	C71240	hypothetical protein	1.97e+02
261	6	1.4	313	2	S59448	hypothetical protein	1.97e+02	334	6	1.4	394	2	S48522	hypothetical protein	1.97e+02
262	6	1.4	316	2	WZBE41	hypothetical protein	1.97e+02	335	6	1.4	396	2	P00813	hypothetical protein	1.97e+02
263	6	1.4	316	2	G70110	hypothetical protein	1.97e+02	336	6	1.4	397	2	H70789	hypothetical protein	1.97e+02
264	6	1.4	316	2	B47157	hypothetical protein	1.97e+02	337	6	1.4	398	2	A71482	hypothetical protein	1.97e+02
265	6	1.4	316	2	E70664	hypothetical protein	1.97e+02	338	6	1.4	398	2	T15846	hypothetical protein	1.97e+02
266	6	1.4	316	2	A47157	hypothetical protein	1.97e+02	339	6	1.4	398	2	J01059	hypothetical protein	1.97e+02
267	6	1.4	316	2	T09591	hypothetical protein	1.97e+02	340	6	1.4	399	1	A26916	hypothetical protein	1.97e+02
268	6	1.4	317	2	A69626	hypothetical protein	1.97e+02	341	6	1.4	400	2	JC2473	hypothetical protein	1.97e+02
269	6	1.4	319	2	A70605	hypothetical protein	1.97e+02	342	6	1.4	401	1	B35177	hypothetical protein	1.97e+02
270	6	1.4	319	2	S79699	hypothetical protein	1.97e+02	343	6	1.4	401	2	A48423	hypothetical protein	1.97e+02
271	6	1.4	322	2	E71137	hypothetical protein	1.97e+02	344	6	1.4	402	2	S56595	hypothetical protein	1.97e+02
272	6	1.4	322	2	S38091	hypothetical protein	1.97e+02	345	6	1.4	403	2	B65989	hypothetical protein	1.97e+02
273	6	1.4	323	2	D70125	hypothetical protein	1.97e+02	346	6	1.4	405	2	I39062	hypothetical protein	1.97e+02
274	6	1.4	323	2	A55773	hypothetical protein	1.97e+02	347	6	1.4	406	1	A48495	hypothetical protein	1.97e+02
275	6	1.4	324	2	D48423	hypothetical protein	1.97e+02	348	6	1.4	407	2	H72573	hypothetical protein	1.97e+02
276	6	1.4	324	2	I50125	hypothetical protein	1.97e+02	349	6	1.4	408	2	S58131	hypothetical protein	1.97e+02
277	6	1.4	325	2	E64998	hypothetical protein	1.97e+02	350	6	1.4	409	2	F72504	hypothetical protein	1.97e+02
278	6	1.4	327	2	C71146	hypothetical protein	1.97e+02	351	6	1.4	411	2	B69886	hypothetical protein	1.97e+02
279	6	1.4	327	2	B65180	hypothetical protein	1.97e+02	352	6	1.4	409	2	E70667	hypothetical protein	1.97e+02
280	6	1.4	330	2	C56931	hypothetical protein	1.97e+02	353	6	1.4	412	1	K4HND	hypothetical protein	1.97e+02
281	6	1.4	333	2	B64085	hypothetical protein	1.97e+02	354	6	1.4	413	2	S46109	hypothetical protein	1.97e+02
282	6	1.4	333	2	E75183	hypothetical protein	1.97e+02	355	6	1.4	416	2	A56486	hypothetical protein	1.97e+02
283	6	1.4	335	2	D71275	hypothetical protein	1.97e+02	356	6	1.4	417	2	T12385	hypothetical protein	1.97e+02
284	6	1.4	336	1	QOBE40	hypothetical protein	1.97e+02	357	6	1.4	417	2	JM0068	hypothetical protein	1.97e+02
285	6	1.4	337	2	G71869	hypothetical protein	1.97e+02	358	6	1.4	421	2	B64819	hypothetical protein	1.97e+02
286	6	1.4	339	2	S20880	hypothetical protein	1.97e+02	359	6	1.4	422	2	S65604	hypothetical protein	1.97e+02
287	6	1.4	343	1	A57014	hypothetical protein	1.97e+02	360	6	1.4	425	2	S76717	hypothetical protein	1.97e+02
288	6	1.4	343	1	T15192	hypothetical protein	1.97e+02	361	6	1.4	426	2	T16406	hypothetical protein	1.97e+02
289	6	1.4	344	2	C69453	hypothetical protein	1.97e+02	362	6	1.4	426	2	E70058	hypothetical protein	1.97e+02
290	6	1.4	344	2	S30706	hypothetical protein	1.97e+02	363	6	1.4	426	2	F64419	hypothetical protein	1.97e+02
291	6	1.4	346	2	C65066	hypothetical protein	1.97e+02	364	6	1.4	428	2	S61623	hypothetical protein	1.97e+02
292	6	1.4	346	2	S42423	hypothetical protein	1.97e+02	365	6	1.4	431	2	G75017	hypothetical protein	1.97e+02
293	6	1.4	346	2	A03308	hypothetical protein	1.97e+02	366	6	1.4	431	2	B75203	hypothetical protein	1.97e+02
294	6	1.4	348	2	S77104	hypothetical protein	1.97e+02	367	6	1.4	432	2	B65190	hypothetical protein	1.97e+02
295	6	1.4	349	2	B49412	hypothetical protein	1.97e+02	368	6	1.4	432	2	T16639	hypothetical protein	1.97e+02
296	6	1.4	349	2	B35114	hypothetical protein	1.97e+02	369	6	1.4	433	2	T04594	hypothetical protein	1.97e+02
297	6	1.4	349	2	S00482	hypothetical protein	1.97e+02	370	6	1.4	433	1	D56CHS	hypothetical protein	1.97e+02
298	6	1.4	349	2	T02506	hypothetical protein	1.97e+02	371	6	1.4	437	2	S70546	hypothetical protein	1.97e+02
299	6	1.4	350	2	I73338	hypothetical protein	1.97e+02	372	6	1.4	437	1	A45569	hypothetical protein	1.97e+02
300	6	1.4	351	2	C72508	hypothetical protein	1.97e+02	373	6	1.4	438	2	S30769	hypothetical protein	1.97e+02
301	6	1.4	352	2	E70797	hypothetical protein	1.97e+02	374	6	1.4	439	2	T15748	hypothetical protein	1.97e+02
302	6	1.4	353	2	B70358	hypothetical protein	1.97e+02	375	6	1.4	441	2	T82242	hypothetical protein	1.97e+02
303	6	1.4	355	2	A41314	hypothetical protein	1.97e+02	376	6	1.4	443	2	T18603	hypothetical protein	1.97e+02
304	6	1.4	358	2	C72643	hypothetical protein	1.97e+02	377	6	1.4	444	2	T12297	hypothetical protein	1.97e+02
305	6	1.4	359	2	A47159	hypothetical protein	1.97e+02	378	6	1.4	445	2	T16025	hypothetical protein	1.97e+02
306	6	1.4	360	1	A49188	hypothetical protein	1.97e+02	379	6	1.4	448	2	S03127	hypothetical protein	1.97e+02
307	6	1.4	363	1	WZBE44	hypothetical protein	1.97e+02	380	6	1.4	449	2	JC5391	hypothetical protein	1.97e+02
308	6	1.4	363	1	T05624	hypothetical protein	1.97e+02	381	6	1.4	449	2	C71156	hypothetical protein	1.97e+02
309	6	1.4	368	2	C72260	hypothetical protein	1.97e+02	382	6	1.4	450	2	E72615	hypothetical protein	1.97e+02
310	6	1.4	369	2	S37314	hypothetical protein	1.97e+02	383	6	1.4	450	1	I03YMC	hypothetical protein	1.97e+02
311	6	1.4	370	2	S70157	hypothetical protein	1.97e+02	384	6	1.4	451	1	S33816	hypothetical protein	1.97e+02
312	6	1.4	373	1	H72756	hypothetical protein	1.97e+02	385	6	1.4	451	2	F66671	hypothetical protein	1.97e+02
313	6	1.4	374	1	S7FURP	hypothetical protein	1.97e+02	386	6	1.4	452	2	F69294	hypothetical protein	1.97e+02
314	6	1.4	378	2	D70515	hypothetical protein	1.97e+02	387	6	1.4	452	2	C72295	hypothetical protein	1.97e+02
315	6	1.4	378	2	S00842	hypothetical protein	1.97e+02	388	6	1.4	458	2	G69123	hypothetical protein	1.97e+02

389	6	1.4	458	2	T11528	NADH dehydrogenase (u	1.97e+02
390	6	1.4	458	2	A71467	probable phosphogluco	1.97e+02
391	6	1.4	458	2	B44407	macrophage scavenger	1.97e+02
392	6	1.4	459	2	S47879	NADH dehydrogenase (u	1.97e+02
393	6	1.4	459	2	T11866	NADH dehydrogenase	1.97e+02
394	6	1.4	459	2	S06607	23S rRNA intron 2 pro	1.97e+02
395	6	1.4	459	2	DESPSP	dihydropolipamide dehy	1.97e+02
396	6	1.4	459	2	T11372	NADH dehydrogenase su	1.97e+02
397	6	1.4	459	2	T11411	NADH dehydrogenase su	1.97e+02
398	6	1.4	462	2	S29503	multi protein - Clostr	1.97e+02
399	6	1.4	462	2	T08199	hypothetical protein	1.97e+02
400	6	1.4	463	2	I40661	methylaspartate mutas	1.97e+02
401	6	1.4	463	2	S75889	hypothetical protein	1.97e+02
402	6	1.4	464	2	T15161	hypothetical protein	1.97e+02
403	6	1.4	470	2	H72105	dicarboxylase translo	1.97e+02
404	6	1.4	473	2	S40507	endoglucanase - rumen	1.97e+02
405	6	1.4	473	2	S64014	probable transport pr	1.97e+02
406	6	1.4	475	1	A56824	dihydropolipamide dehy	1.97e+02
407	6	1.4	478	2	H70474	ATP synthase F1 beta	1.97e+02
408	6	1.4	479	2	B69399	activator 1, replicat	1.97e+02
409	6	1.4	480	2	D75050	hypothetical protein	1.97e+02
410	6	1.4	481	2	S69808	lincomycin resistance	1.97e+02
411	6	1.4	481	2	JE0377	P70 S6 Kinase (EC 2.7	1.97e+02
412	6	1.4	482	2	G71603	chromatin-binding pro	1.97e+02
413	6	1.4	483	2	JH0532	catalase (EC 1.11.1.6	1.97e+02
414	6	1.4	484	2	S58868	G protein-coupled rec	1.97e+02
415	6	1.4	484	2	S58869	G protein-coupled rec	1.97e+02
416	6	1.4	485	2	E75015	IMP dehydrogenase (EC	1.97e+02
417	6	1.4	485	2	I39557	ribulose-bisphosphate	1.97e+02
418	6	1.4	486	2	RKRRL	ribulose-bisphosphate	1.97e+02
419	6	1.4	486	2	I39559	ribulose-bisphosphate	1.97e+02
420	6	1.4	487	1	RKALE	ribulose-bisphosphate	1.97e+02
421	6	1.4	487	2	F70765	hypothetical protein	1.97e+02
422	6	1.4	488	1	RKQXIX	ribulose-bisphosphate	1.97e+02
423	6	1.4	489	1	NIBCAT	nitrogenase (EC 1.18	1.97e+02
424	6	1.4	489	2	I51532	potassium channel - A	1.97e+02
425	6	1.4	492	2	A64498	hypothetical protein	1.97e+02
426	6	1.4	492	2	S49147	ERF-2 protein - human	1.97e+02
427	6	1.4	492	2	A34272	lecithinase 2 - human	1.97e+02
428	6	1.4	494	2	A27442	triacylglycerol lipas	1.97e+02
429	6	1.4	494	2	S10483	lipase, hepatic - rat	1.97e+02
430	6	1.4	495	2	I57680	potassium channel KCN	1.97e+02
431	6	1.4	495	2	B39113	potassium channel KVI	1.97e+02
432	6	1.4	495	2	A40090	potassium channel KVI	1.97e+02
433	6	1.4	495	2	G69360	probable ribose ABC t	1.97e+02
434	6	1.4	505	2	S54302	zinc transporter Znt-	1.97e+02
435	6	1.4	505	2	SYECKU	lysine-tRNA ligase (1.97e+02
436	6	1.4	507	2	S54303	zinc transport protei	1.97e+02
437	6	1.4	508	2	A70125	UDP-N-acetylmutamoyla	1.97e+02
438	6	1.4	509	2	S76731	hypothetical protein	1.97e+02
439	6	1.4	509	2	C70624	probable two componen	1.97e+02
440	6	1.4	521	2	T01923	hypothetical protein	1.97e+02
441	6	1.4	521	2	T05684	hypothetical protein	1.97e+02
442	6	1.4	527	2	T03427	hypothetical protein	1.97e+02
443	6	1.4	527	2	C70130	glycerol-3-phosphate	1.97e+02
444	6	1.4	527	2	S64060	probable membrane pro	1.97e+02
445	6	1.4	528	2	A70915	conserved hypothetical	1.97e+02
446	6	1.4	529	2	F69989	conserved hypothetical	1.97e+02
447	6	1.4	529	2	YRH01	monophenol monooxygen	1.97e+02
448	6	1.4	530	2	NMBE2T	anthranilate synthase	1.97e+02
449	6	1.4	530	2	C38497	anthranilate synthase	1.97e+02
450	6	1.4	531	1	NNEC2	anthranilate synthase	1.97e+02
451	6	1.4	533	2	I49736	monophenol monooxygen	1.97e+02
452	6	1.4	533	2	YRMSCS	transposase - rice bl	1.97e+02
453	6	1.4	535	2	S51577	transposase - rice bl	1.97e+02
454	6	1.4	536	2	H72535	hypothetical protein	1.97e+02
455	6	1.4	536	2	A36395	spore wall maturation	1.97e+02
456	6	1.4	536	2	T04234	calmodulin-binding pr	1.97e+02
457	6	1.4	537	2	A46611	myosin-binding protei	1.97e+02
458	6	1.4	538	2	S76481	hypothetical protein	1.97e+02
459	6	1.4	540	2	B64829	membrane protein b089	1.97e+02
460	6	1.4	541	2	T01394	hypothetical protein	1.97e+02
461	6	1.4	542	1	S25276	D-alanine/glycine tra	1.97e+02
462	6	1.4	545	2	JU0341	intercellular adhesio	1.97e+02
463	6	1.4	548	1	YCEC	acetoacetate synthase	1.97e+02
464	6	1.4	551	1	Q0V225	N3L protein - vaccini	1.97e+02
465	6	1.4	551	2	A36848	N3L protein - variola	1.97e+02
466	6	1.4	552	2	S71811	probable transcrip	1.97e+02
467	6	1.4	552	1	OREBDT	aspartate chemorecept	1.97e+02
468	6	1.4	552	2	C45710	R transactivator homo	1.97e+02
469	6	1.4	554	2	G72361	hypothetical protein	1.97e+02
470	6	1.4	554	2	S59235	hypothetical protein	1.97e+02
471	6	1.4	555	2	F72555	probable molybdenum t	1.97e+02
472	6	1.4	555	2	F72111	fructose-6-phosphot	1.97e+02
473	6	1.4	557	2	T03137	minor capsid protein	1.97e+02
474	6	1.4	557	2	B28182	hemolysin B - Serrat	1.97e+02
475	6	1.4	559	1	A35029	t-plasminogen activat	1.97e+02
476	6	1.4	559	1	A29941	t-plasminogen activat	1.97e+02
477	6	1.4	564	2	S01110	potassium channel pro	1.97e+02
478	6	1.4	564	2	E69860	hypothetical protein	1.97e+02
479	6	1.4	566	2	S54629	hypothetical protein	1.97e+02
480	6	1.4	568	2	S42225	major envelope glycop	1.97e+02
481	6	1.4	568	2	T16024	hypothetical protein	1.97e+02
482	6	1.4	570	1	C69985	probable DNA-dependen	1.97e+02
483	6	1.4	572	1	S28762	gene DBP730 protein -	1.97e+02
484	6	1.4	573	2	B43675	64k protein - intercl	1.97e+02
485	6	1.4	573	2	S12838	Ig mu chain precursor	1.97e+02
486	6	1.4	574	2	S37762	225k protein - Babesi	1.97e+02
487	6	1.4	574	2	B29677	complement C9 precurs	1.97e+02
488	6	1.4	574	2	T05002	probable gamma-glutam	1.97e+02
489	6	1.4	575	2	JH0827	glutamate decarboxyla	1.97e+02
490	6	1.4	575	2	T12896	probable single-stran	1.97e+02
491	6	1.4	581	2	T04844	probable serine/threo	1.97e+02
492	6	1.4	589	2	S60159	serine/threonine-spec	1.97e+02
493	6	1.4	591	2	S33078	G1L protein - variola	1.97e+02
494	6	1.4	591	2	F42511	G1L protein - vaccini	1.97e+02
495	6	1.4	593	2	F64523	hypothetical protein	1.97e+02
496	6	1.4	594	2	S36502	LI protein (alternat	1.97e+02
497	6	1.4	599	2	S64136	methylaspartatehyro	1.97e+02
498	6	1.4	601	2	G70983	probable glycosyl hyd	1.97e+02
499	6	1.4	602	2	A44409	gamma-aminobutyric ac	1.97e+02
500	6	1.4	602	2	A45078	gamma-aminobutyric ac	1.97e+02
501	6	1.4	604	2	T12651	NADH dehydrogenase su	1.97e+02
502	6	1.4	605	2	E71441	hypothetical protein	1.97e+02
503	6	1.4	606	2	S14942	RNA helicase SPB - y	1.97e+02
504	6	1.4	606	2	B69805	conserved hypothetical	1.97e+02
505	6	1.4	609	2	I38596	calcium-activated pot	1.97e+02
506	6	1.4	616	2	A200479	potassium channel pro	1.97e+02
507	6	1.4	619	2	S71114	s/t protein kinase -	1.97e+02
508	6	1.4	620	2	T16657	hypothetical protein	1.97e+02
509	6	1.4	626	2	S53871	pne1 Y protein - mou	1.97e+02
510	6	1.4	627	2	E70122	flagellar hook-associ	1.97e+02
511	6	1.4	627	2	S50583	hypothetical protein	1.97e+02
512	6	1.4	629	2	A46500	ly-9.2 antigen - mous	1.97e+02
513	6	1.4	629	2	S42629	keratin K3 - rabbit	1.97e+02
514	6	1.4	632	2	T00325	hypothetical protein	1.97e+02
515	6	1.4	632	2	A25784	hypothetical 70k prot	1.97e+02
516	6	1.4	633	2	C70358	hypothetical protein	1.97e+02
517	6	1.4	633	2	S57714	csbp protein - Clostr	1.97e+02
518	6	1.4	638	1	KORRPL	plasma kallikrein (EC	1.97e+02
519	6	1.4	638	1	KOHUP	plasma kallikrein (EC	1.97e+02
520	6	1.4	638	2	S36546	El protein - human pa	1.97e+02
521	6	1.4	639	2	S48959	mitochondrial outer m	1.97e+02
522	6	1.4	642	2	I39839	beta-hexosaminidase h	1.97e+02
523	6	1.4	643	2	B75055	hypothetical protein	1.97e+02
524	6	1.4	643	2	S00480	potassium channel pro	1.97e+02
525	6	1.4	647	1	ESRCPC	2',3'-cyclic-nucleot	1.97e+02
526	6	1.4	649	2	S33813	kinesin light chain -	1.97e+02
527	6	1.4	651	2	S35708	NADH oxidase - Thermo	1.97e+02
528	6	1.4	651	2	S25102	NADH oxidase - Thermo	1.97e+02
529	6	1.4	652	1	S52695	2',3'-cyclic-nucleot	1.97e+02
530	6	1.4	653	2	C70742	probable rsbu protein	1.97e+02
531	6	1.4	653	2	T16553	hypothetical protein	1.97e+02
532	6	1.4	656	2	JH0193	potassium channel sha	1.97e+02
533	6	1.4	656	2	A64208	exonuclease ABC chal	1.97e+02
534	6	1.4	656	2	A71916	DNA ligase - Helicoba	1.97e+02

535	6	1.4	657	2	S73946	excinuclease ABC chait	1.97e+02	608	6	1.4	700	2	T13661	NADH dehydrogenase su	1.97e+02
536	6	1.4	657	2	S25184	cspl1 protein - Coryne	1.97e+02	609	6	1.4	701	2	T12296	NADH dehydrogenase su	1.97e+02
537	6	1.4	658	2	A64584	hypothetical protein	1.97e+02	610	6	1.4	702	2	T13708	NADH dehydrogenase su	1.97e+02
538	6	1.4	660	2	S16159	dnak-type molecular c	1.97e+02	611	6	1.4	702	2	A34434	atp1p1r1n alpha chait	1.97e+02
539	6	1.4	661	2	A23398	hypothetical protein c	1.97e+02	612	6	1.4	704	2	T13729	NADH dehydrogenase su	1.97e+02
540	6	1.4	664	2	C71106	hypothetical protein	1.97e+02	613	6	1.4	704	2	T13581	NADH dehydrogenase su	1.97e+02
541	6	1.4	664	2	OKHOAP	alcohol oxidase (EC 1	1.97e+02	614	6	1.4	705	2	T12152	NADH dehydrogenase su	1.97e+02
542	6	1.4	667	2	S74254	homeotic protein six5	1.97e+02	615	6	1.4	705	2	T13459	NADH dehydrogenase su	1.97e+02
543	6	1.4	667	2	T13566	tail protein - phage	1.97e+02	616	6	1.4	706	2	C71929	hypothetical protein	1.97e+02
544	6	1.4	669	2	D70369	ATP-dependent DNA hel	1.97e+02	617	6	1.4	711	2	B64169	phosphate acetyltrans	1.97e+02
545	6	1.4	670	2	T02092	beta-fructofuranosida	1.97e+02	618	6	1.4	716	2	E66772	peptide-binding pr	1.97e+02
546	6	1.4	675	2	S46952	phosphotransferase sy	1.97e+02	619	6	1.4	718	2	T05840	subtilisin-like prote	1.97e+02
547	6	1.4	677	2	S33814	kinesin light chain -	1.97e+02	620	6	1.4	719	2	T13793	NADH dehydrogenase su	1.97e+02
548	6	1.4	681	2	T13566	NADH dehydrogenase	1.97e+02	621	6	1.4	719	2	T139815	NADH dehydrogenase su	1.97e+02
549	6	1.4	681	2	S73550	DNA polymerase III ga	1.97e+02	622	6	1.4	719	2	T10590	insecticidal protein	1.97e+02
550	6	1.4	682	2	T12715	NADH dehydrogenase su	1.97e+02	623	6	1.4	719	2	T10590	insecticidal protein	1.97e+02
551	6	1.4	682	2	T12294	NADH dehydrogenase	1.97e+02	624	6	1.4	719	2	S25383	insecticidal protein	1.97e+02
552	6	1.4	683	2	T12295	NADH dehydrogenase	1.97e+02	625	6	1.4	721	2	T12212	parasporal crystal pr	1.97e+02
553	6	1.4	683	2	T12123	NADH dehydrogenase	1.97e+02	626	6	1.4	725	2	JC5016	NADH dehydrogenase	1.97e+02
554	6	1.4	684	2	T13491	NADH dehydrogenase	1.97e+02	627	6	1.4	726	2	T12216	hyaluronan receptor	1.97e+02
555	6	1.4	684	2	T12151	NADH dehydrogenase	1.97e+02	628	6	1.4	726	2	T12215	NADH dehydrogenase	1.97e+02
556	6	1.4	684	2	T13695	NADH dehydrogenase su	1.97e+02	629	6	1.4	727	2	T12221	NADH dehydrogenase	1.97e+02
557	6	1.4	686	2	T13234	NADH dehydrogenase	1.97e+02	630	6	1.4	728	2	S04641	NADH dehydrogenase	1.97e+02
558	6	1.4	686	2	T13252	NADH dehydrogenase	1.97e+02	631	6	1.4	728	2	T13794	NADH dehydrogenase	1.97e+02
559	6	1.4	686	2	T13235	NADH dehydrogenase	1.97e+02	632	6	1.4	729	2	T12227	NADH dehydrogenase	1.97e+02
560	6	1.4	686	2	T13768	NADH dehydrogenase	1.97e+02	633	6	1.4	730	2	T12224	NADH dehydrogenase	1.97e+02
561	6	1.4	686	2	T13766	NADH dehydrogenase	1.97e+02	634	6	1.4	731	2	T14231	NADH dehydrogenase	1.97e+02
562	6	1.4	686	2	S33815	kinesin light chain 1	1.97e+02	635	6	1.4	731	2	T12226	NADH dehydrogenase	1.97e+02
563	6	1.4	686	2	T10969	DNA topoisomerase (AT	1.97e+02	636	6	1.4	732	2	T14233	NADH dehydrogenase	1.97e+02
564	6	1.4	686	2	S36727	kinesin light chain 1	1.97e+02	637	6	1.4	732	2	T13814	NADH dehydrogenase	1.97e+02
565	6	1.4	687	2	D57713	chloride channel ClC-	1.97e+02	638	6	1.4	732	2	T12194	NADH dehydrogenase	1.97e+02
566	6	1.4	688	2	T13242	NADH dehydrogenase	1.97e+02	639	6	1.4	733	2	T12213	NADH dehydrogenase	1.97e+02
567	6	1.4	688	2	T13237	NADH dehydrogenase	1.97e+02	640	6	1.4	734	2	T13785	NADH dehydrogenase	1.97e+02
568	6	1.4	688	2	T13243	NADH dehydrogenase	1.97e+02	641	6	1.4	735	2	E69139	hypothetical protein	1.97e+02
569	6	1.4	688	2	T13248	NADH dehydrogenase	1.97e+02	642	6	1.4	736	2	T12218	NADH dehydrogenase	1.97e+02
570	6	1.4	688	2	T13253	NADH dehydrogenase	1.97e+02	643	6	1.4	736	2	T12217	NADH dehydrogenase	1.97e+02
571	6	1.4	688	2	T13278	NADH dehydrogenase	1.97e+02	644	6	1.4	736	2	T12214	NADH dehydrogenase	1.97e+02
572	6	1.4	688	2	T09604	NADH dehydrogenase	1.97e+02	645	6	1.4	736	2	E71414	NADH dehydrogenase	1.97e+02
573	6	1.4	688	2	T13249	NADH dehydrogenase	1.97e+02	646	6	1.4	736	2	T12225	NADH dehydrogenase	1.97e+02
574	6	1.4	688	2	T13373	NADH dehydrogenase	1.97e+02	647	6	1.4	737	2	T12193	NADH dehydrogenase	1.97e+02
575	6	1.4	688	2	T13282	NADH dehydrogenase	1.97e+02	648	6	1.4	738	2	T14230	NADH dehydrogenase	1.97e+02
576	6	1.4	688	2	T09836	NADH dehydrogenase	1.97e+02	649	6	1.4	738	2	T12192	NADH dehydrogenase	1.97e+02
577	6	1.4	689	2	T13280	NADH dehydrogenase	1.97e+02	650	6	1.4	740	2	T12223	NADH dehydrogenase	1.97e+02
578	6	1.4	689	2	T13681	NADH dehydrogenase su	1.97e+02	651	6	1.4	740	2	T12753	NADH dehydrogenase	1.97e+02
579	6	1.4	690	2	T12763	NADH dehydrogenase	1.97e+02	652	6	1.4	740	2	DENTN5	NADH dehydrogenase	1.97e+02
580	6	1.4	691	2	S28222	myeloperoxidase (EC 1	1.97e+02	653	6	1.4	741	2	T13791	NADH dehydrogenase	1.97e+02
581	6	1.4	692	2	T12293	NADH dehydrogenase	1.97e+02	654	6	1.4	742	2	VGBERT	glycoprotein H precu	1.97e+02
582	6	1.4	693	2	T12587	NADH dehydrogenase su	1.97e+02	655	6	1.4	743	2	VGBERT	glycoprotein H precu	1.97e+02
583	6	1.4	693	2	T12587	NADH dehydrogenase su	1.97e+02	656	6	1.4	743	2	VGBERT	glycoprotein H precu	1.97e+02
584	6	1.4	696	2	S44912	hypothetical protein	1.97e+02	657	6	1.4	747	2	S47327	chloride channel prot	1.97e+02
585	6	1.4	697	2	T13754	NADH dehydrogenase	1.97e+02	658	6	1.4	747	2	S47327	gene clc4 protein -	1.97e+02
586	6	1.4	697	2	T13754	large T antigen - lym	1.97e+02	659	6	1.4	755	2	W2BE45	gene 45 protein - hum	1.97e+02
587	6	1.4	698	2	T12563	NADH dehydrogenase su	1.97e+02	660	6	1.4	760	2	A5174	eye cell development	1.97e+02
588	6	1.4	698	2	T12560	NADH dehydrogenase su	1.97e+02	661	6	1.4	760	2	A5174	eye cell development	1.97e+02
589	6	1.4	698	2	T12559	NADH dehydrogenase su	1.97e+02	662	6	1.4	762	2	T137242	chloride channel	1.97e+02
590	6	1.4	698	2	T12565	NADH dehydrogenase su	1.97e+02	663	6	1.4	762	2	NNNC2	anthranilate synthase	1.97e+02
591	6	1.4	698	2	T12564	NADH dehydrogenase su	1.97e+02	664	6	1.4	763	2	A29562	PKR1 protein - yeast	1.97e+02
592	6	1.4	698	2	T12567	NADH dehydrogenase su	1.97e+02	665	6	1.4	769	2	T05839	subtilisin-like prote	1.97e+02
593	6	1.4	698	2	T12569	NADH dehydrogenase su	1.97e+02	666	6	1.4	772	2	T05838	subtilisin-like prote	1.97e+02
594	6	1.4	698	2	T12590	NADH dehydrogenase su	1.97e+02	667	6	1.4	773	2	H70108	phenylalanine--RNA 1	1.97e+02
595	6	1.4	698	2	T12586	NADH dehydrogenase su	1.97e+02	668	6	1.4	790	2	H71509	phenylalanine--RNA 1	1.97e+02
596	6	1.4	698	2	T12586	NADH dehydrogenase su	1.97e+02	669	6	1.4	806	2	T08932	retrovirus-related po	1.97e+02
597	6	1.4	698	2	T12586	NADH dehydrogenase su	1.97e+02	670	6	1.4	814	2	GMSIP	hypothetical protein	1.97e+02
598	6	1.4	698	2	T12586	NADH dehydrogenase su	1.97e+02	671	6	1.4	815	2	H69775	hypothetical protein	1.97e+02
599	6	1.4	699	2	T13772	NADH dehydrogenase su	1.97e+02	672	6	1.4	817	2	S53921	hypothetical protein	1.97e+02
600	6	1.4	699	2	T13778	NADH dehydrogenase su	1.97e+02	673	6	1.4	826	2	F64746	probable membrane pro	1.97e+02
601	6	1.4	699	2	G70142	DNA helicase (uvrD) h	1.97e+02	674	6	1.4	830	2	T08556	hypothetical protein	1.97e+02
602	6	1.4	700	2	T13470	NADH dehydrogenase su	1.97e+02	675	6	1.4	830	2	A57060	setine/threonine-spec	1.97e+02
603	6	1.4	700	2	T13726	NADH dehydrogenase su	1.97e+02	676	6	1.4	830	2	B44047	glycoprotein B precu	1.97e+02
604	6	1.4	700	2	T13763	NADH dehydrogenase su	1.97e+02	677	6	1.4	831	2	A44047	glycoprotein B precu	1.97e+02
605	6	1.4	700	2	T13702	NADH dehydrogenase su	1.97e+02	678	6	1.4	831	2	S39835	hypothetical protein	1.97e+02
606	6	1.4	700	2	T13668	NADH dehydrogenase su	1.97e+02	679	6	1.4	839	2	G71659	translation initiatio	1.97e+02
607	6	1.4	700	2	T12589	NADH dehydrogenase su	1.97e+02	680	6	1.4	840	2	H71114	hypothetical protein	1.97e+02
														probable cell divisio	1.97e+02

681	6	1.4	842	2	T05400	hypothetical protein	1.97e+02	734	6	1.4	1335	2	S62497	hypothetical protein	1.97e+02
682	6	1.4	842	2	T16198	hypothetical protein	1.97e+02	735	6	1.4	1332	2	F69732	p53 prophage ORF xkd	1.97e+02
683	6	1.4	842	2	T50159	anion transporter - c	1.97e+02	756	6	1.4	1358	2	A29930	SIR4 prophage - yeast	1.97e+02
684	6	1.4	848	2	A43810	band 3 anion transport	1.97e+02	757	6	1.4	1379	2	JC5778	apoptosis signal-regu	1.97e+02
685	6	1.4	862	1	A49346	aldehyde dehydrogenas	1.97e+02	758	6	1.4	1391	2	S50608	hypothetical protein	1.97e+02
686	6	1.4	869	1	S45757	replication licensing	1.97e+02	759	6	1.4	1429	2	S06434	hypothetical protein	1.97e+02
687	6	1.4	869	2	S49844	probable membrane pro	1.97e+02	760	6	1.4	1444	1	A30588	homeotic protein lin	1.97e+02
688	6	1.4	872	2	B75073	ATP-dependent RNA hel	1.97e+02	761	6	1.4	1445	1	A30588	140K adhesin precursor	1.97e+02
689	6	1.4	885	2	S33015	hypothetical protein	1.97e+02	762	6	1.4	1473	2	S53599	DNA topoisomerase (Ar	1.97e+02
690	6	1.4	892	2	H71558	probable initiation f	1.97e+02	763	6	1.4	1477	2	T13797	tumor suppressor prote	1.97e+02
691	6	1.4	896	2	H70233	hypothetical protein	1.97e+02	764	6	1.4	1495	2	S27001	alpha-2-macroglobulin	1.97e+02
692	6	1.4	909	2	S64038	probable membrane pro	1.97e+02	765	6	1.4	1497	2	S72250	sex-determining trans	1.97e+02
693	6	1.4	919	2	T53474	kinase receptor - ra	1.97e+02	766	6	1.4	1536	1	DVMS	multidrug resistance	1.97e+02
694	6	1.4	919	2	JC5394	exostose-related prot	1.97e+02	767	6	1.4	1556	2	S59393	probable membrane pro	1.97e+02
695	6	1.4	919	2	S19810	glutamate receptor GL	1.97e+02	768	6	1.4	1589	1	RGBYC5	cell division control	1.97e+02
696	6	1.4	922	2	A30816	band 3 anion transport	1.97e+02	769	6	1.4	1596	2	A35927	190K DNA-binding prot	1.97e+02
697	6	1.4	925	2	A55748	protein kinase (EC 2	1.97e+02	770	6	1.4	1602	2	H70984	probable polypeptide s	1.97e+02
698	6	1.4	929	2	A25314	band 3 protein - mous	1.97e+02	771	6	1.4	1628	2	S52588	clathrin heavy chain	1.97e+02
699	6	1.4	932	2	S76501	preprotein translocas	1.97e+02	772	6	1.4	1701	2	T09327	probable erythrocyte	1.97e+02
700	6	1.4	944	2	S56306	vacuolar protein-sort	1.97e+02	773	6	1.4	1735	2	S54784	sex-limited protein S	1.97e+02
701	6	1.4	946	1	JC5667	multidrug resistance	1.97e+02	774	6	1.4	1736	2	A29176	complement C4 precursor	1.97e+02
702	6	1.4	953	2	S19427	probable membrane pro	1.97e+02	775	6	1.4	1745	1	A24558	light junction-associ	1.97e+02
703	6	1.4	955	2	A60990	alpha-amylase (EC 3.2	1.97e+02	776	6	1.4	1762	2	T03222	probable polypeptide s	1.97e+02
704	6	1.4	956	2	J50685	glutamate receptor ch	1.97e+02	777	6	1.4	1774	2	RKMEF9	collagen alpha 1(XVII	1.97e+02
705	6	1.4	966	2	JH0826	glutamate ionotropic	1.97e+02	778	6	1.4	1894	2	B56101	probable polypeptide s	1.97e+02
706	6	1.4	973	2	F72076	polymorphic outer mem	1.97e+02	779	6	1.4	1894	2	JC4980	transcription factor	1.97e+02
707	6	1.4	973	2	T16232	hypothetical protein	1.97e+02	780	6	1.4	2061	2	T13751	transcription factor	1.97e+02
708	6	1.4	984	2	A41996	NF-kappa-B p50 subun1	1.97e+02	781	6	1.4	2100	2	T03223	probable polypeptide s	1.97e+02
709	6	1.4	985	1	VCLJSP	env polypeptide - hum	1.97e+02	782	6	1.4	2126	2	H70621	probable polypeptide s	1.97e+02
710	6	1.4	987	2	S62752	probable DNA-directed	1.97e+02	783	6	1.4	2136	2	A33672	crumbs protein - frul	1.97e+02
711	6	1.4	987	2	A31666	transposase - Escheri	1.97e+02	784	6	1.4	2157	2	S71461	probable polypeptide s	1.97e+02
712	6	1.4	992	2	T56963	transposase - Escheri	1.97e+02	785	6	1.4	2159	2	S71461	probable polypeptide s	1.97e+02
713	6	1.4	1002	2	G70876	probable transmembran	1.97e+02	786	6	1.4	2292	2	S55401	capaid polypeptide pr	1.97e+02
714	6	1.4	1005	2	A42265	alpha-mannosidase (EC	1.97e+02	787	6	1.4	2292	1	GNNYED	genome polypeptide -	1.97e+02
715	6	1.4	1008	2	S72698	transport protein tpi	1.97e+02	788	6	1.4	2321	1	GNNYEB	genome polypeptide -	1.97e+02
716	6	1.4	1026	2	A46945	paracrystalline surfa	1.97e+02	789	6	1.4	2311	1	TYCHSR	kinase-related protel	1.97e+02
717	6	1.4	1039	2	S76747	hypothetical protein	1.97e+02	790	6	1.4	2366	1	S10317	toxlin B - Clostridium	1.97e+02
718	6	1.4	1040	2	T08190	CopI like protein - A	1.97e+02	791	6	1.4	2367	2	S70172	toxlin B - Clostridium	1.97e+02
719	6	1.4	1044	2	DVBEX3	translation elongatio	1.97e+02	792	6	1.4	2524	2	A35844	Xotch protein - Afric	1.97e+02
720	6	1.4	1044	2	S62926	probable membrane pro	1.97e+02	793	6	1.4	2633	2	S28261	centromere protein E	1.97e+02
721	6	1.4	1050	2	S25363	cell surface glycopro	1.97e+02	794	6	1.4	2723	2	T03221	probable polypeptide s	1.97e+02
722	6	1.4	1051	2	A35761	hypothetical protein	1.97e+02	795	6	1.4	2893	2	A64556	toxlin-like outer memb	1.97e+02
723	6	1.4	1055	2	H70951	hypothetical protein	1.97e+02	796	6	1.4	3020	2	C71953	toxlin-like outer memb	1.97e+02
724	6	1.4	1056	2	A53767	tracheobronchial muc1	1.97e+02	797	6	1.4	3187	2	JC5837	mucin 2 precursor, in	1.97e+02
725	6	1.4	1064	2	S74861	hypothetical protein	1.97e+02	798	6	1.4	3268	2	S69625	364K Golgi complex-as	1.97e+02
726	6	1.4	1070	1	RNMB	DNA-directed RNA poly	1.97e+02	799	6	1.4	3411	1	GNNYF	hypothetical protein	1.97e+02
727	6	1.4	1073	1	SYECCP	cardamoml-phosphate s	1.97e+02	800	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
728	6	1.4	1074	2	T04777	hypothetical protein	1.97e+02	801	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
729	6	1.4	1081	2	S15040	pleiotropic drug, resi	1.97e+02	802	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
730	6	1.4	1087	1	S41797	cellulose 1,4-beta-ce	1.97e+02	803	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
731	6	1.4	1113	2	S62904	calcium-regulated pot	1.97e+02	804	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
732	6	1.4	1118	2	S44641	hypothetical protein	1.97e+02	805	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
733	6	1.4	1120	2	T14275	myosin-like protein m	1.97e+02	806	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
734	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	807	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
735	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	808	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
736	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	809	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
737	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	810	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
738	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	811	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
739	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	812	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
740	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	813	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
741	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	814	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
742	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	815	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
743	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	816	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
744	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	817	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
745	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	818	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
746	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	819	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
747	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	820	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
748	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	821	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
749	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	822	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
750	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	823	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
751	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	824	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
752	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	825	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02
753	6	1.4	1132	2	JC4127	protein tyrosine kina	1.97e+02	826	6	1.4	3411	1	GNNYF	genome polypeptide -	1.97e+02

827	5	1.1	168	2	S16800	hypothetical protein	4.87e+03	900	5	1.1	470	2	S30598	H+ transporting ATP s	4.87e+03
828	5	1.1	172	2	G70443	conserved hypothetical	4.87e+03	901	5	1.1	471	1	RKRRL2	ribulose-bisphosphate	4.87e+03
829	5	1.1	173	2	H69644	translation initiation	4.87e+03	902	5	1.1	472	2	JS00623	site-specific DNA-met	4.87e+03
830	5	1.1	180	2	E71929	heat shock protein	4.87e+03	903	5	1.1	473	2	S59984	hypd. protein - Rhodob	4.87e+03
831	5	1.1	180	2	C64584	heat shock protein	4.87e+03	904	5	1.1	473	2	A55275	gamma-aminobutyric ac	4.87e+03
832	5	1.1	184	1	FSFR	phaseolin - kidney be	4.87e+03	905	5	1.1	480	2	G36213	F3U. protein - vaccini	4.87e+03
833	5	1.1	184	2	A42219	light harvesting and	4.87e+03	906	5	1.1	498	1	VHIV61	nucleoprotein - Infl	4.87e+03
834	5	1.1	188	2	A42957	carbon monoxide-induc	4.87e+03	907	5	1.1	498	1	S11150	amC protein - Strept	4.87e+03
835	5	1.1	193	2	S70279	outer surface protein	4.87e+03	908	5	1.1	501	1	RGE008	sensor protein ubp	4.87e+03
836	5	1.1	205	2	S59048	phosphoribosylanthran	4.87e+03	909	5	1.1	510	2	A56442	phosphoglycerate muca	4.87e+03
837	5	1.1	208	2	B70174	hypothetical protein	4.87e+03	910	5	1.1	522	2	B71926	cag island protein -	4.87e+03
838	5	1.1	219	2	B43664	phosphoribosylanthran	4.87e+03	911	5	1.1	526	2	S34945	nitrogenase (EC 1.18	4.87e+03
839	5	1.1	225	2	S23568	adenylate kinase (EC	4.87e+03	912	5	1.1	527	2	A36695	catalase (EC 1.11.1.6	4.87e+03
840	5	1.1	241	2	FS1211	cytoskeletal protein	4.87e+03	913	5	1.1	528	2	H70163	phenylalanine--tRNA	4.87e+03
841	5	1.1	247	1	FWPMA6	H+ transporting ATP s	4.87e+03	914	5	1.1	529	2	S57345	m-impotin (nuclear p	4.87e+03
842	5	1.1	247	1	FWSP26	H+ transporting ATP s	4.87e+03	915	5	1.1	535	1	I38607	p53-binding protein 2	4.87e+03
843	5	1.1	248	2	S34995	surface lipoprotein p	4.87e+03	916	5	1.1	535	2	A44475	N-acetylglucosamine	4.87e+03
844	5	1.1	253	2	H72388	shikimate 5-dehydroge	4.87e+03	917	5	1.1	536	1	C64728	probable membrane pro	4.87e+03
845	5	1.1	253	2	T04435	hypothetical protein	4.87e+03	918	5	1.1	536	1	D70184	probable pyrrolone-5-	4.87e+03
846	5	1.1	262	2	S24727	ornithine carbamoylitr	4.87e+03	919	5	1.1	543	1	S19095	transcription factor	4.87e+03
847	5	1.1	265	2	C72287	hypothetical protein	4.87e+03	920	5	1.1	549	2	SS3427	protein-tyrosine-phos	4.87e+03
848	5	1.1	268	2	E64613	cell division membran	4.87e+03	921	5	1.1	550	2	I55679	integral membrane pro	4.87e+03
849	5	1.1	270	2	S74993	hypothetical protein	4.87e+03	922	5	1.1	552	2	F70372	dihydroxyacid dehydra	4.87e+03
850	5	1.1	273	2	A43862	29k peripheral membra	4.87e+03	923	5	1.1	555	2	RMIVSV	hemagglutinin precurs	4.87e+03
851	5	1.1	278	2	G65165	DNA-damage-inducible	4.87e+03	924	5	1.1	563	1	RMIVSV	polymerase-associated	4.87e+03
852	5	1.1	288	2	B72272	liron-sulfur cluster-b	4.87e+03	925	5	1.1	568	2	RMIVSV	GRSAG protein - tyrp	4.87e+03
853	5	1.1	295	2	JC5671	methionyl aminopeptid	4.87e+03	926	5	1.1	572	2	S14200	phosphotransferase sy	4.87e+03
854	5	1.1	296	2	I40264	outer surface protein	4.87e+03	927	5	1.1	572	2	B28474	ABC transporter, ATP-	4.87e+03
855	5	1.1	303	2	J01386	hypothetical 33k prot	4.87e+03	928	5	1.1	577	2	C72275	type II secretion pat	4.87e+03
856	5	1.1	309	2	I41075	site-specific DNA-met	4.87e+03	929	5	1.1	585	2	T00212	hypothetical protein	4.87e+03
857	5	1.1	319	2	JH0135	genome polyploid	4.87e+03	930	5	1.1	590	2	A35928	hypothetical 86k prot	4.87e+03
858	5	1.1	320	2	S75911	hypothetical protein	4.87e+03	931	5	1.1	597	2	B67189	glutathione-regulated	4.87e+03
859	5	1.1	322	2	T11127	NADH dehydrogenase (u	4.87e+03	932	5	1.1	601	2	A65129	cell division protein	4.87e+03
860	5	1.1	325	2	H72329	phenylalanine--tRNA	4.87e+03	933	5	1.1	615	2	D64714	NADH dehydrogenase su	4.87e+03
861	5	1.1	332	2	S06424	MHC class I histocomp	4.87e+03	934	5	1.1	616	2	T14235	DNA topoisomerase (AT	4.87e+03
862	5	1.1	334	2	S47762	dipeptide transport p	4.87e+03	935	5	1.1	640	5	S35734	serine proteinase (EC	4.87e+03
863	5	1.1	334	2	D22735	hypothetical nox p	4.87e+03	936	5	1.1	645	1	SUBSMP	endopeptidase Clp ATP	4.87e+03
864	5	1.1	341	2	H36841	E5R protein - variola	4.87e+03	937	5	1.1	649	2	S11163	histidine kinase - Ha	4.87e+03
865	5	1.1	344	2	S73555	MG415 homolog C12-ori	4.87e+03	938	5	1.1	652	2	A57071	endo-1,4-beta-mannosi	4.87e+03
866	5	1.1	344	2	T03499	integrase/recombinase	4.87e+03	939	5	1.1	659	2	S58666	hypothetical protein	4.87e+03
867	5	1.1	345	2	S30579	succinate--COA ligase	4.87e+03	940	5	1.1	668	2	D72278	ribo-nucleoside family	4.87e+03
868	5	1.1	360	2	F69333	chorismate synthase (4.87e+03	941	5	1.1	669	2	A50224	2'-5A-dependent RNAse	4.87e+03
869	5	1.1	363	1	A47620	3-isopropylmalate deh	4.87e+03	942	5	1.1	672	2	B72071	probable nucleic acid	4.87e+03
870	5	1.1	364	1	ADCHB	fructose-bisphosphate	4.87e+03	943	5	1.1	676	2	R45771	outer membrane protei	4.87e+03
871	5	1.1	365	1	S77963	MHC class I histocomp	4.87e+03	944	5	1.1	679	2	S28042	E2L protein - variola	4.87e+03
872	5	1.1	365	1	A43324	3-isopropylmalate deh	4.87e+03	945	5	1.1	706	2	J02210	translation initiatio	4.87e+03
873	5	1.1	367	2	S45312	Rockbeta2 protein - ra	4.87e+03	946	5	1.1	723	2	A49613	endothelin converting	4.87e+03
874	5	1.1	367	2	S66502	potassiun channel sha	4.87e+03	947	5	1.1	725	2	A57148	phenylalanine--tRNA	4.87e+03
875	5	1.1	373	2	J02646	SHL2 protein - human	4.87e+03	948	5	1.1	728	2	E59486	probable DNA-directed	4.87e+03
876	5	1.1	373	2	A69847	cystathionine gamma-s	4.87e+03	949	5	1.1	731	2	A37892	anthranilate synthase	4.87e+03
877	5	1.1	380	2	S75348	hypothetical protein	4.87e+03	950	5	1.1	747	2	A27892	DNA polymerase BI (po	4.87e+03
878	5	1.1	381	2	S44094	beta-lactamase (EC 3	4.87e+03	951	5	1.1	754	2	A53679	ribonuclease-diphos	4.87e+03
879	5	1.1	385	2	JC2298	RNA-binding protein H	4.87e+03	952	5	1.1	764	2	B64570	probable lipase (EC	4.87e+03
880	5	1.1	386	1	KMECPM	chorismate mutase (EC	4.87e+03	953	5	1.1	764	2	S75407	AMP deaminase (EC 3.5	4.87e+03
881	5	1.1	386	1	C72013	succinyl-coa synthetase	4.87e+03	954	5	1.1	768	2	S04518	leucine--tRNA ligase	4.87e+03
882	5	1.1	387	1	S26053	probable aspartate am	4.87e+03	955	5	1.1	781	2	A69312	transforming growth f	4.87e+03
883	5	1.1	389	2	E71009	hypothetical protein	4.87e+03	956	5	1.1	781	2	S44868	conserved hypothetical	4.87e+03
884	5	1.1	393	2	D70858	hypothetical protein	4.87e+03	957	5	1.1	788	1	JC1351	DNA mismatch repair p	4.87e+03
885	5	1.1	397	1	NMCMTC	major outer membrane	4.87e+03	958	5	1.1	794	2	S73877	receptor tyrosine kin	4.87e+03
886	5	1.1	402	2	A37049	myosin alpha heavy ch	4.87e+03	959	5	1.1	803	1	A64070	surface-layer protein	4.87e+03
887	5	1.1	402	2	A70559	hypothetical protein	4.87e+03	960	5	1.1	810	2	T10020	progesterone receptor	4.87e+03
888	5	1.1	406	2	JS0343	tryptophan synthase (4.87e+03	961	5	1.1	824	2	S44868	probable cytochrome C	4.87e+03
889	5	1.1	417	2	C64167	hypothetical protein	4.87e+03	962	5	1.1	843	1	JC1351	subtilisin-like prote	4.87e+03
890	5	1.1	418	2	S40380	phosphoglycerate kin	4.87e+03	963	5	1.1	848	1	JC1351	legumain protein 63 -	4.87e+03
891	5	1.1	422	2	S40824	hypothetical 48k prot	4.87e+03	964	5	1.1	852	2	D72230		
892	5	1.1	422	2	S52790	glutamine--phenylpro	4.87e+03	965	5	1.1	904	2	S53896		
893	5	1.1	424	2	C64362	aconitate hydratase (4.87e+03	966	5	1.1	907	2	T04820		
894	5	1.1	424	2	S09884	hypothetical protein	4.87e+03	967	5	1.1	913	2	A48280		
895	5	1.1	428	2	G70838	probable isocitrate 1	4.87e+03	968	5	1.1	917	2	S26365		
896	5	1.1	429	2	T07809	S-receptor kinase (EC	4.87e+03	969	5	1.1	933	1	ORHUP		
897	5	1.1	433	2	G64594	hemolysin secretion p	4.87e+03	970	5	1.1	936	2	H1862		
898	5	1.1	460	2	C70576	probable mgtE protein	4.87e+03	971	5	1.1	957	2	D64659		
899	5	1.1	466	2	J00077	gamma-aminobutylic ac	4.87e+03	972	5	1.1	965	2	S55658		

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973 5 1.1 985 1 DUBEL1 DNA-directed DNA poly 4.87e+03
974 5 1.1 1010 1 H+-transporting ATPas 4.87e+03
975 5 1.1 1020 2 A64641 cation efflux system 4.87e+03
976 5 1.1 1034 1 HNLCA pol polyprotein - hum 4.87e+03
977 5 1.1 1042 2 H70203 isoleucine--tRNA-119 4.87e+03
978 5 1.1 1072 2 A38457 integrin alpha 6 chal 4.87e+03
979 5 1.1 1156 2 A29125 paraspinal crystal for 4.87e+03
980 5 1.1 1175 2 C35815 myosin heavy chain 3 4.87e+03
981 5 1.1 1276 2 A34786 multidrug resistance 4.87e+03
982 5 1.1 1291 1 S05465 retrovirus-related po 4.87e+03
983 5 1.1 1318 1 Q08B1 membrane antigen p140 4.87e+03
984 5 1.1 1328 1 S04273 retrovirus-related re 4.87e+03
985 5 1.1 1358 2 A03905 genome polyprotein (v 4.87e+03
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987 5 1.1 1409 1 OEFPCP copta polyprotein 4.87e+03
988 5 1.1 1464 1 S29159 glutamate receptor, N 4.87e+03
989 5 1.1 1588 1 B5YVY1 ARO1 protein - yeast 4.87e+03
990 5 1.1 1694 2 J01896 hypothetical 191.1k p 4.87e+03
991 5 1.1 1729 2 A49282 fusion protein 1a/1b 4.87e+03
992 5 1.1 1734 2 A54602 microtubule-associate 4.87e+03
993 5 1.1 1869 1 S02771 myosin heavy chain A 4.87e+03
994 5 1.1 2188 2 A70984 probable polyketide s 4.87e+03
995 5 1.1 2201 2 S73014 polyketide synthase p 4.87e+03
996 5 1.1 2385 2 A32491 myosin heavy chain 1 4.87e+03
997 5 1.1 2469 2 H36812 hypothetical protein 4.87e+03
998 5 1.1 2796 2 JCA743 fatty acid synthase 4.87e+03
999 5 1.1 3924 2 S37431 ankyrin 2, neuronal 4.87e+03
1000 5 1.1 4452 1 YCBSG2 gramicidin S syntheta 4.87e+03

```

ALIGNMENTS

```

RESULT 1
ENTRY A32694 #type complete
TITLE Interferon alpha receptor precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change
24-Sep-1998

```

```

ACCESSIONS A32694
REFERENCE A32694
#authors Uze, G.; Lutfalla, G.; Gresser, I.
#journal Cell (1990) 60:225-234
#title Genetic transfer of a functional human interferon alpha
receptor into mouse cells: cloning and expression of its
cDNA.

```

```

#cross-references NUID:90124632
#accession A32694
#status preliminary
#molecule_type mRNA
#residues 1-557 #label UZE
#cross-references GB:J03171; NID:9184645; PID:906914

```

```

GENETICS GDB:IFNARI; IFNAR; IFRC
#gene #cross-references GDB:120078; OMIM:107450
#map_position 21q22.1-21q22.1
KEYWORDS cytokine receptor; transmembrane protein
SUMMARY #length 557 #molecular_weight 63525; #checksum 7035

```

```

Query Match 100.0% Score 436; DB 2; Length 557;
Best Local Similarity 100.0% Pred. No. 0.00e+00;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 1 MMYVLLGATTVLVAVGPMVLSAAGGKRLKSPKVEVDIIDNFIILMNRSDSEVGANT 60
Oy 1 MMYVLLGATTVLVAVGPMVLSAAGGKRLKSPKVEVDIIDNFIILMNRSDSEVGANT 60
Db 61 FSDYOKTGMDNWKILSCQNTSTKCNFSSILKNVEEIKIRIRAEKENTSSWTEVDSF 120
Oy 61 FSDYOKTGMDNWKILSCQNTSTKCNFSSILKNVEEIKIRIRAEKENTSSWTEVDSF 120
Db 61 FSDYOKTGMDNWKILSCQNTSTKCNFSSILKNVEEIKIRIRAEKENTSSWTEVDSF 120
Oy 61 FSDYOKTGMDNWKILSCQNTSTKCNFSSILKNVEEIKIRIRAEKENTSSWTEVDSF 120
Db 121 TPFRAOIGPPEVHLEADKALVHIISPTKDSVMMALDGLSFTSLIMKNSGVEERI 180
Oy 121 TPFRAOIGPPEVHLEADKALVHIISPTKDSVMMALDGLSFTSLIMKNSGVEERI 180

```

```

Db 181 ENIYRHKIKYLSPTTYCLKAKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240
Oy 181 ENIYRHKIKYLSPTTYCLKAKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240
Db 241 NONVYLAQDYTYANNTFQVOMLAFLKRNPGNHLKMKQIPDCENVKTTQCFQNVFQK 300
Oy 241 NONVYLAQDYTYANNTFQVOMLAFLKRNPGNHLKMKQIPDCENVKTTQCFQNVFQK 300
Db 301 GYLIRVQASDQNTSFSSEIKFTEIOAFLPPVFNIRSLSDSFHLYIGAPKOSGNT 360
Oy 301 GYLIRVQASDQNTSFSSEIKFTEIOAFLPPVFNIRSLSDSFHLYIGAPKOSGNT 360
Db 361 VIQDPLVIEIIFMENTSNAERKITEKTDVTPNLKPLTYVCVAAHATNDEKLNKSSV 420
Oy 361 VIQDPLVIEIIFMENTSNAERKITEKTDVTPNLKPLTYVCVAAHATNDEKLNKSSV 420
Db 421 FSDVCEKTKRGNTSK 436
Oy 421 FSDVCEKTKRGNTSK 436

```

```

RESULT 2
ENTRY SI7112 #type complete
TITLE Interferon alpha/beta receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
30-May-1997

```

```

ACCESSIONS SI7112
REFERENCE SI7112
#authors Lutfalla, G.; Gardiner, X.Y.Z.; Proudman, D.; Vleth, E.;
Mogensen, X.Y.Z.; Uze, G.
#submission Submitted to the EMBL Data Library, July 1991
#description The structure of the human interferon alpha/beta receptor
gene.

```

```

#accession SI7112
#status preliminary
#molecule_type DNA
#residues 1-545 #label LUT
#cross-references EMBL:X60459

```

```

GENETICS #introns 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 330/1; 369/3; 420/1;
468/3
KEYWORDS cytokine receptor; transmembrane protein
SUMMARY #length 545 #molecular_weight 62169 #checksum 672

```

```

Query Match 71.6% Score 312; DB 2; Length 545;
Best Local Similarity 100.0% Pred. No. 0.00e+00;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 18 PVLVLSAAGGKRLKSPKVEVDIIDNFIILMNRSDSEVGANTSFSDYOKTGMDNWKILS 77
Oy 18 PVLVLSAAGGKRLKSPKVEVDIIDNFIILMNRSDSEVGANTSFSDYOKTGMDNWKILS 77
Db 78 GCQNTSTKCNFSSILKNVEEIKIRIRAEKENTSSWTEVDSFPPFRAOIGPPEVHLEA 137
Oy 78 GCQNTSTKCNFSSILKNVEEIKIRIRAEKENTSSWTEVDSFPPFRAOIGPPEVHLEA 137
Db 138 EDKAVIHIISCTKDSVMMALDGLSFTSLIMKNSGVEERIENIYRHKIKYLSPTT 197
Oy 138 EDKAVIHIISCTKDSVMMALDGLSFTSLIMKNSGVEERIENIYRHKIKYLSPTT 197
Db 198 YCLAKKALLTSWKIGVSPVHCITTYENELPPENIEVSQNONVYLAQDYTYANNTF 257
Oy 198 YCLAKKALLTSWKIGVSPVHCITTYENELPPENIEVSQNONVYLAQDYTYANNTF 257
Db 258 OVOMLAFLKRNPGNHLKMKQIPDCENVKTTQCFQNVFQKGYLLRVAQSDQNTSF 317
Oy 258 OVOMLAFLKRNPGNHLKMKQIPDCENVKTTQCFQNVFQKGYLLRVAQSDQNTSF 317
Db 318 WSEIKFTEIO 329
Oy 318 WSEIKFTEIO 329

```

```
RESULT 3
ENTRY 3
TITLE S41602 #type fragments
ORGANISM Interferon alpha receptor 2 - human (fragments)
DATE 25-Dec-1994 #sequence_revision 01-Dec-1995 #text_change
ACCESSIONS S41602
REFERENCE #authors Abramovich, C.; Ratovitski, E.; Lundgren, E.; Revel, M.
#journal FEBS Lett. (1994) 338:295-300
#title Identification of mRNAs encoding two different soluble forms
#cross-references MIMD:94139943
#accession S41602
#molecule_type mRNA
#residues 1-56 #label ABR
#length 56 #checksum 845
KEYWORDS SUMMARY
Query Match 3.7%; Score 16; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.22e-22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 PLUYVCARAHMTDE 16
OY 398 PLUYVCARAHMTDE 413

RESULT 4
ENTRY 4
TITLE S27387 #type complete
ORGANISM Interferon alpha receptor type 1 precursor - bovine
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
ACCESSIONS S27387; S33770
REFERENCE #authors Mouchel-Vieilh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
#journal FEBS Lett. (1992) 313:255-259
#title Specific antiviral activities of the human alpha interferons
#cross-references MIMD:93076908
#accession S27387
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-560 #label MOU
#cross-references EMBL:X68443; NID:g431; PID:g432
#experimental_source MDR cells
REFERENCE S33770
#authors Lhm, J.K.; Langer, J.A.
#journal Blochim. Biophys. Acta (1993) 1173:314-319
#title Cloning and characterization of a bovine alpha interferon
#cross-references MIMD:93305725
#accession S33770
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-421, 'V', 423-560 #label LIM
#cross-references EMBL:L06320; NID:g163187; PID:g163188
#experimental_source lung
KEYWORDS antiviral; cytokine receptor; transmembrane protein
FEATURE 1-24 #domain signal sequence #status predicted #label SIG
1-560 #product interferon alpha receptor type 1 #status
predicted #label MAT
SUMMARY #length 560 #molecular-weight 63818 #checksum 4991
Query Match 3.0%; Score 13; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.82e-14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 397 LKPLUYVCARARA 409
```

```
OY 396 LKPLUYVCARARA 408

RESULT 5
ENTRY 5
TITLE A45283 #type complete
ORGANISM Interferon alpha/delta receptor - mouse
DATE 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
ACCESSIONS A45283; I48424; I48425; I48426; I48427; I48428;
REFERENCE #authors Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen,
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4774-4778
#title Behavior of a cloned murine interferon alpha/delta receptor
#cross-references MIMD:92262522
#accession A45283
#status preliminary
#molecule_type mRNA
#residues 1-590 #label UZE
#cross-references GB:M89641; NID:g194111; PID:g194112
#note Sequence extracted from NCBI database (NCBI:102354,
NCBI:102357)
REFERENCE I48423
#authors Lutfalla, G.; Uze, G.
#journal Gene (1994) 148:343-346
#title Structure of the murine interferon alpha/delta
receptor-encoding gene: high-frequency rearrangements in
the interferon-resistant L1210 cell line.
#cross-references MIMD:95047447
#accession I48423
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 118-125 #label RES
#cross-references EMBL:U06237; NID:g497103; PID:g755810
#accession I48424
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 127-224 #label RE2
#cross-references EMBL:U06238; NID:g497104; PID:g755811
#accession I48425
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 243-264 #label RE3
#cross-references EMBL:U06239; NID:g497106; PID:g510261
#accession I48426
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 265-375 #label RE4
#cross-references EMBL:U06240; NID:g497108; PID:g510262
#accession I48427
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 397-424 #label RE5
#cross-references EMBL:U06242; NID:g497112; PID:g755812
#accession I48428
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 426-445 #label RE6
#cross-references EMBL:U06244; NID:g497114; PID:g510265
#accession I48429
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 473-590 #label RE7
#cross-references EMBL:U06244; NID:g497114; PID:g510265
GENETICS IFNAR
#gene 177/3; 331/1
KEYWORDS cytokine receptor; transmembrane protein
SUMMARY #length 590 #molecular-weight 65776 #checksum 833
```

Query Match 2.58; Score 11; DB 2; Length 590;
 Best Local Similarity 100.0%; Pred. No. 4.53e-09;
 Matches 11; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

DB 363 YEIIEMTSN 373
 |||||
 QY 369 YEIIEMTSN 379

RESULT 6
 ENTRY T00676 #type complete
 TITLE hypothetical protein F6E13.9 - Arabidopsis thaliana
 ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear
 DATE 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change
 30-Apr-1999
 T00676
 214198

ACCESSIONS
 REFERENCE
 #authors Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby,
 M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage,
 A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
 #description Arabidopsis thaliana chromosome II BAC F6E13 genomic
 sequence.
 #accession T00676
 #status translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 1-421 #label ROU
 #cross-references EMBL:AC004005; NID:G3212846; PID:G3212853
 #experimental_source cultivar Columbia

GENETICS
 #map_position 2
 #note F6E13.9
 SUMMARY #length 421 #molecular_weight 48397 #checksum 8249

Query Match 1.8%; Score 8; DB 2; Length 421;
 Best Local Similarity 100.0%; Pred. No. 3.98e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 300 FLKRNPN 307
 |||||
 QY 265 FLKRNPN 272

RESULT 7
 ENTRY T13710 #type fragment
 TITLE protein-tyrosine kinase (EC 2.7.1.112) - fruit fly
 ORGANISM #formal_name Drosophila melanogaster (fragment)
 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
 13-Aug-1999
 T13710
 217703

ACCESSIONS
 REFERENCE
 #authors Ito, M.; Matsui, T.; Taniguchi, T.; Chihara, K.
 #journal Gene (1994) 139:215-218
 #title Alternative splicing generates two distinct transcripts for
 the Drosophila melanogaster fibroblast growth factor
 receptor homolog.
 #accession T13710
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-1235 #label ITO
 #cross-references EMBL:U17550; NID:d1007694; PID:d1005014;
 PDB:BA04486.1
 SUMMARY #length 1235 #checksum 4817

KEYWORDS phosphotransferase;
 #length 1235 #checksum 4817

Query Match 1.8%; Score 8; DB 2; Length 1235;
 Best Local Similarity 100.0%; Pred. No. 3.98e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 731 TLVAVNG 738

QY 10 TLVAVNG 17
 |||||

RESULT 8
 ENTRY B26744 #type complete
 TITLE megascollaxinin garden dagger wasp
 ALTERNATE_NAMES 6-Thr-bradykinin-Lys-Ala
 ORGANISM #formal_name Megascollia flavifrons #common_name garden dagger
 wasp
 DATE 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change
 02-Dec-1994
 B26744; A28609
 B26744; A28609

ACCESSIONS
 REFERENCE
 #authors Yasuhara, T.; Mantel, P.; Nakajima, T.; Plek, T.
 #journal Toxicon (1987) 25:527-535
 #title Two kinins isolated from an extract of the venom reservoirs
 of the solitary wasp Megascollia flavifrons.
 #cross-references MUID:87293024
 #accession B26744
 #molecule_type protein
 #residues 1-11 #label YAS
 REFERENCE A28609
 #authors Nakajima, T.; Plek, T.; Yasuhara, T.; Mantel, P.
 #journal Toxicon (1988) 26:34
 #title Two kinins isolated from the venom of Megascollia flavifrons.
 #accession A28609
 #molecule_type protein
 #residues 1-11 #label NAK
 KEYWORDS bradykinin; presynaptic neurotoxin; venom
 SUMMARY #length 11 #molecular_weight 1273 #checksum 4943

Query Match 1.6%; Score 7; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.73e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 5 FTFPRKA 11
 |||||
 QY 120 FTFPRKA 126

RESULT 9
 ENTRY PC4027 #type fragment
 TITLE hypothetical protein 93 - Saccharopolyspora erythraea
 ORGANISM #formal_name Saccharopolyspora erythraea
 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
 09-Sep-1997
 PC4027
 JC4089

ACCESSIONS
 REFERENCE
 #authors Zolchev, S.B.; Hutchinson, C.R.
 #journal Gene (1995) 156:101-106
 #title Cloning and heterologous expression of the genes encoding
 nonspecific electron transport components for a cytochrome
 P450 system of Saccharopolyspora erythraea involved in
 erythromycin production.
 #cross-references MUID:95255650
 #accession PC4027
 #molecule_type DNA
 #residues 1-93 #label ZOF
 #cross-references GB:J3846; NID:G603921; PID:G603922
 SUMMARY #length 93 #checksum 8543

Query Match 1.6%; Score 7; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 3.73e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 48 TTLVAVA 54
 |||||
 QY 9 TTLVAVA 15

RESULT 10

ENTRY / SAVLDM #type complete
TITLE delta large antigen - hepatitis delta virus (strain Japanese M-1)
ALTERNATE_NAMES #formal_name hepatitis delta virus
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic rabbit
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999

ACCESSIONS A36409
REFERENCE #authors Imazeki, F.; Omata, M.; Ohno, M.
#journal J. Virol. (1990) 64:5594-5599
#title Heterogeneity and evolution rates of delta virus RNA sequences
#cross-references MUID:91012805
#accession A36409
##molecule_type genomic RNA
##residues 1195 #label TMA
##cross-references GB:D90190; GB:M58299; NID:9221691; PIDN:BAAL4214.1; PID:dl014919; PID:9221692

CLASSIFICATION #superfamily hepatitis delta virus large antigen
KEYWORDS Core protein
FEATURE 2-195
#product delta large antigen #status predicted #label Mat

SUMMARY #length 195 #molecular_weight 21811 #checksum 7815

Query Match 1.6% Score 7; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 AAGKNT 122
|||
OY 24 AAGKNT 30

RESULT 11
ENTRY B44459 #type fragment
TITLE tropoin T, fast skeletal muscle splice form alpha - rabbit (fragment)
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic rabbit

DATE 30-Apr-1993 #sequence_revision 17-May-1996 #text_change 17-May-1996

ACCESSIONS B44459
REFERENCE A44459
#authors Pan, B.S.; Potter, J.D.
#journal J. Biol. Chem. (1992) 267:23052-23056
#title Two genetically expressed tropoin T fragments representing alpha and beta isoforms exhibit functional differences.
#cross-references MUID:93054628
#accession B44459
##status nucleic acid sequence not shown; not compared with
##molecule_type mRNA
##residues 1-234 #label PAN
##experimental_source neonatal skeletal muscle clone PT7

COMMENT #note
The two carboxyl-terminal isoforms of tropoin T are designated alpha and beta. Alternative splicing to create varied amino-terminal isoforms adds considerable additional complexity to the expression of tropoin T.
#superfamily tropoin T
#alternative splicing; differentiation; skeletal muscle

CLASSIFICATION #length 234 #checksum 3857

KEYWORDS

SUMMARY

Query Match 1.6% Score 7; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 84 RIRAEKE 90
|||
OY 103 RIRAEKE 109

RESULT 12
ENTRY A44459 #type complete
TITLE tropoin T, fast skeletal muscle splice form beta - rabbit
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic rabbit
DATE 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 13-Aug-1999

ACCESSIONS A44459; I46517
REFERENCE A44459
#authors Pan, B.S.; Potter, J.D.
#journal J. Biol. Chem. (1992) 267:23052-23056
#title Two genetically expressed tropoin T fragments representing alpha and beta isoforms exhibit functional differences.
#cross-references MUID:93054628
#accession A44459
##status nucleic acid sequence not shown; not compared with
##molecule_type mRNA
##residues 1-249 #label PAN
##experimental_source neonatal skeletal muscle clone PT5

COMMENT #note
The two carboxyl-terminal isoforms of tropoin T are designated alpha and beta. Alternative splicing to create varied amino-terminal isoforms adds considerable additional complexity to the expression of tropoin T.
#superfamily tropoin T
#alternative splicing; differentiation; skeletal muscle

CLASSIFICATION #length 249 #molecular_weight 29683 #checksum 3853

KEYWORDS

SUMMARY

Query Match 1.6% Score 7; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 RIRAEKE 105
|||
OY 103 RIRAEKE 109

RESULT 13
ENTRY A34327 #type complete
TITLE tropoin T, fast skeletal muscle, embryonic alpha (clone 501) - Japanese quail
ORGANISM #formal_name Coturnix coturnix japonica #common_name Japanese quail
DATE 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 13-Aug-1999

ACCESSIONS A34327
REFERENCE A34327
#authors Bucher, E.A.; Charles de la Brousse, F.; Emerson Jr., C.P.
#journal J. Biol. Chem. (1989) 264:12482-12491
#title Developmental and muscle-specific regulation of avian fast skeletal tropoin T isoform expression by mRNA splicing.
#cross-references MUID:89308680
#accession A34327
##status preliminary
##molecule_type mRNA
##residues 1-249 #label BUC
##cross-references GB:M26599; NID:9213627; PIDN:AAA49505.1; PID:9213628; GB:J05006

CLASSIFICATION #superfamily tropoin T
KEYWORDS skeletal muscle

SUMMARY #length 249 #molecular-weight 29735 #checksum 5504

Query Match 1.6%; Score 7; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 RIRAEKE 107
11111111
OY 103 RIRAEKE 109

RESULT 14

ENTRY D31957 #type complete
TITLE troponin T, skeletal muscle, isoform 4 - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999

ACCESSIONS D31957
REFERENCE A92698
#authors Smillie, L.B.; Golosinska, K.; Reinach, F.C.
#journal J. Biol. Chem. (1988) 263:18816-18820
#title Sequences of complete cDNAs encoding four variants of chicken skeletal muscle troponin T

#cross-references M01D:8906672
#accession D31957
#molecule_type mRNA
#residues 1-251 #label SMI
#cross-references GB:M22158; GB:J04198; NID:g212791; PIDN:AAA9103.1;

CLASSIFICATION #superfamily troponin T
KEYWORDS alternative splicing; muscle; phosphoprotein; skeletal muscle
SUMMARY #length 251 #molecular-weight 29648 #checksum 7133

Query Match 1.6%; Score 7; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 RIRAEKE 109
11111111
OY 103 RIRAEKE 109

RESULT 15

ENTRY B34327 #type complete
TITLE troponin T, fast skeletal muscle, adult alpha (clone 605) - Japanese quail
ORGANISM #formal_name Coturnix coturnix japonica #common_name Japanese quail
DATE 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 13-Aug-1999

ACCESSIONS B34327
REFERENCE B34327
#authors Bucher, E.A.; Charles de la Brousse, F.; Emerson Jr., C.P.
#journal J. Biol. Chem. (1989) 264:12482-12491
#title Developmental and muscle-specific regulation of avian fast skeletal troponin T isoform expression by mRNA splicing.

#cross-references M01D:89308680
#accession B34327
#status Preliminary
#molecule_type mRNA
#residues 1-253 #label BUC
#cross-references GB:M26600; NID:g213629; PIDN:AAA9506.1; PID:g213630;

CLASSIFICATION #superfamily troponin T
KEYWORDS skeletal muscle
SUMMARY #length 253 #molecular-weight 30098 #checksum 1070

Query Match 1.6%; Score 7; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 105 RIRAEKE 111
11111111

OY 103 RIRAEKE 109

RESULT 16

ENTRY B31957 #type complete
TITLE troponin T, skeletal muscle, isoform 2 - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999

ACCESSIONS B31957
REFERENCE A92698
#authors Smillie, L.B.; Golosinska, K.; Reinach, F.C.
#journal J. Biol. Chem. (1988) 263:18816-18820
#title Sequences of complete cDNAs encoding four variants of chicken skeletal muscle troponin T

#cross-references M01D:8906672
#accession B31957
#molecule_type mRNA
#residues 1-257 #label SMI
#cross-references GB:M22155; GB:J04198; NID:g212787; PIDN:AAA9101.1;

CLASSIFICATION #superfamily troponin T
KEYWORDS alternative splicing; muscle; phosphoprotein; skeletal muscle
SUMMARY #length 257 #molecular-weight 30361 #checksum 7402

Query Match 1.6%; Score 7; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 109 RIRAEKE 115
11111111
OY 103 RIRAEKE 109

RESULT 17

ENTRY I53021 #type complete
TITLE troponin T - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

ACCESSIONS I53021
REFERENCE I53021

#authors Wu, Q.L.; Jha, P.K.; Raychowdhury, N.K.; Du, Y.; Leavis, P.C.; Sarkar, S.
#journal DNA Cell Biol. (1994) 13:217-233
#title Isolation and characterization of human fast skeletal troponin T cDNA: Comparative sequence analysis of isoforms and insight into the evolution of members of a multigene family.

#cross-references M01D:94226695
#accession I53021
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-258 #label RES
#cross-references GB:M21984; NID:g508854; PIDN:AAA36777.1; PID:g508855

GENETICS GDB:TNT3
#cross-references GDB:350962; OMIM:600692
#map_position 11p15.5-11p15.5
CLASSIFICATION #superfamily troponin T
SUMMARY #length 258 #molecular-weight 30596 #checksum 6005

Query Match 1.6%; Score 7; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 108 RIRAEKE 114
11111111
OY 103 RIRAEKE 109

RESULT 18
ENTRY C31957 #type complete

#introns 6/2; 11/1 17/1; 23/1; 28/1; 32/1; 37/1; 43/2; 58/3; 97/3;
123/3; 161/3; 198/2; 228/3; 241/3; 255/2
CLASSIFICATION #superfamily tropoin T
KEYWORDS #alternative splicing; muscle; phosphoprotein; skeletal muscle
SUMMARY #length 272 #molecular-weight 32263 #checksum 8900

Query Match 1.6%; Score 7; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 109 RIRAEKE 115
|||
QY 103 RIRAEKE 109

RESULT 21
ENTRY A31957 #type complete
TITLE tropoin T, skeletal muscle, isoform 1 - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999

ACCESSIONS A31957
REFERENCE A92698
#authors Smille, L.B.; Golosinska, K.; Reinach, F.C.
#journal J. Biol. Chem. (1988) 263:18816-18820
#title Sequences of complete cDNAs encoding four variants of chicken skeletal muscle tropoin T.
#cross-references MUID:8906672

#accession A31957
#molecule_type mRNA
#residues 1-274 #label SMI
#cross-references GB:M22154; GB:Y04198; NID:g212785; PIDN:AAA6100.1;
PID:g212786
CLASSIFICATION #superfamily tropoin T
KEYWORDS #alternative splicing; muscle; phosphoprotein; skeletal muscle
SUMMARY #length 274 #molecular-weight 32340 #checksum 8022

Query Match 1.6%; Score 7; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 126 RIRAEKE 132
|||
QY 103 RIRAEKE 109

RESULT 22
ENTRY S75156 #type complete
TITLE hypothetical protein slr1768 - Synechocystis sp. (strain PCC 6803)
ORGANISM #formal_name Synechocystis sp.
DATE 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998

ACCESSIONS S75156
REFERENCE S74322
#authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugita, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naro, K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Mada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the uniceellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
#cross-references MUID:97061201

#accession S75156
#status preliminary
#molecule_type DNA
#residues 1-298 #label KAN
#cross-references EMBL:D90903; GB:AB001339; NID:g1652127; PID:d1017803;

#note PIR:q1652146
the nucleotide sequence was submitted to the EMBL Data Bank Library, June 1996

SUMMARY #length 298 #molecular-weight 32828 #checksum 788

Query Match 1.6%; Score 7; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 236 AERKIE 242
|||
QY 380 AERKIE 386

RESULT 23
ENTRY I38500 #type complete
TITLE interferon gamma receptor accessory factor-1 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 30-May-1997

ACCESSIONS I38500
REFERENCE A49946
#authors Soh, J.; Donnelly, R.J.; Kotenko, S.; Maritano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.L.; Schwartz, B.; Miki, T.; Pestka, S.
#journal Cell (1994) 76:793-802
#title Identification and sequence of an accessory factor regulated for activation of the human interferon gamma receptor.
#cross-references MUID:94170380

#accession I38500
#molecule_type mRNA
#residues 1-337 #label RES
#cross-references EMBL:U05875; NID:g463549; PID:g463550
#experimental_source clone pSKI
#accession I38501
#molecule_type mRNA
#residues 1-63, 0, 65-337 #label RES2
#cross-references EMBL:U05877; NID:g463551; PID:g463552

GENETICS
#map position 21
#keywords cytokine receptor
SUMMARY #length 337 #molecular-weight 37834 #checksum 749

Query Match 1.6%; Score 7; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 142 PRENIEV 148
|||
QY 231 PRENIEV 237

RESULT 24
ENTRY B26952 #type complete
TITLE electron transfer flavoprotein alpha chain homology - Rhizobium meliloti
ALTERNATE_NAMES flxB protein
ORGANISM #formal_name Rhizobium meliloti
DATE 05-Oct-1988 #sequence_revision 12-Jul-1996 #text_change 11-Jun-1999

ACCESSIONS B26952
REFERENCE A26952
#authors Earl, C.D.; Ronson, C.W.; Ausubel, F.M.
#journal J. Bacteriol. (1987) 169:1127-1136
#title Genetic and structural analysis of the Rhizobium meliloti flxA, flxB, flxC, and flxD genes.
#cross-references MUID:87137267
#accession B26952
#molecule_type DNA
#residues 1-353 #label EAR
#cross-references GB:M15546; NID:g340664; PIDN:AAA21769.1; PID:g551199

COMMENT This protein is essential for symbiotic nitrogen fixation.

GENETICS

#gene fixB

CLASSIFICATION operon containing fixA, fixB, fixC, and fixX genes

KEYWORDS #superfamily electron transfer flavoprotein alpha chain

SUMMARY #electron transfer; flavoprotein; nitrogen fixation

#length 353 #molecular-weight 37786 #checksum 7176

Query Match 1.6% Score 7; DB 1; Length 353;

Best Local Similarity 100.0%; Pred. No. 3.73e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 109 LIGATTL 115

|||||

Oy 5 LIGATTL 11

RESULT 25

ENTRY S14071 #type complete

TITLE electron transfer flavoprotein alpha chain fixB homolog -

ORGANISM Acetivibrium caulinodans

DATE #formal-name Acetivibrium caulinodans

10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change

ACCESSIONS S14071

REFERENCE S14070

#authors Arisoni, F.; Kaminski, P.A.; Hennecke, H.; Elmerich, C.

#journal Mol. Gen. Genet. (1991) 225:514-520

#title Nucleotide sequence of the fixABC region of Acetivibrium caulinodans ORS571: similarity of the fixB product with eukaryotic flavoproteins, characterization of fixA, and identification of nifH.

#cross-references MUID:91203829

#accession S14071

#status preliminary

CLASSIFICATION #molecule-type DNA

KEYWORDS #residues 1-369 #label ARI

#cross-references EMBL:X55450; NID:g38695; PTDN:CA39092.1; PTD:g38697

SUMMARY #superfamily electron transfer flavoprotein alpha chain

#electron transfer; flavoprotein

#length 369 #molecular-weight 39712 #checksum 897

Query Match 1.6% Score 7; DB 1; Length 369;

Best Local Similarity 100.0%; Pred. No. 3.73e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 125 LIGATTL 131

|||||

Oy 5 LIGATTL 11

RESULT 26

ENTRY B32495

TITLE Rep-1 protein B - mouse

ORGANISM #formal-name Mus musculus #common-name house mouse

DATE 12-Oct-1989 #sequence-revision 12-Oct-1989 #text-change

10-Sep-1997

ACCESSIONS B32495

REFERENCE A32495

#authors Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellems, R.E.; Crouse, G.F.

#journal Mol. Cell. Biol. (1989) 9:3058-3072

#title Dual bidirectional promoters at the mouse dhfr locus: cloning and characterization of two mRNA classes of the divergently transcribed Rep-1 gene.

#cross-references MUID:89384567

#accession B32495

#status preliminary

KEYWORDS #molecule-type mRNA

#residues 1-394 #label LIN

#cross-references GB:M24919; NID:g200703; PTD:g200704; GB:J04244

SUMMARY DNA binding

#length 394 #molecular-weight 44599 #checksum 606

Query Match 1.6% Score 7; DB 2; Length 394;

Best Local Similarity 100.0%; Pred. No. 3.73e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 247 NKSSVFS 253

|||||

Oy 416 NKSSVFS 422

RESULT 27

ENTRY I52590

TITLE m3-B isoform - mouse

ORGANISM #formal-name Mus sp. #common-name mouse

DATE 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change

ACCESSIONS I52590

REFERENCE I52590

#authors Tchilian, E.Z.; Beverley, P.C.; Young, B.D.; Watt, S.M.

#journal Blood (1994) 83:3188-3198

#title Molecular cloning of two isoforms of the murine homolog of the myeloid CD3 antigen.

#cross-references MUID:94250900

#accession I52590

#status preliminary; translated from GB/EMBL/DBJ

KEYWORDS #molecule-type mRNA

#residues 1-403 #label RES

#cross-references GB:S71345; NID:g551352; PTD:g551353

SUMMARY #length 403 #molecular-weight 44824 #checksum 4331

Query Match 1.6% Score 7; DB 2; Length 403;

Best Local Similarity 100.0%; Pred. No. 3.73e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 LVLVAVG 247

|||||

Oy 11 LVLVAVG 17

RESULT 28

ENTRY T15309

TITLE hypothetical protein B0286.3 - Caenorhabditis elegans

ORGANISM #formal-name Caenorhabditis elegans

DATE 20-Sep-1999 #sequence-revision 20-Sep-1999 #text-change

20-Sep-1999

ACCESSIONS T15309

REFERENCE S69011

#authors Johnson, D.

#description The sequence of C. elegans cosmid B0286.

#accession T15309

#status preliminary; translated from GB/EMBL/DBJ

KEYWORDS #molecule-type DNA

#residues 1-423 #label JOH

#cross-references EMBL:U39848; NID:g1053217; PTD:g1053219;

#cross-references EMBL:AAA80690.1; CESP:B0286.3

GENETICS

#gene CESP:B0286.3

#introns 32/3; 195/3; 254/3; 349/3; 416/3

SUMMARY #length 423 #molecular-weight 46977 #checksum 9992

Query Match 1.6% Score 7; DB 2; Length 423;

Best Local Similarity 100.0%; Pred. No. 3.73e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 112 FLKRNPG 118

|||||

Oy 265 FLKRNPG 271

RESULT 29

ENTRY S14147

TITLE multifunctional purine biosynthesis protein - human

CONTAINS
phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21);
phosphoribosylaminoimidazole succinocarboxamide synthase (EC 6.3.2.6)
#formal_name Homo sapiens #common_name man
#date 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 12-Jun-1998
#accession S14147
#authors Minet, M.; Lacroste, F.
#journal Curr. Genet. (1990) 18:287-291
#title Cloning and sequencing of a human cDNA coding for a multifunctional polypeptide of the purine pathway by complementation of the ade2-101 mutant in *Saccharomyces cerevisiae*.
#cross-references MUID:91070616
#accession S14147
#status Preliminary
#molecule_type mRNA
#residues 1-425 #label MTN
#cross-references GB:X53793; MUID:928383; PID:928384
GENETICS
#gene GDB:ADE2C1
#map_position 8pter-8p23
#cross-references GDB:4627430
CLASSIFICATION
#superfamily phosphoribosylaminoimidazole carboxylase
#catalytic_chain_homology catalytic chain homology
#keywords carbon-carbon lyase; carboxy-lyase; ligase; purine nucleotide biosynthesis
FEATURE
266-397
#domain phosphoribosylaminoimidazole carboxylase
#catalytic_chain_homology #label PCC
#length 425 #molecular_weight 47079 #checksum 3489
SUMMARY
Query Match 1.6%; Score 7; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 108 FLKRNPG 114
QY 265 FLKRNPG 271
RESULT 30
ENTRY S55684 #type complete
TITLE aminoimidazole ribonucleotide carboxylase - rat
#organism #formal_name Rattus norvegicus #common_name Norway rat
#date 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 29-Jan-1999
#accessions S55684
#reference S55684
#authors Iwahana, H.; Honda, S.; Tsujisawa, T.; Takahashi, Y.; Adzuma, K.; Katsushima, R.; Yamaoka, T.; Moritani, M.; Yoshimoto, K.; Itakura, M.
#journal Blochm. Biophys. Acta (1995) 1261:369-380
#title Rat genomic structure of aminoimidazole ribonucleotide transferase, cDNA sequence of aminoimidazole ribonucleotide carboxylase, and cell cycle-dependent expression of these two physically linked genes.
#cross-references MUID:95260861
#accession S55684
#status Preliminary
#molecule_type mRNA
#residues 1-425 #label IWA
#cross-references GB:D37979; MUID:9976251; PID:d1007775; PID:9976252
CLASSIFICATION
#superfamily phosphoribosylaminoimidazole carboxylase
#catalytic_chain_homology catalytic chain homology
FEATURE
266-397
#domain phosphoribosylaminoimidazole carboxylase
#catalytic_chain_homology #label PCC
#length 425 #molecular_weight 47096 #checksum 2993
SUMMARY
Query Match 1.6%; Score 7; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 108 FLKRNPG 114
QY 265 FLKRNPG 271
RESULT 31
ENTRY A35641 #type complete
TITLE 5-aminimidazole-5-aminimidazole-4-N-succinocarboxamide ribonucleotide - chicken
#organism #formal_name Gallus gallus #common_name chicken
#date 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 16-Dec-1998
#accessions A35641
#reference A35641
#authors Chen, Z.; Dixon, J.E.; Zalkin, H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:3097-3101
#title Cloning of a chicken liver cDNA encoding 5-aminimidazole ribonucleotide carboxylase and 5-aminimidazole-4-N-succinocarboxamide ribonucleotide synthetase by functional complementation of *Escherichia coli* pur mutants.
#cross-references MUID:90222176
#accession A35641
#status Preliminary
#molecule_type mRNA
#residues 1-426 #label CHE
#cross-references GB:M31764; MUID:9211193; PID:9211194
CLASSIFICATION
#superfamily phosphoribosylaminoimidazole carboxylase
#catalytic_chain_homology catalytic chain homology
FEATURE
267-398
#domain phosphoribosylaminoimidazole carboxylase
#catalytic_chain_homology #label PCC
#length 426 #molecular_weight 47240 #checksum 5538
SUMMARY
Query Match 1.6%; Score 7; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 109 FLKRNPG 115
QY 265 FLKRNPG 271
RESULT 32
ENTRY S74801 #type complete
TITLE ammonium transport protein - *Synechocystis* sp. (strain PCC 6803)
#organism #formal_name *Synechocystis* sp.
#date 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 28-Sep-1999
#accessions S74801
#reference S74322
#authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugita, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naito, K.; Okumura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
#cross-references MUID:97061201
#accession S74801
#status Preliminary
#molecule_type DNA
#residues 1-442 #label KAN
nucleic acid sequence not shown; translation not shown

#cross-references EMBL:D90901; GB:AB001339; NID:91651897;
 #note PIDN:BA016952.1; PID:d1017685; PID:g1652026
 the nucleotide sequence was submitted to the EMBL Data
 Library, June 1996

GENETICS

#gene ant1
 #superfamily ammonium transport protein ant1
 #length 442 #molecular-weight 47172 #checksum 310

Query Match 1.68; Score 7; DB 2; Length 442;
 Best Local Similarity 100.08; Pred. No. 3.73e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 277 LSNAAG 283
 11111111
 21 LSNAAG 27

RESULT 33

ENTRY #type complete
 TITLE 49.2K membrane protein - equine herpesvirus 1 (strain Ab4p)
 ORGANISM #formal_name equine herpesvirus 1
 #host Equus caballus (domestic horse)
 DATE 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999

ACCESSIONS

REFERENCE A36800
 #authors Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
 #submission submitted to Genbank, March 1992
 #description The DNA sequence of equine herpesvirus-1.
 #accession G36800
 #molecule_type DNA

#residues 1-450 ##label TEL

#cross-references GB:A86664; NID:g330791; PIDN:AB02487.1; PID:g330843

REFERENCE A41831
 #authors Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
 #journal Virology (1992) 189:304-316
 #title The DNA sequence of equine herpesvirus-1.
 #cross-references NID:92295566
 #contents annotation; possible protein-coding frames
 #note neither amino acid nor nucleotide sequence is given

GENETICS

#gene 52
 #superfamily herpesvirus 51K protein
 #transmembrane protein

FEATURE

37-53 #domain transmembrane #status predicted #label TM1
 111-127 #domain transmembrane #status predicted #label TM2
 156-173 #domain transmembrane #status predicted #label TM3
 179-195 #domain transmembrane #status predicted #label TM4
 241-257 #domain transmembrane #status predicted #label TM5
 271-287 #domain transmembrane #status predicted #label TM6
 297-314 #domain transmembrane #status predicted #label TM7
 341-358 #domain transmembrane #status predicted #label TM8
 #length 450 #molecular-weight 49221 #checksum 9416

SUMMARY

Query Match 1.68; Score 7; DB 1; Length 450;
 Best Local Similarity 100.08; Pred. No. 3.73e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 109 TTVLVA 115
 11111111
 9 TTVLVA 15

RESULT 34

ENTRY #type complete
 TITLE multidrug resistance protein homolog - Archaeoglobus fulgidus
 ORGANISM #formal_name Archaeoglobus fulgidus
 DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jun-1998

ACCESSIONS

REFERENCE G69392
 A69250

#authors

Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwin, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kervatage, A.R.; Graham, D.E.; Kyriakides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Arlrich, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.

#journal Nature (1997) 390:364-370
 #title The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Archaeoglobus fulgidus.
 #accession M01D:98049343
 #status preliminary; nucleic acid sequence not shown; translation not shown

#cross-references M01D:98049343
 #residues 1-451 ##label KLE
 #cross-references GB:AE001025; GB:AE000782; NID:92689348; PID:g2649446;
 #length 451 #molecular-weight 47918 #checksum 4428

SUMMARY

Query Match 1.68; Score 7; DB 2; Length 451;
 Best Local Similarity 100.08; Pred. No. 3.73e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 5 KAA1LTS 11
 11111111
 203 KAA1LTS 209

RESULT 35

ENTRY #type complete
 TITLE T02100
 #description hypothetical protein T3K9.4 - Arabidopsis thaliana
 ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear cress
 DATE 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 23-Apr-1999

ACCESSIONS

REFERENCE T02100
 214570
 #authors Rounsley, S.D.; Kaul, S.; Llin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kervatage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.

#submission submitted to the EMBL Data Library, February 1999
 #description Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence.
 #accession T02100
 #status translated from GB/EMBL/DBJ
 #molecule_type DNA
 #residues 1-454 ##label ROU
 #cross-references EMBL:AC004261; NID:g4402695; PID:g3402699
 #experimental_source cultivar Columbia

GENETICS

#map_position 2
 #infrons 72/2; 156/1; 227/3; 235/3; 296/1; 337/1; 392/2; 407/1; 428/1
 #length 454 #molecular-weight 50448 #checksum 3623

SUMMARY

Query Match 1.68; Score 7; DB 2; Length 454;
 Best Local Similarity 100.08; Pred. No. 3.73e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 9 EKKTDVT 15
 11111111
 386 EKKTDVT 392

RESULT 36

ENTRY #type complete
 TITLE B75080
 #type complete
 ENTRY hypothetical protein PAB0690 - Pyrococcus abyssi (strain

```

ORGANISM      #formal_name Pyrococcus abyssi
DATE          20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
ACCESSIONS    B75080
REFERENCE      A75001
#authors      anonymous, Genoscope
#submission   submitted to the EMBL Data Library, July 1999
#description   Pyrococcus abyssi genome sequence: insights into archaeal
                chromosome structure and evolution.
#accession    B75080
#status       preliminary
#molecule_type DNA
#residues     1-530 #label KAM
#cross-references GB:AJ248286; GB:AL096836; NID:95458366;
                PID:CA84943.1; PID:e1515840; PID:95458455
#experimental_source strain Orsay
GENETICS
#gene         PAB0690
SUMMARY       #length 530 #molecular_weight 58629 #checksum 5873
Query Match   1.6%: Score 7; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 445 CENKTT 451
OY 283 CENKTT 289

RESULT 37
ENTRY    B70682 #type complete
TITLE    Probable nitrite reductase - Mycobacterium tuberculosis
          (strain H37RV)
ORGANISM #formal_name Mycobacterium tuberculosis
DATE     17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
ACCESSIONS B70682
REFERENCE   A70500
#authors    Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
            C.; Harris, D.; Gordon, S.V.; Eiglmeyer, K.; Gass, S.; Barry,
            III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;
            Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
            Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
            Hornsby, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
            Rajandream, M.A.; Rogers, J.; Sanger, S.; Seeger, K.;
            Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.;
            Taylor, K.; Whitehead, S.; Barrett, B.G.
#journal    Nature (1998) 393:537-544
#title     Deciphering the biology of Mycobacterium tuberculosis from
            the complete genome sequence.
#cross-references MUID:98295987
#accession B70682
#status     preliminary; nucleic acid sequence not shown;
            translation not shown
#molecule_type DNA
#residues   1-563 #label COL
#cross-references GB:281368; GB:AL123456; NID:93261656; PID:e279651;
            PID:g1655669
#experimental_source strain H37RV
GENETICS
#gene       ntrA
SUMMARY     #length 563 #molecular_weight 62997 #checksum 1223
Query Match 1.6%: Score 7; DB 2; Length 563;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 48 ERENIT 54
OY 178 ERENIT 184

```

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RESULT 38
ENTRY    C71661 #type complete
TITLE    penicillin-binding protein (pbpA) RP565 - Rickettsia
          prowazekii.
ORGANISM #formal_name Rickettsia prowazekii
DATE     21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change
ACCESSIONS C71661
REFERENCE   A71630
#authors    Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.;
            Sichelitz-Ponten, T.; Alsmark, U.C.M.; Podowski, R.M.;
            Naeslund, A.K.; Eriksson, A.S.; Winkler, H.H.; Kurland,
            C.G.
#journal    Nature (1998) 396:133-140
#title     The genome sequence of Rickettsia prowazekii and the origin
            of mitochondria
#cross-references MUID:99039499
#accession C71661
#status     preliminary; nucleic acid sequence not shown;
            translation not shown
#molecule_type DNA
#residues   1-594 #label AND
#cross-references GB:AJ235272; GB:AJ235269; NID:93861033; PID:e1342857;
            PID:93861113
#experimental_source strain Madrid E
GENETICS
#gene       pbpA; RP565
CLASSIFICATION #superfamily penicillin-binding protein 3
SUMMARY      #length 594 #molecular_weight 67195 #checksum 9752
Query Match 1.6%: Score 7; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 186 NIRSLS 192
OY 338 NIRSLS 344

RESULT 39
ENTRY    F64889 #type complete
TITLE    membrane protein mroc - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE     12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
ACCESSIONS F64889
REFERENCE   A64720
#authors    Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
            Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
            Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
            Kirpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
            Y.
#journal    Science (1997) 277:1453-1462
#title     The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426517
#accession F64889
#status     nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues   1-681 #label BLAT
#cross-references GB:AF000236; GB:U00096; NID:91787652; PID:g1787653;
            UMG:p1387
#experimental_source strain K-12, substrain MG1655
FEATURE
301-317     #domain transmembrane #status predicted #label TM01\
588-604     #domain transmembrane #status predicted #label TM02
SUMMARY     #length 681 #molecular_weight 73002 #checksum 2628
Query Match 1.6%: Score 7; DB 2; Length 681;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 587 VLSAAG 593

```

```

OY 20 VLSAABG.26
RESULT 40
ENTRY 670559 #type complete
TITLE Probable uvrB protein - Mycobacterium tuberculosis (strain H37Rv)
ORGANISM #formal_name Mycobacterium tuberculosis
DATE 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 26-Aug-1999
ACCESSIONS 670559
REFERENCE A70500
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; G. Barry, III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rastread, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
#cross-references M01D:98295987
#accession 670559
#status preliminary; nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-698 #label COL
#cross-references GB:295554; GB:AL123456; NID:93261771; PIDN:CA808886.1; PID:ej16899; PID:92113917
#experimental_source strain H37Rv
GENETICS
#gene uvrB
CLASSIFICATION #superfamily exonuclease ABC chain B; DEAD/H box helicase homology
KEYWORDS ATP; P-loop
FEATURE
41-545 #domain DEAD/H box helicase homology #label DEAD\
335-340 #region nucleotide-binding motif A (P-loop)\
339-342 #region DEXH motif
SUMMARY #length 698 #molecular_weight 78070 #checksum 3125
Query Match 1.6%; Score 7; DB 2; Length 698; Best Local Similarity 100.0%; Pred. No. 3,73e+00; Mismatches 0; Indels 0; Gaps 0; Matches 7; Conservative 0;
DB 37 VVILGAT 43
OY 3 VVILGAT 9
RESULT 41
ENTRY A32495 #type complete
TITLE rep-1 protein, form A - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Feb-1997
ACCESSIONS A32495; A30939
REFERENCE A32495
#authors Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellems, R.E.; Crouse, G.F.
#journal Mol. Cell. Biol. (1989) 9:3058-3072
#title Dual bidirectional promoters at the mouse dhfr locus: cloning and characterization of two mRNA classes of the divergently transcribed Rep-1 gene.
#cross-references M01D:89384557
#accession A32495
#molecule_type mRNA

```

```

#residues 1-929 #label LIN
#cross-references GB:M24919; GB:004244
GENETICS
#gene rep-1
KEYWORDS DNA binding
SUMMARY #length 929 #molecular_weight 104652 #checksum 8244
Query Match 1.6%; Score 7; DB 2; Length 929; Best Local Similarity 100.0%; Pred. No. 3,73e+00; Mismatches 0; Indels 0; Gaps 0; Matches 7; Conservative 0;
DB 279 NKSSVES 285
OY 416 NKSSVES 422
RESULT 42
ENTRY A40021 #type complete
TITLE Integrin VLA-3 alpha-3 chain precursor - human
ALTERNATE_NAMES fusion regulatory protein FRP2; galactoprotein b3; very late antigen-3 alpha chain
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 29-Sep-1999
ACCESSIONS A40021; JX0161; C28018; S44356
REFERENCE A40021
#authors Takada, Y.; Murphy, E.; Pil, P.; Chen, C.; Ginsberg, M.H.; Hemler, M.E.
#journal J. Cell Biol. (1991) 115:257-266
#title Molecular cloning and expression of the cDNA for alpha-3 subunit of human alpha-3beta-1 (VLA-3), an integrin receptor for fibronectin, laminin, and collagen.
#cross-references M01D:92011866
#accession A40021
#molecule_type mRNA
#residues 1-1051 #label TAK
REFERENCE JX0161
#authors Tsuji, T.; Hakomori, S.; Osawa, T.
#journal J. Biochem. (1991) 109:659-665
#title Identification of human galactoprotein b3, an oncogenic transformation-induced membrane glycoprotein, as VLA-3 alpha subunit: The primary structure of human integrin alpha 3.
#cross-references M01D:91331981
#accession JX0161
#molecule_type mRNA
#residues 33-1051 #label TSU
#cross-references GB:PD01038; NID:9220140; PIDN:BAA00845.1; PID:dl001309; PID:9220141
REFERENCE A94151
#authors Takada, Y.; Strominger, J.L.; Hemler, M.E.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:3239-3243
#title The very late antigen family b3 heterodimers is part of a superfamily of molecules involved in adhesion and embryogenesis.
#cross-references M01D:87204112
#accession C28018
#molecule_type protein
#residues 33-46 #label TAZ
REFERENCE S44356
#authors Ohta, H.; Tsurudome, M.; Matsumura, H.; Koga, Y.; Morikawa, S.; Kawano, M.; Kusugawa, S.; Komada, H.; Nishio, M.; Ito, Y.
#journal EMBO J. (1994) 13:2044-2055
#title Molecular and biological characterization of fusion regulatory proteins (FRPs): anti-FRP mAbs induced HIV-mediated cell fusion via an integrin system.
#cross-references M01D:94244603
#accession S44356
#status preliminary
#molecule_type protein
#residues 33-43, 'X', 45-49 #label OHT

```

GENETICS
#gene GDB:ITGA3
#map_position 17q21.32-17q21.32
#supfamily integrin alpha-2b chain
#classification calcium binding; cell adhesion; duplication; glycoprotein; heterodimer; metal binding; transmembrane protein

FEATURE
1-32
33-871
168-176
241-249
315-323
378-386
439-447
874-1051
992-1019
86,107,265,500,511,
573,605,656,697,
841,857,926,935,
969

SUMMARY
#length 1051 #molecular_weight 116611 #checksum 8842
#predicted
#binding_site carbohydrate (asn) (covalent) #status predicted

Query Match 1.6% Score 7; DB 2; Length 1051;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 994 LVLVAVG 1000
11 LVLVAVG 17

RESULT 43
ENTRY I55534 #type complete
TITLE VLA-3 alpha subunit - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 29-Sep-1999

ACCESSIONS
REFERENCE I55534
#authors Takeuchi, K.; Hirano, K.; Tsuji, T.; Osawa, T.; Irimura, T.
#journal J. Cell. Biochem. (1995) 57:371-377
#title CDNA cloning of mouse VLA-3 alpha subunit.
#cross-references MUID:95279462.
#accession I55534

CLASSIFICATION
#molecule_type mRNA
#residues 1-1053 #label RES
#cross-references GB:D18867; NID:9220634; PIDN:BAA02980.1; PID:9220635
#supfamily integrin alpha-2b chain
#length 1053 #molecular_weight 116744 #checksum 976

SUMMARY
Query Match 1.6% Score 7; DB 2; Length 1053;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 996 LVLVAVG 1002
11 LVLVAVG 17

RESULT 44
ENTRY JC4019 #type complete
TITLE DNA mismatch repair protein rep-3 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 17-Mar-1999

ACCESSIONS
REFERENCE JC4019
#authors Liu, K.; Niu, L.; Linton, J.P.; Crouse, G.F.

#journal Gene (1994) 147:169-177
#title Characterization of the mouse Rep-3 gene: Sequence similarities to bacterial and yeast mismatch-repair proteins.
#cross-references MUID:95011610
#accession JC4019
#molecule_type mRNA
#residues 1-1126 #label L10
#cross-references GB:L10295
REFERENCE A32495
#authors Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellems, R.E.; Crouse, G.F.
#journal Mol. Cell. Biol. (1994) 9:3058-3072
#title Dual bidirectional promoters at the mouse dirr locus: cloning and characterization of two mRNA classes of the divergently transcribed Rep-1 gene.
#cross-references MUID:89384567
#accession C32495
#status preliminary
#molecule_type mRNA
#residues 47-60 #label L1N
#cross-references GB:M24918; GB:J04244

GENETICS
#gene Rep-3
#introns 86/2; 159/3; 222/3; 261/3; 301/1; 349/3; 405/2; 443/2; 481/1; 546/2; 650/2; 706/1; 728/2; 767/2; 803/2; 840/2; 892/1; 998/2; 1055/2
#note gene previously known as Rep-1

SUMMARY
#length 1126 #molecular_weight 127207 #checksum 9169

Query Match 1.6% Score 7; DB 2; Length 1126;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 NKSSVFS 299
416 NKSSVFS 422

RESULT 45
ENTRY G70600 #type complete
TITLE hypothetical protein RV3910 - Mycobacterium tuberculosis (strain H37RV)
ORGANISM #formal_name Mycobacterium tuberculosis
DATE 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998

ACCESSIONS
REFERENCE G70600
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Hornby, T.; Jagers, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.; Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
#cross-references MUID:98295987
#accession G70600
#status preliminary; nucleic acid sequence not shown; translation not shown

GENETICS
#gene RV3910
#length 1184 #molecular_weight 123562 #checksum 6654

Tue Aug 22 08:32:28 2000

US-09-240-675-2.rpr

Page 21

Query Match 1.68; Score 7; DB 2; Length 1184;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 LGATT 119
|||||
QY 5 LGATT 11

Search completed: Mon Aug 21 10:31:39 2000
Job time : 61 secs.

01 08 1980

Page 51

201 A 201
67 s 67

seq_name: A_Geneseq_36:R14487

seq_documentation_block:

ID R14487 standard; Protein: 436 AA.
AC R14487;
DE 16-JAN-1992 (first entry)
DE Soluble interferon alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-APR-1991.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G;
DR MPI; 91-31978/44.
DR N-PSDB; 014239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 45; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor
CC have been deleted to obtain a soluble, circulating form of the
CC receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence
CC are also claimed as are hybrid molecules comprising the soluble
CC receptor (or deriv.) and an immunoglobulin such as IgG.
CC See also 014240.
SQ Sequence 436 AA.

alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R14487

Align seg 1/1 to: R14487 from: 1 to: 436

```

1 ATGATGCTGCTCTCTGCGCGGAGACCCCTAGTCTGCTGCGCGGTGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValG1 17
51 CCATGGCTGTGTCGCCAGCCGAGGTGGAATAAATCTAATCTCTCT 100
17 YProTPrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTGCACATCATATGACAACTTATCTGAGGTGGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuAyrTrpAsn 50
151 AGGAGCATGAGTCTGCGGGAATGTGACTTTTCATTCGATTATCAAA 200
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTyrGlnL 67
201 A 201
67 s 67

```

seq_name: A_Geneseq_36:R28495

seq_documentation_block:

ID R28495 standard; Protein: 436 AA.
AC R28495;
DE 31-MAR-1993 (first entry)

DE Sequence of a soluble form of the interferon (IFN) receptor
DE with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN M09218626-A.
PD 29-OCT-1992.
PR 17-APR-1991; F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G;
DR MPI; 92-382110/46.
DR N-PSDB; 030532.

PT Water-soluble polypeptide(s) strongly bind interferon(s) alpha
PT and -beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
CC IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies, so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 436 AA.

alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R28495

Align seg 1/1 to: R28495 from: 1 to: 436

```

1 ATGATGCTGCTCTCTGCGCGGAGACCCCTAGTCTGCTGCGCGGTGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValG1 17
51 CCATGGCTGTGTCGCCAGCCGAGGTGGAATAAATCTAATCTCTCT 100
17 YProTPrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTGCACATCATATGACAACTTATCTGAGGTGGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuAyrTrpAsn 50
151 AGGAGCATGAGTCTGCGGGAATGTGACTTTTCATTCGATTATCAAA 200
51 ArgSerAspGlnSerValGlyAsnValThrPheSerPheAspTyrGlnL 67
201 A 201
67 s 67

```

seq_name: A_Geneseq_36:R71723

seq_documentation_block:

ID R71723 standard; Protein: 436 AA.
AC R71723;
DE 16-OCT-1995 (first entry)
DE IFN receptor extracellular domain.
KW IFN receptor; Interferon receptor; Interferon alpha;
KW Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.
OS Homo sapiens.
PN W09507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E03114.

PR 17-SEP-1993, EP-402279.
 PA (EMBL) LAB EURO BIOTECHNOLOGIE SA.
 PI Benlizi E, Tovey M;
 DR WPI: 95-131187/17.
 DR N-PSDB: 086457.
 PT Compn. of monoclonal antibodies against interferon receptor
 useful as immunomodulator, eg. for treating AIDS.
 PS Disclosure: Fig. 2A-2B; 105pp; English.
 CC A recombinant soluble form of the human interferon class I receptor
 protein extracellular domain, given in R71723, was expressed in
 CC either E. coli or COS cell hosts. The protein was used to raise
 CC immunomodulatory monoclonal antibodies.
 SO Sequence 436 AA.

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R71723

Align seg 1/1 to: R71723 from: 1 to: 436

```

1 ATGATGTCGTCCTCTCGGCGCGAGACCTAGTCGTCGCGCGTGGG 50
|||||
1 Mectetvalvalleuenglialathrthrleuvallevalalvalgl 17
51 CCCAGGCGTGTGTCGCGAGCCGCGAGTGAATAATCTAAATCTCC 100
|||||
17 yprotrpvalleuserialalalaglylysasnleulysserprog 34
|||||
101 AAAAGTAGAGTCGACATCATGATGACACTTATCTCTGAGGTGGA 150
|||||
34 Intlyvalgluvalaspilleleaspaspaspaspaspaspasp 50
|||||
151 AGGACCGATGATGTCGCGGAGATGACTTTTCATTGATTAACAAA 200
|||||
51 Argseraspgluservalgllyasnvalthrpheserphesaptygl 67
201 A 201
67 s 67

```

seq_name: A_Geneseq_36:W21806

seq_documentation_block:

ID W21806 standard; Protein; 496 AA.

AC W21806;

DT 23-SEP-1997 (first entry)

DE Spliced-deleted interferon alpha-receptor form 2.

KM Interferon alpha-receptor; IFNAR.

OS Homo sapiens.

EH Key

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

PS Example 3; Fig 7; 46pp; English.
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
 CC (W21806) is characterised by a double deletion when compared to
 CC transmembrane IFNAR (W21804). The extracellular domain is
 CC shortened by 6 amino acid residues and is followed by a truncated
 CC intracellular domain. There is no transmembrane region. The amino
 CC acid sequence is predicted from a cDNA clone (see also W73521) obtd.
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
 CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
 CC response of human cells to IFNs, either by acting as IFN
 CC antagonists or by regulating IFN activities. They can be expressed
 CC in host cells and used to inhibit, modulate or modify the
 CC activities of IFNs alpha and beta in cells, tissues and organisms,
 CC or for diagnostic purposes.
 SO Sequence 496 AA.

alignment_scores:
 Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x W21806

Align seg 1/1 to: W21806 from: 1 to: 496

```

1 ATGATGTCGTCCTCTCGGCGCGAGACCTAGTCGTCGCGCGTGGG 50
|||||
1 Mectetvalvalleuenglialathrthrleuvallevalalvalgl 17
51 CCCAGGCGTGTGTCGCGAGCCGCGAGTGAATAATCTAAATCTCC 100
|||||
17 yprotrpvalleuserialalalaglylysasnleulysserprog 34
|||||
101 AAAAGTAGAGTCGACATCATGATGACACTTATCTCTGAGGTGGA 150
|||||
34 Intlyvalgluvalaspilleleaspaspaspaspaspaspasp 50
|||||
151 AGGACCGATGATGTCGCGGAGATGACTTTTCATTGATTAACAAA 200
|||||
51 Argseraspgluservalgllyasnvalthrpheserphesaptygl 67
201 A 201
67 s 67

```

seq_name: A_Geneseq_36:R11958

seq_documentation_block:

ID R11958 standard; Protein; 557 AA.

AC R11958;

DT 18-JUL-1991 (first entry)

DE Human alpha-interferon receptor protein.

KM Human alpha IFN; IFN agonists; antiviral; anti tumour agent;

OS Homo sapiens.

EH Key

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

CC nosis of viral diseases and tumours. Antibodies raised against
 CC this protein can be used for blocking the receptor when required,
 CC eg where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the protein,
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 SO Sequence 557 AA;

alignment_scores:

Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R1958

Align seg 1/1 to: R1958 from: 1 to: 557

1 ATGATGTCGTCCTCTGCGCGGCGAGACCTAGTCTGTCGCGCGG 50
 1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
 51 CCCATGGTGTGTCGCCGACGCCGAGTGGAATAAATCTCTCTC 100
 17 YProTyrValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
 101 AAAAGTAGAGTGCATCATGATGACACTTATCTAGGTGAGAC 150
 34 InLysValGluValAspLeuLeuLeuAspAsnPhelleuArgTyrPasn 50
 151 AGGAGCGATGCTGTCGGGAATGTGACTTTTCATTCGATTATCAAA 200
 51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
 201 A 201
 67 s 67

seq_name: A_Geneseq_36:R14488

seq_documentation_block:

ID R14488 standard; Protein: 557 AA.
 AC R14488;
 DT 16-JAN-1992 (first entry)
 DE Complete interferon-alpha/beta receptor.
 KW IFN; autoimmune disease; graft rejection; histocompatibility.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 437..457
 FT /label= transmembrane
 FT 458..557
 FT /label= cytoplasmic
 FN domain
 FR2657881-A;
 PD 09-AUG-1991.
 PR 05-FEB-1990; 001298.
 PR 05-FEB-1990; FR-001298.
 PA (EUBI-) LAB EURO BIOECHO.
 EId P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
 Tovey M, Uze G;
 WPI: 91-319778/44.
 DR N-PSDB; Q14240.
 PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
 PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
 PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
 PS Disclosure; Page 47; 52pp; French.
 CC The invention covers derivatives of the interferon-alpha and/or beta
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains
 CC of the native receptor or by substitution. Potentially immunogenic
 CC epitopes are eliminated and the deriv. can be secreted from
 CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
 CC and can be used to treat autoimmune diseases or to inhibit graft
 CC rejection. See also Q14239.

SO Sequence 557 AA;

alignment_scores:

Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R14488

Align seg 1/1 to: R14488 from: 1 to: 557

1 ATGATGTCGTCCTCTGCGCGGCGAGACCTAGTCTGTCGCGCGG 50
 1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
 51 CCCATGGTGTGTCGCCGACGCCGAGTGGAATAAATCTCTCTC 100
 17 YProTyrValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
 101 AAAAGTAGAGTGCATCATGATGACACTTATCTAGGTGAGAC 150
 34 InLysValGluValAspLeuLeuLeuAspAsnPhelleuArgTyrPasn 50
 151 AGGAGCGATGCTGTCGGGAATGTGACTTTTCATTCGATTATCAAA 200
 51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67
 201 A 201
 67 s 67

seq_name: A_Geneseq_36:R28496

seq_documentation_block:

ID R28496 standard; Protein: 557 AA.
 AC R28496;
 DT 31-MAR-1993 (first entry)
 DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KW Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN WC9218626-A.
 PD 29-OCT-1992.
 PR 17-APR-1991; F00318.
 PR 17-APR-1991; WO-F00318.
 PA (EUBI-) LAB EURO BIOECHOLOGIE.
 EId P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
 Tovey M, Uze G;
 WPI: 92-382110/46.
 DR N-PSDB; Q30533.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating auto-immune
 PT diseases and transplant rejection
 PS Claim 3; Fig 2; 58pp; English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template. For example,
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SO Sequence 557 AA;

alignment_scores:

Quality: 340.00 Length: 67
 Ratio: 5.075 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_229 x R28496

Align seg 1/1 to: R28496 from: 1 to: 557

1 ATGATGGTCTCTCTGGCGGAGACCCATGCTGCTGCGCGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValG1 17
51 CCCATGGGTGTGTCGCGAGCCGAGCGGAGGAAAAATCTAAATCTCC 100
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATCATGATGACACTTTTTCCTGAGGTGAGAC 150
34 IntyValGluValAlaAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGAGCGATGAGTCTGTCGCGAATGACTTTTTCATTGATTATCAAA 200
51 ArgSerAspGluSerValGlyLysValThrPheSerPheAspTyrGlnLys 67

201 A 201

67 s 67

seq_name: A_Geneseq_36:R42635

seq_documentation_block:

ID R42635 standard; Protein: 557 AA.
AC R42635.
DT 20-APR-1994 (first entry)
DE Human interferon receptor.
KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
cell proliferation; allograft rejection; systemic lupus erythematosus;
psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
immunodeficiency; measles virus; Interferon-alpha-beta.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= extracellular_domain
FT /note= "soluble, immunogenic form of IFN-R"
PN EP-563487-A.
PD 06-OCT-1993.
PF 31-MAR-1992; 400902.
PR 31-MAR-1992; EP-400902.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
DR WPI: 93-312951/40.
DR N-PSDB; R42635.
PT Monoclonal antibody to human interferon type-I receptor - having
neutralising activity against human type I interferon, used for
therapy and diagnosis
PS Disclosure; Fig 3; 21pp; English.
CC Monoclonal antibodies produced against soluble forms of the human
interferon alpha-beta receptor based on the full-length human IFN-R
sequence are claimed. The antibodies are useful for treatment and
CC prophylaxis of disorders involving cell proliferation and/or viral
infection.
CC Sequence 557 AA;

alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R42635

Align seg 1/1 to: R42635 from: 1 to: 557

1 ATGATGGTCTCTCTGGCGGAGACCCATGCTGCTGCGCGG 50

1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValG1 17
51 CCCATGGGTGTGTCGCGAGCCGAGCGGAGGAAAAATCTAAATCTCC 100
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATCATGATGACACTTTTTCCTGAGGTGAGAC 150
34 IntyValGluValAlaAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGAGCGATGAGTCTGTCGCGAATGACTTTTTCATTGATTATCAAA 200
51 ArgSerAspGluSerValGlyLysValThrPheSerPheAspTyrGlnLys 67

201 A 201

67 s 67

seq_name: A_Geneseq_36:R75356

seq_documentation_block:

ID R75356 standard; Protein: 557 AA.
AC R75356.
DT 16-OCT-1995 (first entry)
DE Human IFN receptor.
KW IFN receptor; Interferon receptor; Interferon-alpha;
Interferon-beta; monoclonal antibody; immunomodulator; AIDS.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..436
FT /label= extracellular_domain
PN W09507716-A.
PD 23-MAR-1995.
PF 16-SEP-1994; E01114.
PR 17-SEP-1993; EP-402279.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
PI Benizri EJ, Tovey MG;
DR WPI: 95-131187/17.
DR N-PSDB; 086458.
PT Compn. of monoclonal antibodies against Interferon receptor -
useful as immunomodulator, eg. for treating AIDS
PS Disclosure; Fig 3A-2B; 105pp; English.
CC The amino acid sequence of human interferon class I receptor is
CC given in R75356. A recombinant soluble form of the extracellular
CC domain of this receptor (R71723) has been used to raise
CC immunomodulatory monoclonal antibodies.
CC Sequence 557 AA;

alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x R75356

Align seg 1/1 to: R75356 from: 1 to: 557

1 ATGATGGTCTCTCTGGCGGAGACCCATGCTGCTGCGCGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValG1 17
51 CCCATGGGTGTGTCGCGAGCCGAGGTGAAAAATCTAAATCTCTC 100
17 yProtrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTCGACATCATGATGACACTTTTTCCTGAGGTGAGAC 150
34 IntyValGluValAlaAspIleIleAspAspAsnPhelIleuArgTrpAsn 50
151 AGAGCGATGAGTCTGTCGCGAATGACTTTTTCATTGATTATCAAA 200

|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67

201 A 201

67 s 67

seq_name: A_Geneseq_36:W21804

seq_documentation_block:

ID: W21804 standard; Protein: 557 AA.

AC W21804

DT 23-SEP-1997 (first entry)

DE Transmembrane Interferon alpha-receptor.

KW Interferon alpha-receptor; IFNAR.

OS Homo sapiens.

FT Key Location/Qualifiers

FT domain 1..436 Extracellular_domain

FT domain 437..457

FT domain 458..557

FT domain /label= Intracellular_domain

FT AU9475977-A.

PD 11-MAY-1995

PD 20-OCT-1994

PR 24-OCT-1993

PA (YEDA) YEDA RES & DEV CO LTD.

PA (ABRA/) ABRAMOVICH C.

PI Abramovich C, Ratovlitaki E, Revel M;

DR WPI: 95-200634/27.

PT New mammalian soluble interferon alpha-receptor forms - used for

PS Inhibiting, modulating or modifying the activities of interferon(s)

CC Disclosure; Fig 7; 46pp; English.

CC Human transmembrane Interferon alpha receptor (IFNAR) (W21804)

CC Includes a 21-amino acid transmembrane region. Novel, splice

CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected

CC that lack this transmembrane domain. These, soluble non-membrane

CC bound polypeptides can be expressed in host cells and used to

CC inhibit, modulate or modify the activities of Interferons alpha

CC and beta in cells, tissues and organisms, or for diagnostic

CC purposes.

CC Sequence 557 AA;

SO

Alignment_scores:

Quality: 340.00 Length: 67

Ratio: 5.075 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:

US-09-240-675-1_COPY_27_229 x W21804

Align seg 1/1 to: W21804 from: 1 to: 557

1 ATGATGCTGCTCTCTGCGCGGAGACCTAGTCTGCTGCGCGGCGG 50
1 MetMetValValLeuLeuValValThrThrLeuValValLeuValValVal 17
51 CCCATGGGCTGTCGCGCGGCGGAGGAGAAATCAATCAATCTCC 100
17 yProTrpValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34
101 AAAAAAGAGGTGACATCATAGATGACACTTATCTGAGGTGGAAC 150
34 LdLyValGlyValAspIleLeuAspAspAspPheIleLeuArgTrpAsn 50
151 AGGACGATGAGTCTGCGGAGATGACTTTTATTCGATTATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67

201 A 201

67 s 67

seq_name: A_Geneseq_36:W93941

seq_documentation_block:

ID: W93941 standard; Protein: 1429 AA.

AC W93941

DT 30-JUN-1999 (first entry)

DE Human bix protein.

KW Bix protein; breast cancer; nuclear receptor-binding auxiliary protein;

KW anti-cancer; anti-proliferative; mitogen; transcription factor; human;

KW tumour suppressor; ovarian cancer; proliferative disorder; treatment;

KW immune tissue; prevention; reproductive tissue.

OS Homo sapiens.

PN W09915544-A1

PD 01-APR-1999

PD 23-SEP-1998

PR 23-SEP-1997; US-059621

PA (DRIG/) DRIGGERS P H.

PA (RUBI/) RUBINO D M.

PA (SEGE/) SEGERS J.

PI Driggers PH, Rubino DM, Segers J;

DR WPI: 99-254688/21.

DR N-PSDB: X24044

PT Breast cancer gene encoding a nuclear receptor-binding auxiliary

PS protein, bix

CC Claim 1b, Page 58-62; 69pp; English.

CC This invention describes a novel human breast cancer gene encoding a

CC nuclear receptor-binding auxiliary protein, bix. The bix encoded protein

CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a

CC transcription factor and tumour suppressor. Levels of expression of bix

CC can be detected using the primers, probes and antibodies (contained in

CC the kit) to determine a predisposition to breast and ovarian cancer and

CC other proliferative disorders of immune tissues. Vectors containing the

CC bix gene can be used for prevention and treatment of cancers and

CC proliferative diseases of mammalian reproductive and immune tissues.

CC Sequence 1429 AA;

SO

Alignment_scores:

Quality: 75.00 Length: 74

Ratio: 1.923 Gaps: 5

Percent Similarity: 52.703 Percent Identity: 41.892

Alignment_block:

US-09-240-675-1_COPY_27_229 x W93941

Align seg 1/1 to: W93941 from: 1 to: 1429

3 GATGTCGCTCTCTGCGCGGAGACCTAGTCTGCTGCGCGGCGG 52
1230 AspGlyArgProSerTrp.....ProSerAlaArgArgArgCysSe 1243
53 CATGGCTGTGTCGCCGCGGAGCGAGGTGGAATAATCTCTCTCA 102
1243 rArgGly.....SerArgThrTrpLysArgSerGlyArgSerSe 1257
103 AAGTAGAGGTGACATCATAGATGACACTT..... 134
1257 eArgArgArgAlaAlaAlaSerGlnTrpAspLeuGluArgLeuArgAla 1273
135rATCTGAGGTGAGMACAGAGGAGTACTGCTGCGGAATGCA 178
1274 GlnLysGlnLeuGluArgGlnGlnGlnHis.....ValArgArgGluAla 1289
179 CTTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 200
1289 u.....ArgLeuSerGln 1293

seq_name: A_Geneseq_36:W93962

seq_documentation_block:

ID: W93962 standard; Protein: 30 AA.

AC W93962;
 DE 30-JUN-1999 (first entry)
 DE Human brx immunogenic peptide 1.
 KW Brx protein; breast cancer; nuclear receptor-binding auxiliary protein;
 KW anti-cancer; anti-proliferative; mitogen; transcription factor; human;
 KW tumour suppressor; ovarian cancer; proliferative disorder; treatment;
 KW Immune tissue; prevention; reproductive tissue; immunogenic.
 OS Homo sapiens.
 PN MO9915544-A1.
 PD 01-APR-1999.
 PF 23-SEP-1998; US-09782.
 PR 23-SEP-1997; US-059621.
 PA (DRIC/) DRIGERS P H.
 PA (RUBI/) RUBINO D M.
 PA (SEGE/) SEGERS J.
 PI Driggers PH, Rubino DM, Segers J;
 WPI: 99-254688/21.
 DR Breast cancer gene encoding a nuclear receptor-binding auxiliary
 PT protein, brx
 PS Disclosure; Page 29; 69pp; English.
 CC This invention describes a novel human breast cancer gene encoding a
 CC nuclear receptor-binding auxiliary protein, brx. The brx encoded protein
 CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a
 CC transcription factor and tumour suppressor. Levels of expression of brx
 CC can be detected using the primers, probes and antibodies (contained in
 CC the kit) to determine a predisposition to breast and ovarian cancer and
 CC other proliferative disorders of immune tissues. Vectors containing the
 CC brx gene can be used for prevention and treatment of cancers and
 CC proliferative diseases of mammalian reproductive and immune tissues.
 SQ Sequence 30 AA;

alignment_scores:
 Quality: 62.00 Length: 33
 Ratio: 3.263 Gaps: 2
 Percent Similarity: 57.576 Percent Identity: 54.545

alignment_block:
 US-09-240-675-1_COPY_27_229 x W93962 ..

Align seg 1/1 to: W93962 from: 1 to: 30

3 GATGCTGCTCCTCGGCGGACAGACCTAGTGTCTCCGCCGCGGCC 52
 |||||
 3 AspGlyArgProSerTrp.....ProSerIlaArgArgCysSe 16
 53 CATGGCTGTTCGCCGACGCCAGGTGGAATAATCTAAATCTCTCA 101
 |||||
 16 rArgGly.....SerArgThrIlePlyArgSerIleArgSerSer 29

seq_name: A_Geneseq_36:W52296

seq_documentation_block:
 ID W52296 standard; Protein; 325 AA.
 AC W52296;
 DE 23-JUN-1998 (first entry)
 DE CREB4 protein.
 KW CREB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection;
 KW vaccine; photosensitivity; inflammation; autoimmune disease;
 KW septic shock; immune response; organ rejection; gene therapy.
 OS Homo sapiens.
 PN MO9802542-A1.
 PD 22-JAN-1998.
 PF 17-JUL-1997; U12455.
 PR 17-JUL-1996; US-683743.
 PA (UYNE-) UNIV NEW JERSEY.
 PI Kotenko SV, Pestka S;
 WPI: 98-110590/10.
 DR N-PS08: V19874.
 PT New recombinant DNA - comprises sequences encoding interleukin-10
 PT and CREB4 linked to operator, useful, e.g. preventing allograft
 PT rejection
 PS Claim 2; Page 7; 79pp; English.

CC This sequence is the human CREB4 sequence, DNA encoding it is used in the
 CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1)
 CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
 CC encoding CREB4, both operably linked to expression control sequences.
 CC Cells containing (I) may be used to identify agonists/antagonist of
 CC IL-10. Agonists are potentially useful, e.g. for preventing allograft
 CC rejection, as vaccine adjuvants, for treatment of photosensitivity,
 CC inflammation, autoimmune disease and septic shock, while antagonists are
 CC potentially useful for increasing immune responses against tumours,
 CC viruses, bacteria and parasites (especially intracellular pathogens) and
 CC for preventing organ rejection. A vector containing (I) is used to
 CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses
 CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a
 CC signal. Antisense CREB4 sequences (especially ribozymes), can inhibit
 CC IL-10 activity in cells. Antibodies specific for CREB4 are used to
 CC measure and localise CREB4, for diagnosis of defective IL-10 activity.
 CC Fragments of (I) are used as primers or probes to assay CREB4-specific
 CC RNA. Agonists/antagonists may be administered parenterally, orally or
 CC rectally especially by intravenous injection or directly into a tumour or
 CC allograft.
 SQ Sequence 325 AA;

alignment_scores:
 Quality: 61.50 Length: 54
 Ratio: 1.922 Gaps: 1
 Percent Similarity: 59.259 Percent Identity: 29.630

alignment_block:
 US-09-240-675-1_COPY_27_229 x W52296 ..

Align seg 1/1 to: W52296 from: 1 to: 325

55 TGGGCTGTTCGCCGACGCCAGGTGGAATAATCTAAATCT..... 96
 ||| ||||| ||||| |||||
 3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuG1 19
 97CCTCAAAAGTAGAGTCGACATCATGATGACAACT 133
 |||||
 19 yMetValProProGluAsnValArgMetAsnSerValAsnPhelysa 36
 134 TTATCCTAGAGTGGAACAGAGCATGAGTGTCTGGCAATGTACTTT 183
 |||||
 36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
 184 TCATTTCATTAT 195
 ::::|
 53 ThrAlaGlnTyr 56

seq_name: A_Geneseq_36:W07702

seq_documentation_block:
 ID W07702 standard; Protein; 543 AA.
 AC W07702;
 DE 06-APR-1997 (first entry)
 DE Mouse ETS2 repressor factor (ERF).
 KW ETS2 repressor factor; ERF; transcriptional repressor;
 KW tumour suppressor; tumour; cancer; oncoprotein; therapy.
 OS Mus sp.
 FH Key
 FT Location/Qualifiers
 FT domain 21..98
 FT /label= "DNA binding domain"
 FT /note= "ets-like DNA binding domain"
 FT 466..525
 FT /label= "Active_repressor_domain"
 PN MO9639517-A1.
 PD 12-DEC-1996.
 PF 04-JUN-1996; U10177.
 PR 05-JUN-1995; US-469412.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Athanasiou MA, Beal GJ, Blair DG, Fisher RJ, Mavrouthalassitis GJ,
 PI Sgouras D N;
 WPI: 97-043139/04.

DR N-PSDB: T47200.
PT New DNA encoding ETS2 repressor factor - useful for reducing
tumourigenicity, esp. oncogene associated tumour cells
PS Disclosure; Page 70-72; 101pp; English.
CC Murine ETS2 repressor factor (ERF) (W07702) is a member of the ETS
family and acts as a transcriptional repressor in mammalian cells.
CC Its amino acid sequence was deduced from the murine ERF gene
(T47198). Human ERF (see also W07700) has also been identified.
CC ERF has tumour suppressor activity. Chimeric molecules comprising
the ERF repressor domain in combination with a heterologous
transcription factor having a binding domain can be used to reduce
tumourigenicity associated with inappropriate expression of
transcription factors.
SQ Sequence 543 AA;

Alignment scores:
Quality: 61.00 Length: 24
Ratio: 3.389 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 45.833

Alignment Block:

US-09-240-675-1_COPY_27_229/rev x W07702

Align seg 1/1 to: W07702 from: 1 to: 543

82 TTCACCTCGGCTGGGAGCAACACCCATGGGCCCGGAGAGAGACT 33
||| :::::||||| ||:::|||||
367 PhetySPhetySPleucInProProLeuGlyArgArgGlnArgLAl 383
32 AGGTCGTGCGCCCGGAGAGA 11
||| :::::|||||
383 aglyglnlysalalProglyGly 390

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MPearch_p protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 10:29:33 2000; MasPar time 12.38 seconds; 834,259 Million cell updates/sec

Tabular output not generated.

Title: >US-09-240-675-2
 Description: (1-436) from US09240675.pep
 Perfect score: 436
 Sequence: 1 MAAVLLCATTLVLAAGVPMV.....KSSVSDAVCEKTRPGNTSK 436

Scoring table:
 TABLE uniprottable
 Gap 60

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 1000 summaries

Database: a-geneseq36
 1:geneseqp

Statistics: Mean 2.943; Variance 0.687; scale 4.285

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description Pred. No.

1	436	100.0	436	1	R28495	Sequence of a soluble	0.00e+00
2	436	100.0	436	1	R14487	Soluble Interferon- α	0.00e+00
3	436	100.0	557	1	R14488	Complete Interferon- α	0.00e+00
4	436	100.0	557	1	R11958	Human alpha-Interferon	0.00e+00
5	436	100.0	557	1	R42635	Human Interferon recep	0.00e+00
6	436	100.0	557	1	R28496	Sequence of a soluble	0.00e+00
7	385	88.3	557	1	R75356	Human IFN receptor.	0.00e+00
8	385	88.3	557	1	W21804	Transmembrane Interfe	0.00e+00
9	376	86.2	434	1	W21805	Spliced-deleted Interf	0.00e+00
10	362	83.0	434	1	W21806	Spliced-deleted Interf	0.00e+00
11	318	72.9	436	1	R7123	IFN receptor, extracell	0.00e+00
12	17	3.9	17	1	R47008	IFN-alpha receptor pos	1.21e-13
13	17	1.6	153	1	W22599	Alpha 3b integrin subu	2.21e-01
14	15	1.6	258	1	W22599	Human fast twitch skel	2.21e-01
15	15	1.6	337	1	R71035	Human IFN-gamma access	2.21e-01
16	15	1.6	337	1	R75783	Human IFN-gamma recep	2.21e-01
17	15	1.6	408	1	R77867	S. ciavalligerus ORF10	2.21e-01
18	15	1.6	441	1	W20402	H. pylori cytoplasmic	2.21e-01
19	15	1.6	553	1	W79159	zycytor7 cytokine recep	2.21e-01
20	15	1.6	1019	1	R14118	Human GAP b3 protein.	2.21e-01
21	15	1.6	1051	1	W54032	Human alpha3 integrin.	2.21e-01
22	7	1.6	2206	1	R22210	True type 3 poliovirus	2.21e-01
23	6	1.4	9	1	W40852	Cytotoxic Epstein-Barr	2.94e+02

24	6	1.4	9	1	R80024	Cytotoxic Epstein-Barr	2.94e+02
25	6	1.4	9	1	R84905	Epstein-Barr virus der	2.94e+02
26	6	1.4	19	1	R73033	Human tyrosinase anti	2.94e+02
27	6	1.4	20	1	R71509	LPX-2.1, peptide frag	2.94e+02
28	6	1.4	20	1	R71510	LPX-3, peptide fragme	2.94e+02
29	6	1.4	23	1	R15517	BMP-8 peptide	2.94e+02
30	6	1.4	37	1	R50181	Fragment of excitatory	2.94e+02
31	6	1.4	38	1	W40091	Seq ID 99 from US57032	2.94e+02
32	6	1.4	38	1	W59202	Seq ID 99 from US 5753	2.94e+02
33	6	1.4	42	1	W78223	Human secreted protein	2.94e+02
34	6	1.4	45	1	W33605	Human secreted protein	2.94e+02
35	6	1.4	60	1	W55271	H. pylori ORF 05ap1091	2.94e+02
36	6	1.4	76	1	W74756	Human secreted protein	2.94e+02
37	6	1.4	85	1	W58848	Human C-C chemokine, DG	2.94e+02
38	6	1.4	92	1	W20172	Human A1168.4, secreted	2.94e+02
39	6	1.4	102	1	W29774	H. pylori protein.	2.94e+02
40	6	1.4	110	1	W20533	Malassezia fungus NF-7	2.94e+02
41	6	1.4	112	1	W60650	H. pylori cytoplasmic	2.94e+02
42	6	1.4	114	1	R38777	Human C-C chemokine, DG	2.94e+02
43	6	1.4	114	1	R25524	Active site peptide, fr	2.94e+02
44	6	1.4	117	1	R25524	Human T lymphocyte rec	2.94e+02
45	6	1.4	130	1	Y12709	Tobacco Ring spot Viru	2.94e+02
46	6	1.4	132	1	R38226	Human 5' EST secreted	2.94e+02
47	6	1.4	137	1	W85613	Sequence of polypeptid	2.94e+02
48	6	1.4	137	1	W19603	Secreted protein clone	2.94e+02
49	6	1.4	151	1	W70219	Myocoplasmia genitalium	2.94e+02
50	6	1.4	151	1	W29881	Leishmania antigen lms	2.94e+02
51	6	1.4	157	1	W46489	Human epithelial membr	2.94e+02
52	6	1.4	157	1	W58867	Human growth arrest pr	2.94e+02
53	6	1.4	157	1	W58869	Human PAP protein.	2.94e+02
54	6	1.4	164	1	W71873	Human TNP protein.	2.94e+02
55	6	1.4	164	1	W69389	Protein encoded by pro	2.94e+02
56	6	1.4	173	1	W28351	Prostate tumour specif	2.94e+02
57	6	1.4	186	1	W77774	Staphylococcus aureus	2.94e+02
58	6	1.4	189	1	R50334	Staphylococcus aureus	2.94e+02
59	6	1.4	197	1	W69423	SPAI peptide.	2.94e+02
60	6	1.4	199	1	W10656	Human secreted protein	2.94e+02
61	6	1.4	199	1	R60359	Rat GM2 activator prot	2.94e+02
62	6	1.4	200	1	W55524	MOSD N-terminal.	2.94e+02
63	6	1.4	205	1	W71872	H. pylori ORF 29ep1072	2.94e+02
64	6	1.4	205	1	W69388	Protein encoded by pro	2.94e+02
65	6	1.4	205	1	W20849	Prostate tumour specif	2.94e+02
66	6	1.4	209	1	W54021	H. pylori inner membra	2.94e+02
67	6	1.4	209	1	R95609	Modified Casein sequen	2.94e+02
68	6	1.4	209	1	R80281	Bovine beta casein AI	2.94e+02
69	6	1.4	218	1	R33259	Methyl or ethyl ester1	2.94e+02
70	6	1.4	221	1	P82521	Sj23-1-like protein.	2.94e+02
71	6	1.4	222	1	W00679	Hepatitis D Virus ORF5	2.94e+02
72	6	1.4	224	1	Y10948	Beta-casein.	2.94e+02
73	6	1.4	229	1	W55386	H. pylori ORF 04ap1201	2.94e+02
74	6	1.4	237	1	Y05282	H. pylori ORF 11ge1030	2.94e+02
75	6	1.4	239	1	W27087	BEF-like homologue PRO	2.94e+02
76	6	1.4	231	1	W60988	Human transforing pro	2.94e+02
77	6	1.4	232	1	W59129	Streptococcus pneumoni	2.94e+02
78	6	1.4	234	1	W96221	Rhmo sapiens Tpb Inter	2.94e+02
79	6	1.4	246	1	R41231	Shad4/DP4 protein C-t	2.94e+02
80	6	1.4	247	1	W28235	GAT-2 transporter gene	2.94e+02
81	6	1.4	248	1	W60592	Amino acid sequence of	2.94e+02
82	6	1.4	250	1	R05421	Human prostate-specific	2.94e+02
83	6	1.4	250	1	R05772	Human adipisin/D encode	2.94e+02
84	6	1.4	264	1	W20199	Human adipisin gene pro	2.94e+02
85	6	1.4	269	1	R48743	H. pylori cytoplasmic	2.94e+02
86	6	1.4	274	1	W02715	G-protein coupled odor	2.94e+02
87	6	1.4	274	1	W02720	G-protein coupled odor	2.94e+02
88	6	1.4	284	1	R48748	G-protein coupled odor	2.94e+02
89	6	1.4	284	1	R48748	G-protein coupled odor	2.94e+02
90	6	1.4	284	1	W02718	G-protein coupled odor	2.94e+02
91	6	1.4	285	1	R82689	G-protein coupled odor	2.94e+02
92	6	1.4	293	1	W55671	Shrimp tropomyosin SA-	2.94e+02
93	6	1.4	296	1	R76767	H. pylori ORF hp5p1564	2.94e+02
94	6	1.4	300	1	R76774	Film protein derived f	2.94e+02
95	6	1.4	300	1	R76772	Film protein derived f	2.94e+02
96	6	1.4	300	1	R76773	Film protein derived f	2.94e+02

97	6	1.4	300	1	R76745	FlmH protein derived f	2.94e+02	170	6	1.4	531	1	R07071	Sequence encoded by hu	2.94e+02
98	6	1.4	300	1	R76764	FlmH protein derived f	2.94e+02	171	6	1.4	538	1	W78755	Human EYA2.	2.94e+02
99	6	1.4	300	1	R76765	FlmH protein derived f	2.94e+02	172	6	1.4	539	1	W87799	Antipeptidase SLPD en	2.94e+02
100	6	1.4	300	1	R76771	FlmH protein derived f	2.94e+02	173	6	1.4	539	1	R80506	S. lividans protease p	2.94e+02
101	6	1.4	300	1	R76763	FlmH protein derived f	2.94e+02	174	6	1.4	546	1	W78756	Human EYA3.	2.94e+02
102	6	1.4	300	1	R76775	FlmH protein derived f	2.94e+02	175	6	1.4	548	1	R88842	E. coli 11VCMDA opero	2.94e+02
103	6	1.4	300	1	R76766	FlmH protein derived f	2.94e+02	176	6	1.4	548	1	W13731	Protein product of Bac	2.94e+02
104	6	1.4	300	1	R76776	FlmH protein derived f	2.94e+02	177	6	1.4	548	1	W22460	E. coli acetoalactate s	2.94e+02
105	6	1.4	300	1	R76768	FlmH protein derived f	2.94e+02	178	6	1.4	548	1	R86881	E. coli theonine-deam	2.94e+02
106	6	1.4	300	1	R76769	FlmH protein derived f	2.94e+02	179	6	1.4	552	1	W14287	Human deleted in panc	2.94e+02
107	6	1.4	300	1	R76770	FlmH protein derived f	2.94e+02	180	6	1.4	559	1	R13263	Human EYA1-B.	2.94e+02
108	6	1.4	301	1	R48639	Ryegrass Lol pV allergy	2.94e+02	181	6	1.4	559	1	W78753	Human EYA1-B.	2.94e+02
109	6	1.4	301	1	R71506	Lol pV (clone 12R); ma	2.94e+02	182	6	1.4	560	1	W38165	Human tyrosinase.	2.94e+02
110	6	1.4	301	1	R33555	Sequence of Lol p Ib.1	2.94e+02	183	6	1.4	563	1	R86989	Human tyrosinase.	2.94e+02
111	6	1.4	304	1	R56480	I-19 B-lymphocyte derl	2.94e+02	184	6	1.4	578	1	W26607	Thermosstable DNA poly	2.94e+02
112	6	1.4	310	1	R23996	B-Hdgag-T recombinant p	2.94e+02	185	6	1.4	592	1	W78754	Human EYA1-B.	2.94e+02
113	6	1.4	322	1	R27336	Plasmidium falciparum	2.94e+02	186	6	1.4	593	1	W98782	Human EYA1-B.	2.94e+02
114	6	1.4	328	1	R76170	PMI.	2.94e+02	187	6	1.4	595	1	W18097	Human EYA1-B.	2.94e+02
115	6	1.4	332	1	R76169	H. pylori ORF 29epi072	2.94e+02	188	6	1.4	602	1	R41228	Xenopus beta-signalin	2.94e+02
116	6	1.4	337	1	Y10964	Absidia sporophora var	2.94e+02	189	6	1.4	608	1	W26606	GAT-2 GABA transporter	2.94e+02
117	6	1.4	337	1	W77402	Absidia reiflexa lipase	2.94e+02	190	6	1.4	608	1	R32657	Thermosstable DNA poly	2.94e+02
118	6	1.4	338	1	W77403	Absidia reiflexa lipase	2.94e+02	191	6	1.4	657	1	R32657	PSI protein from C.mel	2.94e+02
119	6	1.4	338	1	W26690	Absidia reiflexa lipase	2.94e+02	192	6	1.4	657	1	R03926	T. cruzi HSP.	2.94e+02
120	6	1.4	338	1	W26691	Absidia reiflexa lipase	2.94e+02	193	6	1.4	658	1	W98873	H. pylori GPO 1739 pr	2.94e+02
121	6	1.4	338	1	W77401	Absidia corymbifera 11	2.94e+02	194	6	1.4	664	1	R11606	Alcohol-oxidase.	2.94e+02
122	6	1.4	338	1	W26689	Absidia corymbifera 11	2.94e+02	195	6	1.4	676	1	R89331	Recombinant alcohol ox	2.94e+02
123	6	1.4	341	1	W02599	G-protein coupled huma	2.94e+02	196	6	1.4	676	1	W97809	Tip adhesin protein an	2.94e+02
124	6	1.4	341	1	R48727	G-protein coupled huma	2.94e+02	197	6	1.4	693	1	W15140	Mammalian cell cycle r	2.94e+02
125	6	1.4	343	1	W60986	Streptococcus pneumoni	2.94e+02	198	6	1.4	719	1	W45089	Bacillus thuringiensis	2.94e+02
126	6	1.4	351	1	W20340	H. pylori secreted or	2.94e+02	199	6	1.4	719	1	R08081	81 kD endotoxin deduce	2.94e+02
127	6	1.4	351	1	W01052	Human umbilical vein e	2.94e+02	200	6	1.4	720	1	W19266	Lactobacillus amylovor	2.94e+02
128	6	1.4	371	1	R98113	Human lymphocyte cell	2.94e+02	201	6	1.4	725	1	W39165	Human RRAM protein.	2.94e+02
129	6	1.4	372	1	W36616	Celebs macegaze Zcytor	2.94e+02	202	6	1.4	736	1	W97809	Cytomegalovirus regu	2.94e+02
130	6	1.4	373	1	W20833	H. pylori secreted or	2.94e+02	203	6	1.4	742	1	R47232	Cytomegalovirus Tome	2.94e+02
131	6	1.4	382	1	R03464	Transglutaminase type	2.94e+02	204	6	1.4	742	1	R21433	CMV Tome gH protein.	2.94e+02
132	6	1.4	385	1	P90551	Bovine substance K rec	2.94e+02	205	6	1.4	743	1	P70290	Human cytomegalovirus	2.94e+02
133	6	1.4	390	1	R25276	SCC antigen.	2.94e+02	206	6	1.4	760	1	W29490	Programmed cell death	2.94e+02
134	6	1.4	390	1	W15241	Psoriastatin type I.	2.94e+02	207	6	1.4	766	1	W55464	H. pylori ORF 07ap1121	2.94e+02
135	6	1.4	398	1	W01335	Psoriastatin type II.	2.94e+02	208	6	1.4	790	1	R95565	Human RRAM protein.	2.94e+02
136	6	1.4	400	1	W80135	Human recombinant neur	2.94e+02	209	6	1.4	798	1	W85013	N. meningitidis seroly	2.94e+02
137	6	1.4	400	1	W83429	Human Doc2-alpha.	2.94e+02	210	6	1.4	806	1	W85025	Smad4-green fluorescen	2.94e+02
138	6	1.4	400	1	W01114	Brain-specific protein	2.94e+02	211	6	1.4	854	1	R72855	Smad4-green fluorescen	2.94e+02
139	6	1.4	412	1	W71369	Death associated protei	2.94e+02	212	6	1.4	865	1	R75790	A. nidulans FKSA.	2.94e+02
140	6	1.4	412	1	R74207	Human death associated	2.94e+02	213	6	1.4	872	1	W26605	Murine predicted PMSL	2.94e+02
141	6	1.4	415	1	W22849	Canine herpes virus pr	2.94e+02	214	6	1.4	909	1	W96250	Thermostable bacter the	2.94e+02
142	6	1.4	415	1	W22849	Canine herpesvirus gly	2.94e+02	215	6	1.4	909	1	W96254	Mouse semaphorin recep	2.94e+02
143	6	1.4	426	1	W55086	Streptococcus pneumoni	2.94e+02	216	6	1.4	909	1	W96249	Mouse semaphorin recep	2.94e+02
144	6	1.4	427	1	W80676	S. pneumoniae trigger	2.94e+02	217	6	1.4	911	1	R15355	Rat semaphorin recep	2.94e+02
145	6	1.4	437	1	R89329	TIP-adhesin protein.	2.94e+02	218	6	1.4	914	1	W96251	Human erythrocyte memb	2.94e+02
146	6	1.4	438	1	R89333	Saccharomyces cerevisi	2.94e+02	219	6	1.4	916	1	W96251	Mouse semaphorin recep	2.94e+02
147	6	1.4	438	1	W01975	Saccharomyces cerevisi	2.94e+02	220	6	1.4	919	1	W86812	Secreted protein clone	2.94e+02
148	6	1.4	438	1	R71934	Sterol-delta-14-reduct	2.94e+02	221	6	1.4	925	1	R50179	Excitatory amino acid	2.94e+02
149	6	1.4	458	1	W20964	H. pylori cytoplasmic	2.94e+02	222	6	1.4	925	1	W96308	Neurotrophin-2.	2.94e+02
150	6	1.4	458	1	W55372	H. pylori ORF hp2el091	2.94e+02	223	6	1.4	925	1	R92177	SAK-a-serine-threonine	2.94e+02
151	6	1.4	459	1	W26529	Branched chain keto ac	2.94e+02	224	6	1.4	926	1	W62166	G6amylyase.	2.94e+02
152	6	1.4	465	1	W60723	36K antigen of Mycobac	2.94e+02	225	6	1.4	926	1	W96255	Mouse semaphorin recep	2.94e+02
153	6	1.4	466	1	Y00027	Enterococcus faecalis	2.94e+02	226	6	1.4	931	1	W96253	Human semaphorin recep	2.94e+02
154	6	1.4	471	1	W56742	Orpomyces cellulase	2.94e+02	227	6	1.4	936	1	R33356	Excitatory amino acid re	2.94e+02
155	6	1.4	485	1	Y00026	Enterococcus faecalis	2.94e+02	228	6	1.4	1026	1	R49013	Caubacter s-layer pr	2.94e+02
156	6	1.4	488	1	W44322	Bacillus thuringiensis	2.94e+02	229	6	1.4	1026	1	R48993	rsaa S-lyase protein.	2.94e+02
157	6	1.4	508	1	W38167	Mutant human tyrosinas	2.94e+02	230	6	1.4	1026	1	W37490	Caubacter crescentus	2.94e+02
158	6	1.4	526	1	W30705	Inositol-1-phosphate s	2.94e+02	231	6	1.4	1038	1	W19766	Mouse Interleukin-1 re	2.94e+02
159	6	1.4	526	1	W79299	Inositol-1-phosphate s	2.94e+02	232	6	1.4	1051	1	R11117	Hamster GAP b3 protein	2.94e+02
160	6	1.4	529	1	W75050	Fragment of human secr	2.94e+02	233	6	1.4	1088	1	Y00892	Isolucy1-LRNA synthet	2.94e+02
161	6	1.4	529	1	W03306	Tyrosinase melanoma an	2.94e+02	234	6	1.4	1088	1	Y00891	Isolucy1-LRNA synthet	2.94e+02
162	6	1.4	529	1	W71234	Tyrosinase.	2.94e+02	235	6	1.4	1132	1	R77417	Human cell cycle prote	2.94e+02
163	6	1.4	529	1	R56309	Human tyrosinase actin	2.94e+02	236	6	1.4	1135	1	W33808	Mouse ataxin-2.	2.94e+02
164	6	1.4	529	1	W36519	Tyrosinase containing	2.94e+02	237	6	1.4	1139	1	W76425	Human JAK2 protein seq	2.94e+02
165	6	1.4	529	1	W00184	Human tyrosinase.	2.94e+02	238	6	1.4	1278	1	W88445	Human NPC1 (Niemann-P1	2.94e+02
166	6	1.4	529	1	R63623	Human tyrosinase prote	2.94e+02	239	6	1.4	1288	1	W92297	Mouse alpha-1 (XVIII)	2.94e+02
167	6	1.4	529	1	W38166	Normal human tyrosinas	2.94e+02	240	6	1.4	1388	1	W26328	Mouse alpha-1 collagen	2.94e+02
168	6	1.4	531	1	R79493	Human tyrosinase actin	2.94e+02	241	6	1.4	1319	1	W88446	Mouse NPC1 orthologue.	2.94e+02
169	6	1.4	531	1	W22083	Human SK29-MEL tyrosin	2.94e+02	242	6	1.4	1358	1	W18824	Human restrictin.	2.94e+02

243	6	1.4	1358	1	W35743	Recombinant human rest	2.94e+02	316	5	1.1	66	1	Y11767	Human 5' EST secreted	2.95e+03
244	6	1.4	1358	1	R99358	Human restrictin	2.94e+02	317	5	1.1	66	1	Y11767	Human 5' EST secreted	2.95e+03
245	6	1.4	1375	1	W27283	Apoptosis inducing pro	2.94e+02	318	5	1.1	68	1	Y13043	Human secreted protein	2.95e+03
246	6	1.4	1390	1	W21636	Grapevine leafroll vi	2.94e+02	319	5	1.1	69	1	W94650	Human secreted protein	2.95e+03
247	6	1.4	1398	1	W94839	Pyococcus furiosus pr	2.94e+02	320	5	1.1	70	1	W11736	Human 5' EST secreted	2.95e+03
248	6	1.4	1398	1	W24124	Protease	2.94e+02	321	5	1.1	70	1	W96719	Human 5' EST secreted	2.95e+03
249	6	1.4	1398	1	R87008	Human multidrug resist	2.94e+02	322	5	1.1	72	1	Y12481	Human 5' EST secreted	2.95e+03
250	6	1.4	1437	1	W80597	O. longistaminata Xaz1	2.94e+02	323	5	1.1	73	1	Y12335	Human 5' EST secreted	2.95e+03
251	6	1.4	1445	1	W93595	H. pylori GPO 1484 pr	2.94e+02	324	5	1.1	77	1	Y12335	Human 5' EST secreted	2.95e+03
252	6	1.4	1481	1	W55686	Helicobacter polypept	2.94e+02	325	5	1.1	81	1	Y12335	Human 5' EST secreted	2.95e+03
253	6	1.4	1891	1	W23720	Platenolide synthase O	2.94e+02	326	5	1.1	81	1	Y12335	Human 5' EST secreted	2.95e+03
254	6	1.4	1891	1	W23720	Platenolide synthase O	2.94e+02	327	5	1.1	81	1	Y12335	Human 5' EST secreted	2.95e+03
255	6	1.4	2353	1	R95011	Haemophilus adhesin p	2.94e+02	328	5	1.1	81	1	Y12335	Human 5' EST secreted	2.95e+03
256	6	1.4	2366	1	R95011	Haemophilus adhesin p	2.94e+02	329	5	1.1	81	1	Y12335	Human 5' EST secreted	2.95e+03
257	6	1.4	2366	1	R95011	Haemophilus adhesin p	2.94e+02	330	5	1.1	82	1	Y12335	Human 5' EST secreted	2.95e+03
258	6	1.4	2893	1	W98828	H. pylori GPO 1484 pr	2.94e+02	331	5	1.1	82	1	Y12335	Human 5' EST secreted	2.95e+03
259	6	1.4	2893	1	W98828	H. pylori GPO 1484 pr	2.94e+02	332	5	1.1	83	1	Y12335	Human 5' EST secreted	2.95e+03
260	6	1.4	3398	1	R44430	erya region polypeptid	2.94e+02	333	5	1.1	85	1	W94884	Human 5' EST secreted	2.95e+03
261	6	1.4	3898	1	R10473	Hog cholera virus geno	2.94e+02	334	5	1.1	88	1	Y12335	Human 5' EST secreted	2.95e+03
262	5	1.1	7	1	W08842	Dolastatin-15 derivati	2.95e+03	335	5	1.1	91	1	Y12335	Human 5' EST secreted	2.95e+03
263	5	1.1	7	1	W08842	Dolastatin-15 derivati	2.95e+03	336	5	1.1	92	1	Y12335	Human 5' EST secreted	2.95e+03
264	5	1.1	8	1	W08842	Dolastatin-15 derivati	2.95e+03	337	5	1.1	96	1	Y12335	Human 5' EST secreted	2.95e+03
265	5	1.1	9	1	W08842	Predicted binding site	2.95e+03	338	5	1.1	96	1	Y12335	Human 5' EST secreted	2.95e+03
266	5	1.1	9	1	W08842	Predicted binding site	2.95e+03	339	5	1.1	96	1	Y12335	Human 5' EST secreted	2.95e+03
267	5	1.1	10	1	W97928	Human MHC class II bin	2.95e+03	340	5	1.1	97	1	Y12335	Human 5' EST secreted	2.95e+03
268	5	1.1	12	1	W97928	Human synaptonemal com	2.95e+03	341	5	1.1	97	1	Y12335	Human 5' EST secreted	2.95e+03
269	5	1.1	16	1	W98117	Collagen assembly inh1	2.95e+03	342	5	1.1	97	1	Y12335	Human 5' EST secreted	2.95e+03
270	5	1.1	17	1	W05607	T-cell membrane protel	2.95e+03	343	5	1.1	100	1	W28142	Human 5' EST secreted	2.95e+03
271	5	1.1	18	1	W05607	Tetanus toxin helper T	2.95e+03	344	5	1.1	103	1	W94883	Human 5' EST secreted	2.95e+03
272	5	1.1	21	1	W53348	Activation domain of h	2.95e+03	345	5	1.1	103	1	W00614	Large monomer of modif	2.95e+03
273	5	1.1	21	1	W53348	Nephila clavipes spide	2.95e+03	346	5	1.1	103	1	W53025	Collagen V prepeptide	2.95e+03
274	5	1.1	21	1	W53025	E2A/bx1 immunogenec f	2.95e+03	347	5	1.1	104	1	Y11335	S. pneumoniae protein	2.95e+03
275	5	1.1	21	1	R95023	Fragment #1 of 30 KD.1	2.95e+03	348	5	1.1	104	1	R30010	Light chain variable r	2.95e+03
276	5	1.1	23	1	R95023	Fragment of human secr	2.95e+03	349	5	1.1	105	1	Y12349	Human 5' EST secreted	2.95e+03
277	5	1.1	24	1	R95023	Glycoprotein anchor se	2.95e+03	350	5	1.1	106	1	W6715	Growth related oncogen	2.95e+03
278	5	1.1	24	1	R81561	Anchor sequence #2 of	2.95e+03	351	5	1.1	106	1	W6715	Growth related oncogen	2.95e+03
279	5	1.1	26	1	Y12058	Human 5' EST secreted	2.95e+03	352	5	1.1	107	1	W96714	H. pylori GPO 304 pro	2.95e+03
280	5	1.1	28	1	W93833	Human 15S. lipoxygenase	2.95e+03	353	5	1.1	107	1	W96714	Growth related oncogen	2.95e+03
281	5	1.1	29	1	Y03012	Fragment of human secr	2.95e+03	354	5	1.1	107	1	R20590	Human macrophage infla	2.95e+03
282	5	1.1	29	1	Y12922	Amino acid sequence of	2.95e+03	355	5	1.1	107	1	W07439	Anti-DNA antibody 9111	2.95e+03
283	5	1.1	30	1	W1569	Hepatocyte nuclear fac	2.95e+03	356	5	1.1	107	1	Y12443	Human 5' EST secreted	2.95e+03
284	5	1.1	33	1	W53349	Human 5' EST secreted	2.95e+03	357	5	1.1	110	1	W92773	Human 5' EST secreted	2.95e+03
285	5	1.1	33	1	W53349	Nephila clavipes spide	2.95e+03	358	5	1.1	111	1	W20254	US5856134 Seq ID 91	2.95e+03
286	5	1.1	35	1	W90039	N. crassa glutamate de	2.95e+03	359	5	1.1	111	1	Y07876	H. pylori transmembran	2.95e+03
287	5	1.1	35	1	Y12514	Human 5' EST secreted	2.95e+03	360	5	1.1	112	1	Y09268	Human secreted protein	2.95e+03
288	5	1.1	39	1	Y12940	Amino acid sequence of	2.95e+03	361	5	1.1	117	1	Y03366	VL-1 thermal hysteresi	2.95e+03
289	5	1.1	41	1	Y11256	Human secreted protein	2.95e+03	362	5	1.1	119	1	Y12790	Fragment of human secr	2.95e+03
290	5	1.1	42	1	R71106	Streptococcus pneumonia	2.95e+03	363	5	1.1	119	1	Y11895	Human 5' EST secreted	2.95e+03
291	5	1.1	44	1	Y12438	HEV antigenic peptide	2.95e+03	364	5	1.1	119	1	Y11895	Human 5' EST secreted	2.95e+03
292	5	1.1	44	1	Y12562	Human 5' EST secreted	2.95e+03	365	5	1.1	120	1	W40417	D. vulgaris flavodoxin	2.95e+03
293	5	1.1	44	1	R72912	E. coli Pripase-alpha N	2.95e+03	366	5	1.1	122	1	Y00976	CRCA-1 protein sequenc	2.95e+03
294	5	1.1	47	1	Y11935	Human 5' EST secreted	2.95e+03	367	5	1.1	122	1	Y11785	Human 5' EST secreted	2.95e+03
295	5	1.1	47	1	Y12256	Human 5' EST secreted	2.95e+03	368	5	1.1	123	1	W00617	Large monomer of modif	2.95e+03
296	5	1.1	47	1	W83947	Human 5' EST secreted	2.95e+03	369	5	1.1	125	1	Y11240	S. pneumoniae protein	2.95e+03
297	5	1.1	47	1	Y02751	Human secreted protein	2.95e+03	370	5	1.1	125	1	W02889	Human 5' EST secreted	2.95e+03
298	5	1.1	48	1	Y11836	Human secreted protein	2.95e+03	371	5	1.1	127	1	W96306	Taungo-59 type II membr	2.95e+03
299	5	1.1	51	1	Y11272	Human 5' EST secreted	2.95e+03	372	5	1.1	128	1	W67716	A platelet basic prote	2.95e+03
300	5	1.1	52	1	W95673	Streptococcus pneumonia	2.95e+03	373	5	1.1	128	1	R13519	Leukocyte derived grow	2.95e+03
301	5	1.1	52	1	Y03015	Pneumocystis carinii c	2.95e+03	374	5	1.1	130	1	R54261	Mab L243 light chain c	2.95e+03
302	5	1.1	56	1	Y03015	Fragment of human secr	2.95e+03	375	5	1.1	130	1	Y01487	acrp30 protein fragmen	2.95e+03
303	5	1.1	57	1	Y11998	Human 5' EST secreted	2.95e+03	376	5	1.1	131	1	W97385	Adipoc protein fragmen	2.95e+03
304	5	1.1	57	1	W75202	Human secreted protein	2.95e+03	377	5	1.1	131	1	W88553	Amino acid sequence of	2.95e+03
305	5	1.1	58	1	W74437	Human Galpha subunit N	2.95e+03	378	5	1.1	132	1	W81106	Secreted protein encod	2.95e+03
306	5	1.1	58	1	W74438	Human Galpha subunit N	2.95e+03	379	5	1.1	132	1	W81106	Secreted protein encod	2.95e+03
307	5	1.1	58	1	W69641	N-terminal region of G	2.95e+03	380	5	1.1	134	1	W04957	Human cytoskeleton spec	2.95e+03
308	5	1.1	59	1	Y12866	Human 5' EST secreted	2.95e+03	381	5	1.1	135	1	W04957	Human cytoskeleton spec	2.95e+03
309	5	1.1	60	1	R80103	Sequence of Elmeria ac	2.95e+03	382	5	1.1	139	1	Y11233	S. pneumoniae gppp pro	2.95e+03
310	5	1.1	61	1	Y10875	Amino acid sequence of	2.95e+03	383	5	1.1	140	1	Y01641	An Arbidolopsis thalian	2.95e+03
311	5	1.1	62	1	Y11659	Human 5' EST secreted	2.95e+03	384	5	1.1	140	1	Y04885	Myobacterium species	2.95e+03
312	5	1.1	64	1	Y12259	Human 5' EST secreted	2.95e+03	385	5	1.1	142	1	Y05309	S. aureus protein sequ	2.95e+03
313	5	1.1	65	1	Y13169	Human secreted protein	2.95e+03	386	5	1.1	142	1	Y00975	CRCA-1 protein sequenc	2.95e+03
314	5	1.1	66	1	Y12073	Human secreted protein	2.95e+03	387	5	1.1	146	1	W80502	Leptin receptor analog	2.95e+03
315	5	1.1	66	1	W67875	Human secreted protein	2.95e+03	388	5	1.1	147	1	Y13074	Human secreted protein	2.95e+03

389	5	1.1	147	1	Y01642	A Brassica napus prote	2.95e+03	462	5	1.1	234	1	W74866	Human secreted protein	2.95e+03
390	5	1.1	148	1	W96307	Tango-69 type-II memb	2.95e+03	463	5	1.1	235	1	R01555	Pertussis toxin clone	2.95e+03
391	5	1.1	148	1	R99496	Genetic Met-X-Ob prot	2.95e+03	464	5	1.1	235	1	R01555	Pertussis toxin clone	2.95e+03
392	5	1.1	150	1	W93583	Mouse mAbO-gamma prot	2.95e+03	465	5	1.1	235	1	W93583	Sensence-protein der	2.95e+03
393	5	1.1	150	1	Y11199	S. pneumoniae protein	2.95e+03	466	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
394	5	1.1	150	1	Y02643	A. actinomycetemcomit	2.95e+03	467	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
395	5	1.1	150	1	W96144	Mouse TRAIIN-R (short)	2.95e+03	468	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
396	5	1.1	154	1	Y11119	S. pneumoniae IS12 pro	2.95e+03	469	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
397	5	1.1	158	1	W97248	Acyladenylation domain	2.95e+03	470	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
398	5	1.1	159	1	W97250	Polypeptide fragment e	2.95e+03	471	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
399	5	1.1	160	1	W97250	Acyladenylation domain	2.95e+03	472	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
400	5	1.1	160	1	W97250	Acyladenylation domain	2.95e+03	473	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
401	5	1.1	162	1	R37863	Deduced from clone lam	2.95e+03	474	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
402	5	1.1	163	1	Y12385	Human 5' EST secreted	2.95e+03	475	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
403	5	1.1	164	1	P70241	Polypeptide conferring	2.95e+03	476	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
404	5	1.1	164	1	W29736	Human H-rev 107-like p	2.95e+03	477	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
405	5	1.1	166	1	W00974	CRCA-1 protein sequenc	2.95e+03	478	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
406	5	1.1	167	1	W46876	Protein sequence encod	2.95e+03	479	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
407	5	1.1	169	1	W88404	Human adult testis sec	2.95e+03	480	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
408	5	1.1	177	1	R98370	Mycobacterial AhpF pol	2.95e+03	481	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
409	5	1.1	178	1	R98370	H. pylori GHPO 1741 pr	2.95e+03	482	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
410	5	1.1	179	1	Y03772	S. aureus spoo2 polyp	2.95e+03	483	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
411	5	1.1	180	1	W98874	H. pylori GHPO 1741 pr	2.95e+03	484	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
412	5	1.1	182	1	Y07759	Human secreted protein	2.95e+03	485	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
413	5	1.1	186	1	W97109	Thermotable polypepti	2.95e+03	486	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
414	5	1.1	187	1	W20795	H. pylori outer membra	2.95e+03	487	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
415	5	1.1	190	1	R67238	Human glial cell grow	2.95e+03	488	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
416	5	1.1	190	1	W92757	US5856134 Seq ID 38	2.95e+03	489	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
417	5	1.1	191	1	Y00771	Human tagr clone prote	2.95e+03	490	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
418	5	1.1	191	1	W64119	Human interferon recep	2.95e+03	491	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
419	5	1.1	192	1	R89548	Hepatitis C virus isol	2.95e+03	492	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
420	5	1.1	193	1	Y01410	Secreted protein encod	2.95e+03	493	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
421	5	1.1	193	1	P60463	Sequence of C-terminus	2.95e+03	494	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
422	5	1.1	193	1	Y10976	H. pylori ORF 01c1110	2.95e+03	495	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
423	5	1.1	194	1	P80624	AA sequence (IV) of po	2.95e+03	496	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
424	5	1.1	195	1	Y07105	Colon cancer associate	2.95e+03	497	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
425	5	1.1	196	1	W98411	H. pylori GHPO 267 pro	2.95e+03	498	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
426	5	1.1	197	1	W97134	Human guanilate kinase	2.95e+03	499	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
427	5	1.1	198	1	W97135	Mouse guanilate kinase	2.95e+03	500	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
428	5	1.1	200	1	W97625	Tomato prosystemin	2.95e+03	501	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
429	5	1.1	200	1	W99101	Tomato prosystemin	2.95e+03	502	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
430	5	1.1	200	1	W88109	A cockroach allergen d	2.95e+03	503	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
431	5	1.1	201	1	W93948	Human regulatory molec	2.95e+03	504	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
432	5	1.1	203	1	W97355	A partial HOOB059 poly	2.95e+03	505	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
433	5	1.1	205	1	W88400	Human foetal brain sec	2.95e+03	506	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
434	5	1.1	206	1	Y07222	MTN6-derived G protein	2.95e+03	507	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
435	5	1.1	207	1	Y07115	Mouse BAK protein sequ	2.95e+03	508	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
436	5	1.1	208	1	Y05432	S. pneumoniae N-(5'-ph	2.95e+03	509	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
437	5	1.1	209	1	Y11177	Human BAK protein sequ	2.95e+03	510	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
438	5	1.1	211	1	Y05433	Human TR-interacting p	2.95e+03	511	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
439	5	1.1	212	1	W92389	Human GSTH protein	2.95e+03	512	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
440	5	1.1	213	1	W92526	Sequence encoded by VP	2.95e+03	513	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
441	5	1.1	213	1	P30199	Mouse mAbO4-alpha (sho	2.95e+03	514	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
442	5	1.1	213	1	P30373	Mouse mAbO4-alpha (sho	2.95e+03	515	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
443	5	1.1	214	1	W93580	Mouse TRAIIN-R (long fr	2.95e+03	516	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
444	5	1.1	214	1	W98145	Recombinant pCO-8pt	2.95e+03	517	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
445	5	1.1	215	1	Y06983	ECF-8 homologous pRO533	2.95e+03	518	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
446	5	1.1	216	1	Y05280	Amino acid sequence of	2.95e+03	519	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
447	5	1.1	216	1	Y13353	A HOOB059 polypeptide	2.95e+03	520	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
448	5	1.1	217	1	W97318	Ancyllostoma secreted p	2.95e+03	521	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
449	5	1.1	218	1	W04323	H. pylori GHPO 453 pro	2.95e+03	522	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
450	5	1.1	218	1	W98656	Human CD53 antigen	2.95e+03	523	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
451	5	1.1	219	1	W80455	Human CD53 antigen	2.95e+03	524	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
452	5	1.1	219	1	W89152	Human CD53 antigen	2.95e+03	525	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
453	5	1.1	219	1	W92524	Human h4-IBSV recepto	2.95e+03	526	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
454	5	1.1	219	1	W92524	Human h4-IBSV recepto	2.95e+03	527	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
455	5	1.1	221	1	W80645	S. pneumoniae protein	2.95e+03	528	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
456	5	1.1	222	1	W20138	H. pylori cell envelop	2.95e+03	529	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
457	5	1.1	222	1	Y02661	Human secreted protein	2.95e+03	530	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
458	5	1.1	230	1	Y00195	Enterococcus faecalis	2.95e+03	531	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
459	5	1.1	230	1	W37993	Mutant Aspergillus ory	2.95e+03	532	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
460	5	1.1	232	1	Y04284	Mouse APRIL protein se	2.95e+03	533	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
461	5	1.1	233	1	P80728	Sequence of human tumo	2.95e+03	534	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03

681	1.1	481	1	Y04145	Rat Tango-76 protein	2.95e+03	754	5	1.1	612	1	W69299	Murine H1AP-2 protein	2.95e+03
682	1.1	482	1	W88321	E. coli O157 antigen p	2.95e+03	755	5	1.1	614	1	W98113	T-cell membrane protel	2.95e+03
683	1.1	485	1	Y00895	Rat GMEB-2' protein se	2.95e+03	756	5	1.1	614	1	W98113	T-cell membrane protel	2.95e+03
684	1.1	487	1	Y11008	H. pylori ORF hp61060	2.95e+03	757	5	1.1	619	1	Y06980	Recombinant p50-11CKS	2.95e+03
685	1.1	489	1	R66220	ADP-glucose-pyrophosph	2.95e+03	758	5	1.1	619	1	W89271	Granulocyte Ehrlichia	2.95e+03
686	1.1	489	1	W90341	G. max SBP2 protein	2.95e+03	759	5	1.1	621	1	W98548	H. pylori GHP0.1588 pr	2.95e+03
687	1.1	490	1	Y06978	Recombinant p50-9CKS p	2.95e+03	760	5	1.1	621	1	R37870	Soluble KE2 protease	2.95e+03
688	1.1	491	1	P70464	Sequence of gfp encode	2.95e+03	761	5	1.1	621	1	Y01402	Secreted protein encod	2.95e+03
689	1.1	495	1	W49070	Streptococcus pneumonia	2.95e+03	762	5	1.1	623	1	R15298	Varicella protein encod	2.95e+03
690	1.1	496	1	W96815	Smad7 protein used to	2.95e+03	763	5	1.1	625	1	W47023	Arabidopsis thaliana S	2.95e+03
691	1.1	497	1	W93362	C. trachomatis Cys5 pro	2.95e+03	764	5	1.1	626	1	W98010	BCG Ag85B antigen phag	2.95e+03
692	1.1	497	1	P60456	Sequence of aldehyde d	2.95e+03	765	5	1.1	631	1	W43105	C. thermococcus scaffo	2.95e+03
693	1.1	498	1	W80439	Feline herpesvirus IE	2.95e+03	766	5	1.1	641	1	W93364	Mouse calpain CAP6 pr	2.95e+03
694	1.1	500	1	R12769	Cl inhibitor muten	2.95e+03	767	5	1.1	642	1	W82741	806.077 heavy chain Rd	2.95e+03
695	1.1	500	1	W18212	Recombinant Cl inhibi	2.95e+03	768	5	1.1	643	1	W82739	Clone pNG4/ASB7VH-19c2	2.95e+03
696	1.1	501	1	W93490	Rat l-alpha-OHase prot	2.95e+03	769	5	1.1	647	1	W00926	Human cyclin D1-human	2.95e+03
697	1.1	503	1	W75500	Canine oral papillomav	2.95e+03	770	5	1.1	647	1	W82747	Plasmid pUC19/muASB7-R	2.95e+03
698	1.1	506	1	Y04840	Mycopacterium species	2.95e+03	771	5	1.1	652	1	R63808	Human amphotropic retr	2.95e+03
699	1.1	506	1	Y01313	Glutamine-oxoglutarate	2.95e+03	772	5	1.1	659	1	W93387	Human HEV ORF 2 protel	2.95e+03
700	1.1	507	1	W93491	Mouse l-alpha-OHase pr	2.95e+03	773	5	1.1	660	1	W93395	Human HEV ORF 2 protel	2.95e+03
701	1.1	507	1	R47517	MEU EPO receptor	2.95e+03	774	5	1.1	660	1	W93391	Human HEV ORF 2 protel	2.95e+03
702	1.1	507	1	W92894	Murine l-alpha-hydroxy	2.95e+03	775	5	1.1	660	1	W93394	Human HEV ORF 2 protel	2.95e+03
703	1.1	509	1	W93304	Amino acid sequence of	2.95e+03	776	5	1.1	660	1	W93393	Human HEV ORF 2 protel	2.95e+03
704	1.1	510	1	W93304	Xenopus activin recept	2.95e+03	777	5	1.1	660	1	W93396	Human HEV ORF 2 protel	2.95e+03
705	1.1	511	1	P81180	Sequence of alpha-amy	2.95e+03	778	5	1.1	660	1	W93392	Swine HEV ORF 2 protel	2.95e+03
706	1.1	511	1	R23997	Immunogenic secretory	2.95e+03	779	5	1.1	660	1	W93388	Human HEV ORF 2 protel	2.95e+03
707	1.1	513	1	R54214	L.lactis branched amin	2.95e+03	780	5	1.1	660	1	W93388	Human HEV ORF 2 protel	2.95e+03
708	1.1	514	1	R80508	S. lividans protease p	2.95e+03	781	5	1.1	660	1	W93388	Human HEV ORF 2 protel	2.95e+03
709	1.1	514	1	W88426	Chlamydia pneumoniae s	2.95e+03	782	5	1.1	660	1	W93390	Human HEV ORF 2 protel	2.95e+03
710	1.1	516	1	W59448	Pea ADP-glucose pyroph	2.95e+03	783	5	1.1	661	1	W47274	Human B-cell activatio	2.95e+03
711	1.1	517	1	W94393	Variant ADP-glucose py	2.95e+03	784	5	1.1	662	1	W81502	Dead Box X (DBX) gene	2.95e+03
712	1.1	518	1	W94392	Variant ADP-glucose py	2.95e+03	785	5	1.1	666	1	W82745	Fusion protein (806.07	2.95e+03
713	1.1	524	1	W90339	G. max SBP1 protein	2.95e+03	786	5	1.1	672	1	W93657	Staphylococcus aureus	2.95e+03
714	1.1	526	1	W97814	Human butyrophilin	2.95e+03	787	5	1.1	673	1	W82742	Plasmid pNG4/55.1scfV/	2.95e+03
715	1.1	527	1	W78914	Bovine butyrophilin pr	2.95e+03	788	5	1.1	675	1	W69354	P. damelsa bst protein	2.95e+03
716	1.1	527	1	W96321	Human catalase sequenc	2.95e+03	789	5	1.1	675	1	W74500	Amino acid sequence of	2.95e+03
717	1.1	529	1	Y00894	Rat GMEB-2 protein seq	2.95e+03	790	5	1.1	675	1	W74499	Human 15S lipoygenase	2.95e+03
718	1.1	530	1	R14405	Protein 1 (1.3-fucosyl	2.95e+03	791	5	1.1	676	1	W93832	Human 15S lipoygenase	2.95e+03
719	1.1	531	1	W47002	Glutathione-S-transfer	2.95e+03	792	5	1.1	678	1	W93654	Human adenovirus nucleo	2.95e+03
720	1.1	532	1	W80446	Human intracellular ad	2.95e+03	793	5	1.1	679	1	W96998	The gibbon ape leukem	2.95e+03
721	1.1	532	1	W86193	Human intracellular ad	2.95e+03	794	5	1.1	679	1	W96998	Mouse 2.5A-dependent R	2.95e+03
722	1.1	543	1	W92498	Glycine max protoporph	2.95e+03	795	5	1.1	685	1	W04209	Mutant streptavidin/liu	2.95e+03
723	1.1	544	1	R82213	Talaromyces flavus glv	2.95e+03	796	5	1.1	686	1	W17597	Bacillus Cftase varian	2.95e+03
724	1.1	547	1	W57261	Human Nramp1 protein	2.95e+03	797	5	1.1	687	1	Y07111	Colon cancer associate	2.95e+03
725	1.1	548	1	W93667	Mutant firefly lucifer	2.95e+03	798	5	1.1	692	1	W93890	Human Rb38 protein	2.95e+03
726	1.1	548	1	R30803	Thermotable luciferas	2.95e+03	799	5	1.1	696	1	W97619	Human neuregulin relat	2.95e+03
727	1.1	548	1	W04212	Luciola lateralis luci	2.95e+03	800	5	1.1	704	1	R41249	B. ohenensis Alal8 cycl	2.95e+03
728	1.1	552	1	Y13373	Amino acid sequence of	2.95e+03	801	5	1.1	708	1	Y13355	Amino acid sequence of	2.95e+03
729	1.1	552	1	W93666	Chimeric firefly lucif	2.95e+03	802	5	1.1	711	1	W73025	Helicobacter pylori 76	2.95e+03
730	1.1	560	1	W93859	Streptococcus pneumonia	2.95e+03	803	5	1.1	712	1	W80485	Islet cell antibody an	2.95e+03
731	1.1	560	1	W95088	Response regulator cog	2.95e+03	804	5	1.1	713	1	W97617	Mouse neuregulin relat	2.95e+03
732	1.1	563	1	Y00893	Human GMEB-1 protein s	2.95e+03	805	5	1.1	720	1	Y05452	Human neuregulin-like f	2.95e+03
733	1.1	565	1	W96316	Acidic leucine aminope	2.95e+03	806	5	1.1	720	1	W97618	Human neuregulin relat	2.95e+03
734	1.1	570	1	P94046	1-plastin protein deri	2.95e+03	807	5	1.1	722	1	W73107	B. f. toxin protein 211	2.95e+03
735	1.1	571	1	W96315	Acidic leucine aminope	2.95e+03	808	5	1.1	726	1	W57306	Rhodotermus marinus D	2.95e+03
736	1.1	571	1	W78491	S. coelicolor AbsA1 pro	2.95e+03	809	5	1.1	727	1	W93798	Human VARP-1 (VR2) cap	2.95e+03
737	1.1	571	1	Y00093	Enterococcus faecalis	2.95e+03	810	5	1.1	729	1	W97619	Staphylococcus aureus	2.95e+03
738	1.1	575	1	W83389	Caenorhabditis elegans	2.95e+03	811	5	1.1	730	1	W13669	C-proteinase encoded b	2.95e+03
739	1.1	576	1	R08069	Murine IL-1 receptor p	2.95e+03	812	5	1.1	732	1	W97207	A. triehaense phosphor	2.95e+03
740	1.1	582	1	W81077	Amino acid sequences o	2.95e+03	813	5	1.1	745	1	W94096	Human I-kappa-B kinase	2.95e+03
741	1.1	585	1	Y01364	Human protein with Zn	2.95e+03	814	5	1.1	745	1	W96157	Human IKK-alpha	2.95e+03
742	1.1	585	1	R41359	Tumour associated 90K	2.95e+03	815	5	1.1	746	1	W80322	Bacillus thuringiensis	2.95e+03
743	1.1	589	1	P60303	Sequence encoded by th	2.95e+03	816	5	1.1	748	1	W98877	H. pylori GHP0.1750 pr	2.95e+03
744	1.1	590	1	Y04736	PDZ domain-containing	2.95e+03	817	5	1.1	748	1	W89272	Granulocyte Ehrlichia	2.95e+03
745	1.1	591	1	W97384	A catalytic telomerase	2.95e+03	818	5	1.1	754	1	W96210	Amyloid precursor prot	2.95e+03
746	1.1	592	1	W97359	A. 6-transmembrane prot	2.95e+03	819	5	1.1	761	1	W97990	Def VRR-1 (VR2) caps	2.95e+03
747	1.1	592	1	W82661	A. thaliana L-galacton	2.95e+03	820	5	1.1	762	1	Y00939	Desulfurococcus M1 TL	2.95e+03
748	1.1	593	1	Y00092	Enterococcus faecalis	2.95e+03	821	5	1.1	766	1	Y00870	S. tuberosum isoamylas	2.95e+03
749	1.1	596	1	W94459	Human neurofibromatost	2.95e+03	822	5	1.1	770	1	W97996	Human amyloid precurs	2.95e+03
750	1.1	596	1	W92643	Rat anti-oestrogen tire	2.95e+03	823	5	1.1	771	1	W97798	Aspergillus oryzae pro	2.95e+03
751	1.1	603	1	R74620	Human lung tumour Polo	2.95e+03	824	5	1.1	785	1	Y06890	Human varts protein	2.95e+03
752	1.1	603	1	Y05277	P. roqueforti beta-fir	2.95e+03	825	5	1.1	787	1	W81064	Amino acid sequence of	2.95e+03
753	1.1	606	1	Y00129	Enterococcus faecalis	2.95e+03	826	5	1.1	788	1	W75919	C-proteinase sequence	2.95e+03

827	5	1.1	789	1	W80321	Bacillus thuringiensis	2.95e+03	900	1.1	1059	1	Y13393	Amino acid sequence of	2.95e+03
828	5	1.1	789	1	W80320	Bacillus thuringiensis	2.95e+03	901	1.1	1060	1	W89314	STIMAC339 genome pol p	2.95e+03
829	5	1.1	789	1	W46863	Bacillus thuringiensis	2.95e+03	902	1.1	1070	1	W08747	Human colon carcinoma	2.95e+03
830	5	1.1	793	1	W81065	Amino acid sequence of	2.95e+03	903	5	1074	1	Y00186	Enterococcus faecalis	2.95e+03
831	5	1.1	800	1	W83165	Rat orphan tyrosine ki	2.95e+03	904	5	1074	1	Y00206	Enterococcus faecalis	2.95e+03
832	5	1.1	802	1	Y04925	Mycobacterium species	2.95e+03	905	5	1077	1	W95559	A partial hepatitis A	2.95e+03
833	5	1.1	803	1	Y07113	W0904265 Seq ID No: 6	2.95e+03	906	5	1079	1	W63154	Human calcium channel	2.95e+03
834	5	1.1	809	1	W19521	B. cereus VIP3A(a) syn	2.95e+03	907	5	1081	1	W03163	Mult reverse transcript	2.95e+03
835	5	1.1	811	1	W93952	Human regulatory molec	2.95e+03	908	5	1086	1	W81600	Candida albicans CANIK	2.95e+03
836	5	1.1	819	1	W04926	Mycobacterium species	2.95e+03	909	5	1103	1	W63153	Human calcium channel	2.95e+03
837	5	1.1	823	1	W81066	Amino acid sequence of	2.95e+03	910	5	1130	1	W63151	Human calcium channel	2.95e+03
838	5	1.1	823	1	W80972	Sequence encoded by 3k	2.95e+03	911	5	1132	1	W05178	Human catalytic telome	2.95e+03
839	5	1.1	831	1	W79961	Thermus flavus DNA pol	2.95e+03	912	5	1136	1	W90251	Caenorhabditis elegans	2.95e+03
840	5	1.1	832	1	W80428	DNA polymerase enzyme	2.95e+03	913	5	1146	1	W47544	Alternative cryIF/cryI	2.95e+03
841	5	1.1	840	1	W73570	Human Hpr-1 protein se	2.95e+03	914	5	1148	1	W83393	Bacillus thuringiensis	2.95e+03
842	5	1.1	840	1	W93569	Human conductin protel	2.95e+03	915	5	1155	1	W88117	CryE(d) protein	2.95e+03
843	5	1.1	843	1	W99799	Chicken VRI capsalain	2.95e+03	916	5	1176	1	W47035	Bacillus thuringiensis	2.95e+03
844	5	1.1	843	1	W99799	BRCA1 mutant from pati	2.95e+03	917	5	1208	1	R81520	BRCA1 mutant from samp	2.95e+03
845	5	1.1	844	1	R81484	Enterococcus faecalis	2.95e+03	918	5	1216	1	W14497	Disease protein	2.95e+03
846	5	1.1	851	1	Y00172	Enterococcus faecalis	2.95e+03	919	5	1220	1	W03664	IBC-1 protein conferril	2.95e+03
847	5	1.1	851	1	Y00174	Enterococcus faecalis	2.95e+03	920	5	1223	1	W03664	Enterococcus faecalis	2.95e+03
848	5	1.1	851	1	Y00176	Amino acid sequence of	2.95e+03	921	5	1239	1	Y00127	Protein containing PDZ	2.95e+03
849	5	1.1	853	1	W81079	Feline immunodefience	2.95e+03	922	5	1255	1	W04734	Mouse mla Rho targett	2.95e+03
850	5	1.1	854	1	W81079	Staphylococcus aureus	2.95e+03	923	5	1262	1	W13505	B. bronchiseptica aden	2.95e+03
851	5	1.1	855	1	R44957	Renal cancer associate	2.95e+03	924	5	1285	1	W97098	Pfu DNA polymerase C s	2.95e+03
852	5	1.1	857	1	W97702	Staphylococcus aureus	2.95e+03	925	5	1289	1	R28890	HIS tagged thiorodoxin	2.95e+03
853	5	1.1	862	1	W87971	Toxin A immunogenic tr	2.95e+03	926	5	1291	1	Y06810	Toxin 1b	2.95e+03
854	5	1.1	862	1	Y07064	Amino acid sequence of	2.95e+03	927	5	1363	1	W47000	Mouse Per gene product	2.95e+03
855	5	1.1	866	1	W96956	Murine developmental t	2.95e+03	928	5	1385	1	R28890	Protein encoded by the	2.95e+03
856	5	1.1	866	1	Y00935	Mycobacterium species	2.95e+03	929	5	1391	1	Y01689	Enterococcus faecalis	2.95e+03
857	5	1.1	873	1	Y06985	M. prunae DNA polymera	2.95e+03	930	5	1391	1	Y01689	Enterococcus faecalis	2.95e+03
858	5	1.1	874	1	R60545	Myobacterium species	2.95e+03	931	5	1391	1	Y00130	Adenyl cyclase type 9	2.95e+03
859	5	1.1	876	1	Y04883	Bacillus cereus 100 KD	2.95e+03	932	5	1391	1	Y00130	Aldehyde oxidase prote	2.95e+03
860	5	1.1	877	1	Y00938	Mycobacterium species	2.95e+03	933	5	1391	1	W88525	Sequence encoded by hu	2.95e+03
861	5	1.1	884	1	R63793	Human brain-specific t	2.95e+03	934	5	1370	1	W57838	Toxin 17a	2.95e+03
862	5	1.1	886	1	Y07286	Human axlin	2.95e+03	935	5	1385	1	R28889	BR toxin 17a	2.95e+03
863	5	1.1	887	1	R80231	Human Hg38 protein	2.95e+03	936	5	1401	1	W97841	Murine MWRN polypeptid	2.95e+03
864	5	1.1	895	1	W96264	A. tigrinum AEI protel	2.95e+03	937	5	1401	1	W97841	Leuotoxin 101	2.95e+03
865	5	1.1	900	1	W93889	Rat metabotropic gluta	2.95e+03	938	5	1403	1	W95754	Enterococcus faecalis	2.95e+03
866	5	1.1	907	1	W90263	Rat semaphorin recepto	2.95e+03	939	5	1416	1	Y00211	Human btx protein	2.95e+03
867	5	1.1	915	1	R80479	Neutrophilin	2.95e+03	940	5	1429	1	W93941	Enterococcus faecalis	2.95e+03
868	5	1.1	921	1	W96247	Human semaphorin recep	2.95e+03	941	5	1448	1	Y00210	Amino acid sequence of	2.95e+03
869	5	1.1	922	1	W96309	Mouse semaphorin recep	2.95e+03	942	5	1481	1	W95160	Canine ribosome recept	2.95e+03
870	5	1.1	923	1	W96246	Chlamydia pneumoniae s	2.95e+03	943	5	1500	1	R30636	hCPS1	2.95e+03
871	5	1.1	928	1	W88421	M. catarrhalis strain	2.95e+03	944	5	1508	1	W96706	Human slit 1 mature pr	2.95e+03
872	5	1.1	930	1	W88424	Human AOMF05 proteln	2.95e+03	945	5	1522	1	Y04138	Human BAI1 protein	2.95e+03
873	5	1.1	941	1	W68205	Human AOMF05 proteln	2.95e+03	946	5	1528	1	W74472	Topoisomerase II, bindl	2.95e+03
874	5	1.1	944	1	W43310	Human AOMF05 proteln	2.95e+03	947	5	1528	1	W95895	Mouse multidrug resist	2.95e+03
875	5	1.1	949	1	W93905	Human AOMF05 proteln	2.95e+03	948	5	1531	1	W95895	Human multidrug resist	2.95e+03
876	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	949	5	1531	1	W95895	Human multidrug resist	2.95e+03
877	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	950	5	1531	1	W95895	Human multidrug resist	2.95e+03
878	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	951	5	1531	1	W95895	Human multidrug resist	2.95e+03
879	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	952	5	1531	1	W95895	Human multidrug resist	2.95e+03
880	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	953	5	1531	1	W95895	Human multidrug resist	2.95e+03
881	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	954	5	1531	1	W95895	Human multidrug resist	2.95e+03
882	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	955	5	1531	1	W95895	Human multidrug resist	2.95e+03
883	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	956	5	1531	1	W95895	Human multidrug resist	2.95e+03
884	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	957	5	1531	1	W95895	Human multidrug resist	2.95e+03
885	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	958	5	1531	1	W95895	Human multidrug resist	2.95e+03
886	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	959	5	1531	1	W95895	Human multidrug resist	2.95e+03
887	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	960	5	1531	1	W95895	Human multidrug resist	2.95e+03
888	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	961	5	1531	1	W95895	Human multidrug resist	2.95e+03
889	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	962	5	1531	1	W95895	Human multidrug resist	2.95e+03
890	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	963	5	1531	1	W95895	Human multidrug resist	2.95e+03
891	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	964	5	1531	1	W95895	Human multidrug resist	2.95e+03
892	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	965	5	1531	1	W95895	Human multidrug resist	2.95e+03
893	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	966	5	1531	1	W95895	Human multidrug resist	2.95e+03
894	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	967	5	1531	1	W95895	Human multidrug resist	2.95e+03
895	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	968	5	1531	1	W95895	Human multidrug resist	2.95e+03
896	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	969	5	1531	1	W95895	Human multidrug resist	2.95e+03
897	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	970	5	1531	1	W95895	Human multidrug resist	2.95e+03
898	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	971	5	1531	1	W95895	Human multidrug resist	2.95e+03
899	5	1.1	951	1	W93906	Human AOMF05 proteln	2.95e+03	972	5	1531	1	W95895	Human multidrug resist	2.95e+03

973	5	1.1	2161	1	W87724	Ruprestis stem pitting	2.95e+03
974	5	1.1	2183	1	W48709	Measles virus Zagreb v	2.95e+03
975	5	1.1	2193	1	W48708	Measles virus Moraten	2.95e+03
976	5	1.1	2193	1	W48710	Measles virus ATK-Cyva	2.95e+03
977	5	1.1	2233	1	W48711	HPIV-1 JS isolate wild	2.95e+03
978	5	1.1	2285	1	W98149	Bacillus subtilis meta	2.95e+03
979	5	1.1	2332	1	W33323	Procoagulant-active hu	2.95e+03
980	5	1.1	2343	1	W80989	Canine factor VIII	2.95e+03
981	5	1.1	2352	1	W11438	Active factor VIII-C a	2.95e+03
982	5	1.1	2352	1	W11439	Active factor VIII-C a	2.95e+03
983	5	1.1	2458	1	R04031	Full length T4 encoded	2.95e+03
984	5	1.1	2471	1	W84841	Candida albicans histi	2.95e+03
985	5	1.1	2860	1	W63651	Hepatitis GB virus E2	2.95e+03
986	5	1.1	2873	1	W92755	US5856134 Seq ID 15	2.95e+03
987	5	1.1	2910	1	W89458	Hepatitis G virus vari	2.95e+03
988	5	1.1	2910	1	W92789	US5856134 Seq ID 183	2.95e+03
989	5	1.1	2963	1	W56444	Fragment HgJ1789 of a	2.95e+03
990	5	1.1	2969	1	W56449	Fragment KJ32(2Y) of a	2.95e+03
991	5	1.1	3030	1	W98022	Infectious hepatitis C	2.95e+03
992	5	1.1	3011	1	R20111	Non-A, non-B viral gen	2.95e+03
993	5	1.1	3011	1	W98020	Infectious hepatitis C	2.95e+03
994	5	1.1	3011	1	W34480	HCV polypeptide	2.95e+03
995	5	1.1	3011	1	W98021	Infectious hepatitis C	2.95e+03
996	5	1.1	3096	1	Y06919	Hexaploid wheat DBE pa	2.95e+03
997	5	1.1	3119	1	W72304	HSV-2 strain S95 Cont1	2.95e+03
998	5	1.1	3165	1	R38889	Sequence encoded by OR	2.95e+03
999	5	1.1	3366	1	R43662	DEN1-S273/90 (PCACC V9	2.95e+03
1000	5	1.1	3801	1	W31949	Human bg protein assoc	2.95e+03

ALIGNMENTS

RESULT 1
ID R28495 standard; Protein: 436 AA.

AC R28495;
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor
with a high affinity for IFN-alpha and -beta.
KW Interferon receptor; alpha-interferon; beta-interferon.
OS Synthetic.
PN WO9218626-A.
PD 29-OCT-1992.
PR 17-APR-1991; F00318.
PR 17-APR-1991; WO-F00318.
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
PI Tovey M, Uze G;
DR MPI: 92-382110/46.
DR N-PSDB: Q30532.
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
and beta - useful as immunosuppressants, for treating auto-immune
PT diseases and transplant rejection
PS Claim 2; Fig 1; 58pp; English.
CC DNA encoding the water-soluble polypeptide with a high affinity for
IFN-alpha and -beta is isolated by PCR, using appropriate
CC oligonucleotides as primers and cloned cDNA as template. For example,
CC bacteriophage lambda ZAP, containing the entire coding sequence of
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495
CC lacks the transmembrane and cytoplasmic domains. Both forms bind
CC IFN in the same way as antibodies so are immunosuppressants e.g. for
CC treating autoimmune diseases and graft rejection. They lack the
CC toxic side-effects of known immunosuppressants such as steroids.
SQ Sequence 436 AA;

Query Match 100.0%; Score 436; DB 1; Length 436;

Best Local Similarity 100.0%; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVLLGATTLVAVGPVWLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESIGNVT 60
1 MMVLLGATTLVAVGPVWLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESIGNVT 60

Db	61	ESPDYOKTGMDNMKIKSGCONITSTKCNFSLKLNYSERIKLRIRAEKNTSSWYVDSE	120
Qy	61	ESPDYOKTGMDNMKIKSGCONITSTKCNFSLKLNYSERIKLRIRAEKNTSSWYVDSE	120
Db	121	TPFRKAQIGPPEVHEAEKKAIVIHISPTKDSVMMALDGLSTYSLLIMKNSGVEERI	180
Qy	121	TPFRKAQIGPPEVHEAEKKAIVIHISPTKDSVMMALDGLSTYSLLIMKNSGVEERI	180
Db	181	ENIYSRHKIKYKSPETTYCLKVAALITSMKIGVSPVACIKTVEENLPPENIEVSQ	240
Qy	181	ENIYSRHKIKYKSPETTYCLKVAALITSMKIGVSPVACIKTVEENLPPENIEVSQ	240
Db	241	NOVYVLMKDYTNAMFQOMLHAFIRKPNGLTYWKQIPDCENKTKQCFPQVNFQK	300
Qy	241	NOVYVLMKDYTNAMFQOMLHAFIRKPNGLTYWKQIPDCENKTKQCFPQVNFQK	300
Db	301	GYLLRVAQSDGNSTFSESEIEKDEIOAFLLPVPFNRLSDSFHIIYIGAPKSGNTP	360
Qy	301	GYLLRVAQSDGNSTFSESEIEKDEIOAFLLPVPFNRLSDSFHIIYIGAPKSGNTP	360
Db	361	VIODYPLIIEIIFEMTSSNAERKIKKIDVYVPIKPLTYVCVKRAHMDKLNKSSV	420
Qy	361	VIODYPLIIEIIFEMTSSNAERKIKKIDVYVPIKPLTYVCVKRAHMDKLNKSSV	420
Db	421	ESDVCETKTPGNTSK 436	
Qy	421	ESDVCETKTPGNTSK 436	

RESULT 2
ID R14487 standard; Protein: 436 AA.

AC R14487;
DT 16-JAN-1992 (first entry)
DE Soluble Interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PR 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tovey M, Uze G;
DR MPI: 91-319778/44.
DR N-PSDB: Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 45; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor
CC have been deleted to obtain a soluble, circulating form of the
CC receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence
CC are also claimed as are hybrid molecules comprising the soluble
CC receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also Q14240.
SQ Sequence 436 AA;

Query Match 100.0%; Score 436; DB 1; Length 436;

Best Local Similarity 100.0%; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVLLGATTLVAVGPVWLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESIGNVT 60
1 MMVLLGATTLVAVGPVWLSAAGKRLKSPQKVEVDIIDNFTLRNRSDESIGNVT 60

DB 61 FSPDYOKTGMDNMKIKSGCONITSTKCNFSLKLNYSERIKLRIRAEKNTSSWYVDSE 120
61 FSPDYOKTGMDNMKIKSGCONITSTKCNFSLKLNYSERIKLRIRAEKNTSSWYVDSE 120

DB 121 TPFRKAQIGPPEVHEAEKKAIVIHISPTKDSVMMALDGLSTYSLLIMKNSGVEERI 180
121 TPFRKAQIGPPEVHEAEKKAIVIHISPTKDSVMMALDGLSTYSLLIMKNSGVEERI 180

Db 181 ENIYSRHKIYKISPEYTCYKAKALITSMKIGVSPVHCITTYENELPPENIEVSQ 240
 QY 181 ENIYSRHKIYKISPEYTCYKAKALITSMKIGVSPVHCITTYENELPPENIEVSQ 240
 Db 241 NONYLKNDYTYANNTFOVOMLHAFKRNPNHLYKMKQIPDCENVKTTQCVFQNVOK 300
 QY 241 NONYLKNDYTYANNTFOVOMLHAFKRNPNHLYKMKQIPDCENVKTTQCVFQNVOK 300
 Db 301 GYLLRVOASGNTSMFSEIEKFDTEIOAFLLPVPVFNIRSLSDSFHYIGAPKOSGNT 360
 QY 301 GYLLRVOASGNTSMFSEIEKFDTEIOAFLLPVPVFNIRSLSDSFHYIGAPKOSGNT 360
 Db 361 VIOPYPLIYEIIFEMNTSMERKIIKERTDVTVPNLKPLFYCYKARAHMTDEKLNSV 420
 QY 361 VIOPYPLIYEIIFEMNTSMERKIIKERTDVTVPNLKPLFYCYKARAHMTDEKLNSV 420
 Db 421 FSDAVCEKTRPGNTSK 436
 QY 421 FSDAVCEKTRPGNTSK 436

RESULT 3
 ID R14488 standard; Protein; 557 AA
 AC R14488;
 DT 16-JAN-1992 (first entry)
 DE Complete interferon-alpha/beta receptor.
 KW IFN; autoimmune disease; graft rejection; histocompatibility.
 OS Homo sapiens.
 FH Key
 FT domain Location/Qualifiers
 FT domain 437..457
 FT domain /label= transmembrane
 FT domain 458..557
 FT domain /label= cytoplasmic
 PN FR2657881-A;
 PD 05-AUG-1991;
 PE 05-FEB-1990; 001298.
 PR (EUBI-) LAB EURO BIOTECNO.
 PA (EUBI-) LAB EURO BIOTECNO.
 PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
 DR WPI; 91-319778/44.
 DR N-PSDB; Q14240.
 PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
 PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
 PS aplastic anemia, diabetes mellitus, rheumatoid arthritis, etc.
 PS Disclosure; Page 47; 52pp; French.
 CC The invention covers derivatives of the interferon-alpha and/or beta
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains
 CC of the native receptor or by substitution. Potentially immunogenic
 CC epitopes are eliminated and the deriv. can be secreted from
 CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
 CC and can be used to treat autoimmune diseases or to inhibit graft
 CC rejection. See also Q14239.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 436; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMVVLGATTLVAVGPPVLSAAGKMLKSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 QY 1 MMVVLGATTLVAVGPPVLSAAGKMLKSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 Db 61 FSDYQKGMNMKILSGCNTSTKCNFSSKLNVYEIKIRIRAEKENTSSWYEVDSF 120
 QY 61 FSDYQKGMNMKILSGCNTSTKCNFSSKLNVYEIKIRIRAEKENTSSWYEVDSF 120
 Db 121 TPFRAQIGPPEVHLAEADKAIVIHISPTKDSVYMAALDGLSFTYSLIMKSSGVEERI 180
 QY 121 TPFRAQIGPPEVHLAEADKAIVIHISPTKDSVYMAALDGLSFTYSLIMKSSGVEERI 180
 Db 181 ENIYSRHKIYKISPEYTCYKAKALITSMKIGVSPVHCITTYENELPPENIEVSQ 240

QY 181 ENIYSRHKIYKISPEYTCYKAKALITSMKIGVSPVHCITTYENELPPENIEVSQ 240
 Db 241 NONYLKNDYTYANNTFOVOMLHAFKRNPNHLYKMKQIPDCENVKTTQCVFQNVOK 300
 QY 241 NONYLKNDYTYANNTFOVOMLHAFKRNPNHLYKMKQIPDCENVKTTQCVFQNVOK 300
 Db 301 GYLLRVOASGNTSMFSEIEKFDTEIOAFLLPVPVFNIRSLSDSFHYIGAPKOSGNT 360
 QY 301 GYLLRVOASGNTSMFSEIEKFDTEIOAFLLPVPVFNIRSLSDSFHYIGAPKOSGNT 360
 Db 361 VIOPYPLIYEIIFEMNTSMERKIIKERTDVTVPNLKPLFYCYKARAHMTDEKLNSV 420
 QY 361 VIOPYPLIYEIIFEMNTSMERKIIKERTDVTVPNLKPLFYCYKARAHMTDEKLNSV 420
 Db 421 FSDAVCEKTRPGNTSK 436
 QY 421 FSDAVCEKTRPGNTSK 436

RESULT 4
 ID R1958 standard; Protein; 557 AA
 AC R1958;
 DT 18-JUL-1991 (first entry)
 DE Human alpha-interferon receptor protein.
 KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
 OS Homo sapiens.
 FH Key
 FT peptide Location/Qualifiers
 FT peptide 1..27
 FT peptide /label= signal peptide
 PN W09105862-A.
 PD 02-MAY-1991.
 PE 19-OCT-1990; F00758
 PR 20-OCT-1989; FR-013770.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Mogensen KE, Uze G, Lutfalla G, Gresser I;
 DR WPI; 91-148740/20.
 DR N-PSDB; Q11701.
 PT New human alpha-interferon receptor protein - useful for testing
 PT interferon agonists and in treatment or diagnosis
 PS Disclosure; fig 4; 30pp; French.
 CC This recombinant human alpha interferon (IFN) receptor protein is
 CC useful for the testing of IFN agonists and for treatment and diag-
 CC nosis of viral diseases and tumours. Antibodies raised against
 CC this protein can be used for blocking the receptor when required,
 CC eg where overexpression of alpha-IFN is harmful. The Abs are
 CC also useful for eg drug targeting. Variants of the protein,
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted
 CC between residues 479 and 480, are also useful.
 SQ Sequence 557 AA;

Query Match 100.0%; Score 436; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMVVLGATTLVAVGPPVLSAAGKMLKSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 QY 1 MMVVLGATTLVAVGPPVLSAAGKMLKSPQKVEVDIIDNFIIRNRSDSEGVNT 60
 Db 61 FSDYQKGMNMKILSGCNTSTKCNFSSKLNVYEIKIRIRAEKENTSSWYEVDSF 120
 QY 61 FSDYQKGMNMKILSGCNTSTKCNFSSKLNVYEIKIRIRAEKENTSSWYEVDSF 120
 Db 121 TPFRAQIGPPEVHLAEADKAIVIHISPTKDSVYMAALDGLSFTYSLIMKSSGVEERI 180
 QY 121 TPFRAQIGPPEVHLAEADKAIVIHISPTKDSVYMAALDGLSFTYSLIMKSSGVEERI 180
 Db 181 ENIYSRHKIYKISPEYTCYKAKALITSMKIGVSPVHCITTYENELPPENIEVSQ 240
 QY 181 ENIYSRHKIYKISPEYTCYKAKALITSMKIGVSPVHCITTYENELPPENIEVSQ 240
 Db 241 NONYLKNDYTYANNTFOVOMLHAFKRNPNHLYKMKQIPDCENVKTTQCVFQNVOK 300

OY 241 NONVLMKDYTNAMTFVOYOMLHAFLKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300
 DB 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKOSGNT 360
 OY 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKOSGNT 360
 DB 361 VIODYPLIYIEMTNSAERKIEKTDVTPNKLPLVYCVKAAHMDKLNKSSV 420
 OY 361 VIODYPLIYIEMTNSAERKIEKTDVTPNKLPLVYCVKAAHMDKLNKSSV 420
 DB 421 FSDVCEKTKPGNTSK 436
 OY 421 FSDVCEKTKPGNTSK 436
 RESULT 5
 ID R24635 standard; Protein: 557 AA.
 AC R42635;
 DT 20-APR-1994 (first entry)
 DE Human interferon receptor.
 KW IFN-R; extracellular domain; monoclonal antibody; viral infection;
 cell proliferation; allograft rejection; systemic lupus erythematosus;
 psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
 immunodeficiency; measles virus; interferon-alpha-beta.
 OS Homo sapiens.
 PI Key Location/Qualifiers
 FT domain 1..436
 FT label= extracellular domain
 FT /note= soluble; immunogenic form of IFN-R
 EN EP-563487-A.
 PD 06-OCT-1993.
 PF 31-MAR-1992: 400902.
 PR 31-MAR-1992: EP-400902.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;
 DR P-PSDB; R42635.
 DR WPI; 93-312951/40.
 PT Monoclonal antibody to human interferon type-I receptor - having
 neutralising activity against human type I interferon, used for
 therapy and diagnosis
 PS Disclosure: Fig 3; 21pp; English.
 CC Monoclonal antibodies produced against soluble forms of the human
 CC interferon alpha-beta receptor based on the full-length human IFN-R
 CC sequence are claimed. The antibodies are useful for treatment and
 CC prophylaxis of disorders involving cell proliferation and/or viral
 CC infection.
 SQ Sequence 557 AA;
 Query Match 100.0%; Score 436; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 MMVVLGATTLVAVGPNWLSAAGKNLSPQKVEVDIIDNFLRNRSDSEVGNVT 60
 OY 1 MMVVLGATTLVAVGPNWLSAAGKNLSPQKVEVDIIDNFLRNRSDSEVGNVT 60
 DB 61 FSPDYQKGTGDMNLIKSGCONITSTKCNFSSKLNTYEETKLRIRAEKENTSSWYEDSF 120
 OY 61 FSPDYQKGTGDMNLIKSGCONITSTKCNFSSKLNTYEETKLRIRAEKENTSSWYEDSF 120
 DB 61 FSPDYQKGTGDMNLIKSGCONITSTKCNFSSKLNTYEETKLRIRAEKENTSSWYEDSF 120
 OY 61 FSPDYQKGTGDMNLIKSGCONITSTKCNFSSKLNTYEETKLRIRAEKENTSSWYEDSF 120
 DB 121 TPRKAOIGPPEVHLEADKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSSGVEERI 180
 OY 121 TPRKAOIGPPEVHLEADKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSSGVEERI 180
 DB 121 TPRKAOIGPPEVHLEADKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSSGVEERI 180
 OY 121 TPRKAOIGPPEVHLEADKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSSGVEERI 180
 DB 181 ENTYSRRIKIKLSPETTYCLAKVAALLTSKIGVSPVHCIKTTVENELPPENIEVSQ 240
 OY 181 ENTYSRRIKIKLSPETTYCLAKVAALLTSKIGVSPVHCIKTTVENELPPENIEVSQ 240
 DB 241 NONVLMKDYTNAMTFVOYOMLHAFLKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300
 OY 241 NONVLMKDYTNAMTFVOYOMLHAFLKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300
 DB 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKOSGNT 360
 OY 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKOSGNT 360

DB 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKOSGNT 360
 OY 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKOSGNT 360
 DB 361 VIODYPLIYIEMTNSAERKIEKTDVTPNKLPLVYCVKAAHMDKLNKSSV 420
 OY 361 VIODYPLIYIEMTNSAERKIEKTDVTPNKLPLVYCVKAAHMDKLNKSSV 420
 DB 421 FSDVCEKTKPGNTSK 436
 OY 421 FSDVCEKTKPGNTSK 436
 RESULT 6
 ID R24496 standard; Protein: 557 AA.
 AC R24496;
 DT 31-MAR-1993 (first entry)
 DE Sequence of a soluble form of the interferon (IFN) receptor
 DE with a high affinity for IFN-alpha and -beta.
 KW Interferon receptor; alpha-interferon; beta-interferon.
 OS Synthetic.
 PN M09218626-A.
 PD 29-OCT-1992.
 PF 17-APR-1991: F00318.
 PR 17-APR-1991: MO-F00318.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
 PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,
 PI Tovey M, Uze G;
 DR WPI; 92-382110/46.
 DR N-PSDB; Q30533.
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha
 PT and beta - useful as immunosuppressants, for treating auto-immune
 PT diseases and transplant rejection
 PS Claim 3; Fig 2; 56pp; English.
 CC DNA encoding the water-soluble polypeptide with a high affinity for
 CC IFN-alpha and -beta is isolated by PCR, using appropriate
 CC oligonucleotides as primers and cloned cDNA as template. For example,
 CC bacteriophage lambda ZAP, containing the entire coding sequence of
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos
 CC Q30534 and Q30535. R24496 represents the complete receptor. R24495
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for
 CC treating autoimmune diseases and graft rejection. They lack the
 CC toxic side-effects of known immunosuppressants such as steroids.
 SQ Sequence 557 AA;
 Query Match 100.0%; Score 436; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 MMVVLGATTLVAVGPNWLSAAGKNLSPQKVEVDIIDNFLRNRSDSEVGNVT 60
 OY 1 MMVVLGATTLVAVGPNWLSAAGKNLSPQKVEVDIIDNFLRNRSDSEVGNVT 60
 DB 61 FSPDYQKGTGDMNLIKSGCONITSTKCNFSSKLNTYEETKLRIRAEKENTSSWYEDSF 120
 OY 61 FSPDYQKGTGDMNLIKSGCONITSTKCNFSSKLNTYEETKLRIRAEKENTSSWYEDSF 120
 DB 61 FSPDYQKGTGDMNLIKSGCONITSTKCNFSSKLNTYEETKLRIRAEKENTSSWYEDSF 120
 OY 61 FSPDYQKGTGDMNLIKSGCONITSTKCNFSSKLNTYEETKLRIRAEKENTSSWYEDSF 120
 DB 121 TPRKAOIGPPEVHLEADKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSSGVEERI 180
 OY 121 TPRKAOIGPPEVHLEADKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSSGVEERI 180
 DB 121 TPRKAOIGPPEVHLEADKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSSGVEERI 180
 OY 121 TPRKAOIGPPEVHLEADKAIYIHISPGTKDSVMALDGLSTYSLLIMKNSSGVEERI 180
 DB 181 ENTYSRRIKIKLSPETTYCLAKVAALLTSKIGVSPVHCIKTTVENELPPENIEVSQ 240
 OY 181 ENTYSRRIKIKLSPETTYCLAKVAALLTSKIGVSPVHCIKTTVENELPPENIEVSQ 240
 DB 241 NONVLMKDYTNAMTFVOYOMLHAFLKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300
 OY 241 NONVLMKDYTNAMTFVOYOMLHAFLKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300
 DB 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKOSGNT 360
 OY 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKOSGNT 360

Db 361 VIODYPLIYEIIFWENTSNAERKITEKTDVTPNKLPLVYCVARAHMDEKLNSSV 420
 OY 361 VIODYPLIYEIIFWENTSNAERKITEKTDVTPNKLPLVYCVARAHMDEKLNSSV 420
 Db 421 FSDAVCEKTPGNTSK 436
 OY 421 FSDAVCEKTPGNTSK 436

RESULT 7
 ID R75356 standard; Protein; 557 AA.
 AC R75356
 DT 16-OCT-1995 (first entry)
 DE Human IFN receptor.
 KW IFN receptor; Interferon receptor; Interferon-alpha;
 OS Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.
 FH Homo sapiens.
 FT Key
 FT domain
 FT 1. 436
 FT /label= Extracellular_domain
 PD MO9507716-A.
 PN 23-MAR-1995.
 PR 16-SEP-1994; E03114.
 PR 17-SEP-1993; EP-402279.
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
 PI Benlizi EJ, Tovey MG;
 DR WPI: 95-131187/17.
 DR N-PSDB: 086458.
 PT Compn. of monoclonal antibodies against Interferon receptor
 PS useful as Immunomodulator, eg. for treating AIDS
 PS Disclosure: Fig. 3A-2B; 105pp; English.
 CC The amino acid sequence of human Interferon class I receptor is
 CC given in R75356. A recombinant soluble form of the extracellular
 CC domain of this receptor (R71723) has been used to raise
 CC immunomodulatory monoclonal antibodies.
 SQ Sequence 557 AA;

Query Match 88.3%; Score 385; DB 1; Length 557;
 Best Local Similarity 99.8%; Pred. No. 0.00e+00;
 Matches 435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MMYVLGATTLVAVGPWVLSAAGKRNKSPQKVEVDIIDDNFILRNKSDSVGNT 60
 OY 1 MMYVLGATTLVAVGPWVLSAAGKRNKSPQKVEVDIIDDNFILRNKSDSVGNT 60
 Db 61 FSPDYOKTGMDNMTIKSLGCONITSTKCNFSSKLNVYEELKIRAKENTSSWYEDSF 120
 OY 61 FSPDYOKTGMDNMTIKSLGCONITSTKCNFSSKLNVYEELKIRAKENTSSWYEDSF 120
 Db 121 TPRKAOIGPPEVHLEADAIYHISPGTKDSVMALDGLSFTYSLILKNSGVEERI 180
 OY 121 TPRKAOIGPPEVHLEADAIYHISPGTKDSVMALDGLSFTYSLILKNSGVEERI 180
 Db 181 ENTYSRRKIYKISPEPTYCLKVAALITSMKIGVSPVHCITKTVENELEPPENIEVSQ 240
 OY 181 ENTYSRRKIYKISPEPTYCLKVAALITSMKIGVSPVHCITKTVENELEPPENIEVSQ 240
 Db 181 ENTYSRRKIYKISPEPTYCLKVAALITSMKIGVSPVHCITKTVENELEPPENIEVSQ 240
 OY 181 ENTYSRRKIYKISPEPTYCLKVAALITSMKIGVSPVHCITKTVENELEPPENIEVSQ 240
 Db 241 NONTYVKMDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENKTTQCVFPOVFEK 300
 OY 241 NONTYVKMDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENKTTQCVFPOVFEK 300
 Db 301 GYLLRVQASDGNNTSFWSEEEKFDEIOAFILPVPFNIRSLSDSFHYIGAPKSGNTP 360
 OY 301 GYLLRVQASDGNNTSFWSEEEKFDEIOAFILPVPFNIRSLSDSFHYIGAPKSGNTP 360
 Db 361 VIODYPLIYEIIFWENTSNAERKITEKTDVTPNKLPLVYCVARAHMDEKLNSSV 420
 OY 361 VIODYPLIYEIIFWENTSNAERKITEKTDVTPNKLPLVYCVARAHMDEKLNSSV 420
 Db 421 FSDAVCEKTPGNTSK 436
 OY 421 FSDAVCEKTPGNTSK 436

RESULT 8
 ID W21804 standard; Protein; 557 AA.
 AC W21804
 DT 23-SEP-1997 (first entry)
 DE Transmembranal Interferon alpha-receptor
 KW Interferon alpha-receptor; IFNAR
 OS Homo sapiens
 FH Key
 FT domain
 FT 1. 436
 FT /label= Extracellular_domain
 FT 437. 457
 FT /label= Transmembrane_domain
 FT 458. 557
 FT /label= Intracellular_domain
 PD AU9475977-A.
 PN 11-MAY-1995.
 PR 20-OCT-1994; 075977.
 PR 24-OCT-1993; IL-107378.
 PA (YEDA) YEDA RES. & DEV. CO LTD.
 PI (ABRA) ABRAMOVICH C.
 PI Abramovich C, Ratovitski E, Revel M;
 DR WPI: 95-200634/27.
 PT New mammalian soluble Interferon alpha-receptor forms - used for
 PT inhibiting, modulating or modifying the activities of Interferon(s)
 PS Disclosure: Fig 7; 46pp; English.
 CC Human transmembranal Interferon alpha receptor (IFNAR) (W21804)
 CC includes a 21-amino acid transmembrane region. Novel, splice-
 CC deleted INAR forms 1 (W21805) and 2 (W21806) have been detected
 CC that lack this transmembrane domain. These soluble non-membrane
 CC bound polypeptides can be expressed in host cells and used to
 CC inhibit, modulate or modify the activities of Interferons alpha
 CC and beta in cells, tissues and organisms, or for diagnostic
 CC purposes.
 SQ Sequence 557 AA;

Query Match 88.3%; Score 385; DB 1; Length 557;
 Best Local Similarity 99.8%; Pred. No. 0.00e+00;
 Matches 435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MMYVLGATTLVAVGPWVLSAAGKRNKSPQKVEVDIIDDNFILRNKSDSVGNT 60
 OY 1 MMYVLGATTLVAVGPWVLSAAGKRNKSPQKVEVDIIDDNFILRNKSDSVGNT 60
 Db 61 FSPDYOKTGMDNMTIKSLGCONITSTKCNFSSKLNVYEELKIRAKENTSSWYEDSF 120
 OY 61 FSPDYOKTGMDNMTIKSLGCONITSTKCNFSSKLNVYEELKIRAKENTSSWYEDSF 120
 Db 121 TPRKAOIGPPEVHLEADAIYHISPGTKDSVMALDGLSFTYSLILKNSGVEERI 180
 OY 121 TPRKAOIGPPEVHLEADAIYHISPGTKDSVMALDGLSFTYSLILKNSGVEERI 180
 Db 181 ENTYSRRKIYKISPEPTYCLKVAALITSMKIGVSPVHCITKTVENELEPPENIEVSQ 240
 OY 181 ENTYSRRKIYKISPEPTYCLKVAALITSMKIGVSPVHCITKTVENELEPPENIEVSQ 240
 Db 181 ENTYSRRKIYKISPEPTYCLKVAALITSMKIGVSPVHCITKTVENELEPPENIEVSQ 240
 OY 181 ENTYSRRKIYKISPEPTYCLKVAALITSMKIGVSPVHCITKTVENELEPPENIEVSQ 240
 Db 241 NONTYVKMDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENKTTQCVFPOVFEK 300
 OY 241 NONTYVKMDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENKTTQCVFPOVFEK 300
 Db 301 GYLLRVQASDGNNTSFWSEEEKFDEIOAFILPVPFNIRSLSDSFHYIGAPKSGNTP 360
 OY 301 GYLLRVQASDGNNTSFWSEEEKFDEIOAFILPVPFNIRSLSDSFHYIGAPKSGNTP 360
 Db 361 VIODYPLIYEIIFWENTSNAERKITEKTDVTPNKLPLVYCVARAHMDEKLNSSV 420
 OY 361 VIODYPLIYEIIFWENTSNAERKITEKTDVTPNKLPLVYCVARAHMDEKLNSSV 420
 Db 421 FSDAVCEKTPGNTSK 436
 OY 421 FSDAVCEKTPGNTSK 436

RESULT 9
ID W21805 standard; Protein; 434 AA.
AC W21805;
DE 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 1.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key: Location/Qualifiers
FT domain 1.427
FT /label= "Extracellular domain
FT /note= "Comprises amino acids 1-427 of the
FT domain 428.434
FT /label= "S-domain
PN AU9475977-A.
PD 11-MAY-1995.
PE 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M.
DR WPI; 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 2; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1.
CC (W21805) is characterised by a new domain (S) which follows an
CC deleted extracellular domain when compared to transmembrane
CC IFNAR (W21804). There is no transmembrane domain. The amino acid
CC sequence is predicted from a cDNA clone (see also T73520) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate
CC the response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating the activity of the multiple IFN
CC subtypes. They can be expressed in host cells and used to inhibit,
CC modulate or modify the activities of IFNs alpha and beta in cells,
CC tissues and organisms, or for diagnostic purposes.
SQ Sequence 434 AA.

Query Match 86.2%; Score 376; DB 1; Length 434;

Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 MMYVLGATTLVLA VGPWVLSAAGKLNKSPKVEVDIIDNFILRMNSDSVGNVT 60
QY 1 MMYVLGATTLVLA VGPWVLSAAGKLNKSPKVEVDIIDNFILRMNSDSVGNVT 60
DB 61 FSPDYKTGMDNMTIKLSGCONITSTKCNFSSLKNTVEIKLRIRAKENTSSVEYDSF 120
QY 61 FSPDYKTGMDNMTIKLSGCONITSTKCNFSSLKNTVEIKLRIRAKENTSSVEYDSF 120
DB 121 TPFKRAOIGPEVLEADKRAIVIHISPGTKDSYVMAALDGLSFYSLIMKNSGVEERI 180
QY 121 TPFKRAOIGPEVLEADKRAIVIHISPGTKDSYVMAALDGLSFYSLIMKNSGVEERI 180
DB 121 TPFKRAOIGPEVLEADKRAIVIHISPGTKDSYVMAALDGLSFYSLIMKNSGVEERI 180
QY 121 TPFKRAOIGPEVLEADKRAIVIHISPGTKDSYVMAALDGLSFYSLIMKNSGVEERI 180
DB 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCITTVENELPPENIEVSQ 240
QY 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCITTVENELPPENIEVSQ 240
DB 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCITTVENELPPENIEVSQ 240
QY 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCITTVENELPPENIEVSQ 240
DB 241 NONVYLMKDYTYAMNTFOVOMLHAFKRNPGNHLKKMKQIPDCENVTQTQCVFQNTFOK 300
QY 241 NONVYLMKDYTYAMNTFOVOMLHAFKRNPGNHLKKMKQIPDCENVTQTQCVFQNTFOK 300
DB 241 NONVYLMKDYTYAMNTFOVOMLHAFKRNPGNHLKKMKQIPDCENVTQTQCVFQNTFOK 300
QY 241 NONVYLMKDYTYAMNTFOVOMLHAFKRNPGNHLKKMKQIPDCENVTQTQCVFQNTFOK 300
DB 301 GYLLLRVQASDGNNTSPWSEIKFDTEIOAFLLPVPVNIISLSDSFHYIGAPROSGNTP 360
QY 301 GYLLLRVQASDGNNTSPWSEIKFDTEIOAFLLPVPVNIISLSDSFHYIGAPROSGNTP 360
DB 301 GYLLLRVQASDGNNTSPWSEIKFDTEIOAFLLPVPVNIISLSDSFHYIGAPROSGNTP 360
QY 301 GYLLLRVQASDGNNTSPWSEIKFDTEIOAFLLPVPVNIISLSDSFHYIGAPROSGNTP 360
DB 361 VIQDYPLIYEIIFEMNTSNAERKIIIEKTDVTVNPKLPLIYCYKARAHMDELKNSV 420
QY 361 VIQDYPLIYEIIFEMNTSNAERKIIIEKTDVTVNPKLPLIYCYKARAHMDELKNSV 420
DB 421 FSDAVCE 427

RESULT 10
ID W21806 standard; Protein; 496 AA.
AC W21806;
DE 23-SEP-1997 (first entry)
DE Spliced-deleted interferon alpha-receptor form 2.
KW Interferon alpha-receptor; IFNAR.
OS Homo sapiens.
FH Key: Location/Qualifiers
FT domain 1.419
FT /label= "Extracellular domain
FT /note= "Comprises amino acid residues 1-413 and
FT domain 420.496
FT /label= "Intracellular domain
FT /note= "Comprises amino acids 481-557 of
FT domain 420.496
FT /label= "transmembrane IFNAR"
PN AU9475977-A.
PD 11-MAY-1995.
PE 20-OCT-1994; 075977.
PR 24-OCT-1993; IL-107378.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (ABRA/) ABRAMOVICH C.
PI Abramovich C, Ratovitski E, Revel M.
DR WPI; 95-200634/27.
PT New mammalian soluble interferon alpha-receptor forms - used for
PT inhibiting, modulating or modifying the activities of interferon(s)
PS Example 3; Fig 7; 46pp; English.
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2
CC (W21806) is characterised by a double deletion when compared to
CC transmembrane IFNAR (W21804). The extracellular domain is
CC shortened by 6 amino acid residues and is followed by a truncated
CC intracellular domain. There is no transmembrane region. The amino
CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the
CC response of human cells to IFNs, either by acting as IFN
CC antagonists or by regulating IFN activities. They can be expressed
CC in host cells and used to inhibit, modulate or modify the
CC activities of IFNs alpha and beta in cells, tissues and organisms,
CC or for diagnostic purposes.
SQ Sequence 496 AA.

Query Match 83.0%; Score 362; DB 1; Length 496;

Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 MMYVLGATTLVLA VGPWVLSAAGKLNKSPKVEVDIIDNFILRMNSDSVGNVT 60
QY 1 MMYVLGATTLVLA VGPWVLSAAGKLNKSPKVEVDIIDNFILRMNSDSVGNVT 60
DB 61 FSPDYKTGMDNMTIKLSGCONITSTKCNFSSLKNTVEIKLRIRAKENTSSVEYDSF 120
QY 61 FSPDYKTGMDNMTIKLSGCONITSTKCNFSSLKNTVEIKLRIRAKENTSSVEYDSF 120
DB 121 TPFKRAOIGPEVLEADKRAIVIHISPGTKDSYVMAALDGLSFYSLIMKNSGVEERI 180
QY 121 TPFKRAOIGPEVLEADKRAIVIHISPGTKDSYVMAALDGLSFYSLIMKNSGVEERI 180
DB 121 TPFKRAOIGPEVLEADKRAIVIHISPGTKDSYVMAALDGLSFYSLIMKNSGVEERI 180
QY 121 TPFKRAOIGPEVLEADKRAIVIHISPGTKDSYVMAALDGLSFYSLIMKNSGVEERI 180
DB 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCITTVENELPPENIEVSQ 240
QY 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCITTVENELPPENIEVSQ 240
DB 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCITTVENELPPENIEVSQ 240
QY 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCITTVENELPPENIEVSQ 240
DB 241 NONVYLMKDYTYAMNTFOVOMLHAFKRNPGNHLKKMKQIPDCENVTQTQCVFQNTFOK 300
QY 241 NONVYLMKDYTYAMNTFOVOMLHAFKRNPGNHLKKMKQIPDCENVTQTQCVFQNTFOK 300
DB 241 NONVYLMKDYTYAMNTFOVOMLHAFKRNPGNHLKKMKQIPDCENVTQTQCVFQNTFOK 300
QY 241 NONVYLMKDYTYAMNTFOVOMLHAFKRNPGNHLKKMKQIPDCENVTQTQCVFQNTFOK 300
DB 301 GYLLLRVQASDGNNTSPWSEIKFDTEIOAFLLPVPVNIISLSDSFHYIGAPROSGNTP 360
QY 301 GYLLLRVQASDGNNTSPWSEIKFDTEIOAFLLPVPVNIISLSDSFHYIGAPROSGNTP 360
DB 301 GYLLLRVQASDGNNTSPWSEIKFDTEIOAFLLPVPVNIISLSDSFHYIGAPROSGNTP 360
QY 301 GYLLLRVQASDGNNTSPWSEIKFDTEIOAFLLPVPVNIISLSDSFHYIGAPROSGNTP 360

RESULT 12
ID R47008 standard; Protein; 17 AA.
AC R47008;
DT 16-SEP-1994 (first entry)
DE IFN-alpha receptor position 271-287.
KW Naturally-occurring, immunomodulatory protein; human; therapy; class I
KW major histocompatibility complex; class II; allotype; type I diabetes
KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
KW multiple sclerosis; transplant rejection; vaccine; MHC.

DT	23-MAR-1993	(first entry)	
DE	Alpha 3B integrin subunit cDNA.		
KN	Mouse; alpha 6A, alpha 6B, integrin; cell surface receptor; adhesion;		
KW	extracellular matrix; cytoskeleton; heterodimer; laminin receptor;		
KW	alpha 3B.		
OS	Mus musculus.		
FH	Key	Location/Qualifiers	
FT	domain	108..112	
FT		/note-"Cytoplasmic sequence CDFK"	
PD	W09219647-A.		
PD	12-NOV-1992.		
PF	27-APR-1992; U03527.		
PF	03-MAY-1991; US-695564.		
PA	(SCRI) SCRIPPS RES INST.		
PR	Quaranta V, Tamura RN;		
DR	WPI; 92-39879/48.		
DR	N-PSDB; Q31192..		
PT	Integrin alpha sub-unit cytoplasmic domain polypeptide(s) - used		
PT	for prodn. of antibodies and in detection of integrin sub-units		
PT	in body samples		
PS	Disclosure; Page 92; 115pp; English.		
CC	The sequences given in R28823-25 are the mouse alpha 6B, 6A and		
CC	3B integrin subunits. Integrins are a family of cell surface		
CC	receptors which serve cellular adhesion functions. These receptors		
CC	form a link between the extracellular matrix and the cytoskeleton		
CC	through their binding to various extracellular components. Each		
CC	integrin receptor is a heterodimer comprised of an alpha and a beta		
CC	subunit. Each alpha subunit tends to associate with only one type of		
CC	beta subunit but there are several exceptions to this rule. The 6A		
CC	and 6B integrin subunits correspond to the laminin receptor and the		
CC	alpha 3B subunit corresponds to the laminin, collagen and fibronectin		
CC	receptors. The cytoplasmic domain of the 6A and 6B integrins differs		
CC	from previously isolated alpha 6 integrins.		
SO	Sequence 153 AA;		

Query Match 1.6%; Score 7; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.21e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 LVLVAVG 92
11 LVLVAVG 17

RESULT 14
ID W2599 standard; protein; 258 AA.
AC W2599; (first entry)
DE Human fast twitch skeletal muscle troponin T
KW Human; fast twitch skeletal muscle troponin; angiogenesis; inhibitor;
KM tumour; ocular neovascularisation; arthritis; psoriasis;
RN atherosclerotic plaque; nonunion fracture
OS Homo sapiens
PN W09730085-A1
PD 21-AUG-1997
PF 14-FEB-1997; U02439
PR 16-FEB-1996; US-602941
PA (CHIL-) CHILDRENS MEDICAL CENT
PI Langer RS, Moses MA, Sytkowski A, Wiedersheim DG,
PI Wu I;
PI WPI: 97-424977/39
PT Use of troponin subunits as angiogenesis inhibitors - used for
PT treating e.g. tumours, ocular neovascularisation, arthritis,
PT psoriasis, atherosclerotic plaques or nonunion fractures
PS Claim 1; Page 9; 51pp; English
CC A novel pharmaceutical composition has been developed which comprises a
CC carrier and an angiogenesis inhibiting amount of a peptide which is:
CC (a) an inhibitor of basic fibroblast growth factor (bFGF) stimulated
CC bovine endothelial cell proliferation having an IC50 of at least
CC 10 mu M; (b) greater than 75 amino acids in length; and (c) greater
CC than 80% homologous with a subunit selected from human fast-twitch
CC troponin subunit C, subunit I or subunit T. The present sequence
CC represents human fast-twitch troponin subunit T. The compositions can
CC be used for inhibiting atopic angiogenesis. They can be used to treat a
CC cancerous condition, or to prevent progression from a pre-neoplastic or
CC non-malignant state into a neoplastic or a malignant state. They can
CC also be used to treat ocular disorders associated with
CC neovascularisation such as neovascular glaucoma, diabetic retinopathy,
CC retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of
CC prematurity, macular degeneration, corneal graft neovascularisation as
CC well as other eye inflammatory diseases, ocular tumour and diseases
CC associated with choroidal or iris neovascularisation. They can also be
CC used to treat other disorders e.g. haemangioma, arthritis, psoriasis,
CC angiodioma, atherosclerotic plaques, delayed wound healing,
CC granuloma, haemophilic joints, hypertrophic scars, nonunion
CC fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma,
CC trachoma, and vascular adhesions.
SQ Sequence 258 AA;

Query Match 1.6%; Score 7; DB 1; Length 258;
Best Local Similarity 100.0%; Pred. No. 2.21e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 108 RIRAEKE 114
103 RIRAEKE 109

RESULT 15
ID R71035 standard; protein; 337 AA.
AC R71035;
DE 11-OCT-1995 (first entry)
DE Human IFN-gamma accessory factor-1
KW Interferon-gamma; AF-1; tumour.
OS Homo sapiens
PN W09505847-A
PD 02-MAR-1995
PF 22-AUG-1994; U09438

PR 20-AUG-1993; US-110119
PA (UYNE-) UNIV NEW JERSEY
PI Cook JR, Donnelly RJ, Emanuel S, Kotenko S, Mariano TM,
PI Pestka S, Schwartz B, Soh J,
DR WPI: 95-106679/14
DR N-PSDB: 084697
PT Suppressing tumours in mammals with accessory factor 1 (AF-1)
PT for interferon gamma, specifically induction of class I HLA
PT antigens, including use of AF-1 DNA in gene therapy
PS Disclosure; Fig 21A; 114pp; English
CC The sequence is that of human interferon-gamma accessory factor-1.
CC Incorporation of AF-1 into immune and tumour cells re-establishes
CC normal function with elimination of malignant cells.
SQ Sequence 337 AA;

Query Match 1.6%; Score 7; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 2.21e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 PPNIEV 148
231 PPNIEV 237

RESULT 16
ID R75783 standard; protein; 337 AA.
AC R75783;
DE 13-NOV-1995 (first entry)
DE IFN-gamma receptor beta-subunit
KW Interferon-gamma receptor beta subunit; huIFN-
KM Interferon-gamma-antagonist
OS Homo sapiens
PN W09516036-A
PD 15-JUN-1995
PF 07-DEC-1994; U14277
PR 09-DEC-1993; US-164596
PA (AGUE/) AGUE M
PA (BOEH/) BOEHNI R
PA (HEMM/) HEMMI S
PI Aguet M, Boehni R, Hemmi S;
PI WPI: 95-224321/29
DR N-PSDB: 090809
PT Novel interferon gamma receptor beta chain polypeptide - for
PT treatment of inflammatory bowel disease and liver damage
PS Claim 6; Fig 5a; 86pp; English
CC The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived
CC from a human cDNA library is given in R75783. Recombinant beta-subunit,
CC pref. with the transmembrane anchoring domain deleted or
CC inactivated and with the cytoplasmic domain deleted, may be
CC used to treat pathological conditions associated with endogenous
CC IFN-gamma production
SQ Sequence 337 AA;

Query Match 1.6%; Score 7; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 2.21e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 PPNIEV 148
231 PPNIEV 237

RESULT 17
ID R77867 standard; protein; 408 AA.
AC R77867;
DE 13-NOV-1995 (first entry)
DE S. clavuligerus ORF10 product
KW Clavulanic acid; clavulinate; antibiotic; beta-lactamase-inhibitor.
OS Streptomyces clavuligerus
PN CA2108113-A
PD 09-APR-1995
PF 08-OCT-1993; 108113
PR 08-OCT-1993; CA-108113

PA (UTAL-) UNIV ALBERTA;
 PI Aldoo KA, Jensen SE, Paradar AS;
 DR WPI: 95-207301/28.
 DR N-PSDB: Q91580.
 PT Clavulanic acid biosynthesis enzymes and corresp. DNA - useful for
 PT biosynthesis of the antidiabetic in Streptomyces hosts which do not
 PT naturally produce clavulanate
 PS Claim 32; Fig. 19; 41pp; English.
 CC A 15 kb fragment S. clavuligerus NRRL 5741 genomic DNA (Q91580),
 CC extending downstream from pcdB, included 10 ORFs encoding the
 CC enzymes required for clavulanate biosynthesis. The ORF10
 CC product (R77867) showed high similarity to cytochrome P450-type
 CC enzymes from other Streptomyces spp.
 SO Sequence 408 AA;

Query Match 1.6%; Score 7; DB 1; Length 408;
 Best Local Similarity 100.0%; Pred. No. 2.21e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 206 VERREN 212
 |||||
 QY 176 VERREN 182

RESULT 18
 ID W20402 standard; protein: 441 AA.
 AC W20402.
 DE 14-JUL-1997 (first entry)
 DT H. pylori cytoplasmic protein: 32422343.aa.
 KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;
 KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
 KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
 RN Helicobacter pylori.
 OS WO9640893-A1.
 PD 19-DEC-1996.
 PF 06-JUN-1996; 009122.
 PR 07-JUN-1995; US-487032.
 PR 01-APR-1996; US-630405.
 PA (ASTR) ASTRA AB.
 PI Berglundh OT, Smith D, Mellgaard BJ;
 DR WPI: 97-052306/05.
 DR N-PSDB: T67585.
 PT Helicobacter pylori nucleic acid sequences and related
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
 PT infection, and to detect Helicobacter
 PS Claim 61; Page 582-583; 1481pp; English.
 CC The present sequence is a H. pylori cytoplasmic protein.
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds,
 CC useful as potential H. pylori life cycle activators or inhibitors.
 CC The genomic sequence of H. pylori (ATCC 55679) was determined from
 CC overlapping contigs generated by mechanically shearing the bacterial
 CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
 CC and the predicted coding regions defined by computer evaluation. To
 CC identify likely H. pylori antigens for vaccine development, the amino
 CC acid sequences predicted from various ORF were analysed for significant
 CC homology to other known or exported membrane proteins. Having identified
 CC and determined the sequences of interest, particular regions can be
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide
 CC production, e.g. in E. coli hosts.
 SO Sequence 441 AA;

Query Match 1.6%; Score 7; DB 1; Length 441;
 Best Local Similarity 100.0%; Pred. No. 2.21e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 406 ELPPEN 412
 |||||
 QY 228 ELPPEN 234

RESULT 19
 ID W79159 standard; protein: 553 AA.

AC W79159;
 DT 20-NOV-1998 (first entry)
 DE zcytor7 cytokine receptor polypeptide.
 KW zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
 KW type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
 KW agonist; cell proliferation; cell differentiation; renal disease; human;
 OS Homo sapiens.
 RN Key.
 FT Domain
 FT Location/Qualifiers
 FT 30..250
 FT /note="extracellular (ligand-binding) domain;
 FT /sequence claimed in claim 1"
 FT 275..553
 FT /note="intracellular domain"

WO9837193-A1
 PN 27-AUG-1998.
 PF 18-FEB-1998; 003029.
 PR 02-OCT-1997; US-943087.
 PR 20-FEB-1997; US-803305.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Adams RL, Fairah TM, Jellberg AC, Kho CJ, Lok S,
 PI Whitmore RE;
 DR WPI: 98-480796/41.
 DR N-PSDB: V57515.
 PT Novel human zcytor7 DNA encodes a type 2 cytokine receptor - useful
 PT for treating renal, neural, pancreatic and prostatic diseases
 PS Claim 1; Pages 55-59; 72pp; English.
 CC This represents the zcytor7 cytokine receptor. zcytor7 is a ligand-
 CC binding receptor polypeptide and is a novel member of the type 2 cytokine
 CC receptor family (CRF). An expression vector containing the zcytor
 CC polynucleotide, operably linked to transcription promoter, a sequence
 CC encoding a transmembrane and intracellular domain, or both, and a
 CC transcriptional terminator can be used to transform host cells for the
 CC recombinant production of the polypeptide. The sequences can be used to
 CC study the zcytor7 gene and to isolate ligands binding to it. zcytor7 is
 CC preferentially expressed in the kidney, pancreas, prostate or nervous
 CC tissue. Agonists of zcytor7 can be used to stimulate proliferation and
 CC differentiation of cell in these organs. The antagonists and agonists can
 CC also be used in the treatment of renal, neural, pancreatic and prostate
 CC diseases.
 SO Sequence 553 AA;

Query Match 1.6%; Score 7; DB 1; Length 553;
 Best Local Similarity 100.0%; Pred. No. 2.21e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 136 QIGPEV 142
 |||||
 QY 127 QIGPEV 133

RESULT 20
 ID R14118 standard; protein: 1019 AA.
 AC R14118;
 DT 10-DEC-1991 (first entry)
 DE Human GAP b3 protein.
 KW Galactoprotein b3; carcinoma; cancer; tumour.
 OS Homo sapiens.
 RN Key.
 FT modified_site
 FT Location/Qualifiers
 FT 54
 FT /label= N-glycosylation
 FT modified_site
 FT 85
 FT /label= N-glycosylation
 FT binding_site
 FT 136..144
 FT /label= divalent cation binding site
 FT binding_site
 FT 209..217
 FT /label= divalent cation binding site
 FT modified_site
 FT 233
 FT /label= N-glycosylation
 FT binding_site
 FT 283..291
 FT /label= divalent cation binding site
 FT binding_site
 FT 346..354
 FT /label= divalent cation binding site

FT binding_site 407.415
 FT modified_site 468 /label- divalent cation binding site
 FT modified_site 479 /label- N-glycosylation
 FT modified_site 541 /label- N-glycosylation
 FT modified_site 573 /label- N-glycosylation
 FT modified_site 624 /label- N-glycosylation
 FT modified_site 665 /label- N-glycosylation
 FT modified_site 809 /label- N-glycosylation
 FT modified_site 825 /label- N-glycosylation
 FT cleavage_site 840.841 /label- N-glycosylation
 FT modified_site 894 /label- N-glycosylation
 FT modified_site 903 /label- N-glycosylation
 FT modified_site 937 /label- N-glycosylation
 FT domain 960.987 /label- transmembrane domain
 FT WO9113983-A.
 PD 19-SEP-1991
 PE 08-APR-1991; 001606.
 PR 12-MAR-1990; US-491910.
 PA (BION-) BIOMEMBRANE INST.
 PI Tsuji T, Yamamoto F, Hakomori S;
 DR N-PSDB; Q13822.
 PT DNA sequences encoding galactoprotein b3 - produced using DNA
 PT constructs also antibodies to gap b3 used to detect tumours that
 PT result in elevated expression of protein.
 PS Disclosure: Fig 6, 46pp; English.
 CC The sequence was deduced from 3 overlapping clones isolated from
 CC a human T24 cell line cDNA library. The DNA can be used to express
 CC the gap b3 protein which is a transformation-dependent cell surface
 CC glycoprotein. The C-terminal 32 AA segment is likely to constitute
 CC the cytoplasmic domain with the longer 959 AA residue segment
 CC forming a glycosylated extracellular domain. The N-terminal region
 CC has seven homologous repeats, three of which include the putative
 CC metal binding sequences. Each repeat consists of a long (21-28 AA)
 CC stretch followed by a short (5 AAs) stretch. The alignment of
 CC glycine and hydrophobic residues in each repeat shows a similar
 CC pattern, especially the presence of XXXGAP (X- a hydrophobic AA) at
 CC the end of most of the longer stretches (except for the 2nd and 7th
 CC repeats. The protein may be used to produce antibodies and these,
 CC or the DNA sequences, can be used to detect and quantify levels of
 CC gap b3 protein or mRNA in biological samples. A high level of the
 CC protein is indicative of certain cancers.
 CC See also R4117.
 SQ Sequence 1019 AA;

Query Match 1.6%; Score 7; DB 1; Length 1019;
 Best Local Similarity 100.0%; Pred. No. 2.21e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 962 LVIYAVG 968
 OY 11 LVIYAVG 17

RESULT 21
 ID W54032 standard; Protein: 1051 AA.
 AC W54032;
 DE Human alpha3 integrin protein.
 KW Anti-Integrin alpha3 antibody; human; anti-tumour agent;

KW chemotherapeutic drug.
 OS Homo sapiens.
 PN WO9809651-A1.
 PD 12-MAR-1998.
 PE 03-SEP-1997; 003085.
 PR 03-SEP-1996; JP-250887.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Hayakawa T, Kawata H, Sekimori Y, Shimizu K, Tomioka E;
 DR WPI: 98-193327/17.
 DR N-PSDB; V23920.
 PT Anti-integrin alpha3 antibody and chemotherapeutic drug - useful in
 PT anti-tumour agents and diagnostic reagent compositions
 PS Disclosure: Page 68-76; 96pp; Japanese.
 CC This sequence is the human alpha3 integrin protein. The alpha3
 CC integrin sequence is targeted by the anti-integrin alpha3 antibody of the
 CC invention. The anti-integrin alpha3 antibody or its antigen binding
 CC fragment are for use as anti-tumour agents, and diagnostic reagent
 CC compositions. They can also be used in a chemotherapeutic drug.
 SQ Sequence 1051 AA;

Query Match 1.6%; Score 7; DB 1; Length 1051;
 Best Local Similarity 100.0%; Pred. No. 2.21e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 994 LVIYAVG 1000
 OY 11 LVIYAVG 17

RESULT 22
 ID R22210 standard; Protein: 2206 AA.
 AC R22210;
 DE 14-JUL-1992 (first entry)
 DE True type 3 poliovirus protein from LED3.
 KW RNA virus; error reduction.
 OS Poliovirus.
 PN WO9203538-A.
 PD 05-MAR-1992.
 PE 20-AUG-1991; 005890.
 PR 20-AUG-1990; US-570000.
 PA (UYNYR-) COLUMBIA UNIV NEM Y.
 PI Racanelli V, Tatem JM, Weekslevy CL;
 DR WPI: 92-096882/12.
 DR N-PSDB; Q22965.
 PT New vaccine against infectious polio-virus comprises RNA virus -
 PT for producing RNA virus cDNA and viable RNA virus
 PS Disclosure: Fig 6, 110pp; English.
 CC The protein sequence was deduced from the cDNA sequence of p3
 CC poliovirus obd as in Q22965. The cDNA sequence is that of a
 CC true RNA virus, i.e. the cDNA directs the prodn. of a viable
 CC RNA virus which is phenotypically similar to the source virus.
 CC The full length cDNA in pLED3 was infectious. In vitro
 CC transcription of pLED3 cDNA using T7 RNA polymerase produced
 CC RNAs which possessed several erroneous amino acids. The RNA
 CC viruses are used in vaccines against polio. The screening method
 CC can be used during amplification of the source virus for vaccine
 CC prodn. to ensure maintenance of C at position 2493 in the viral
 CC genome i.e. increasing the attenuation. The new prod. overcomes
 CC the problem of errors introduced during replication of ss RNA,
 CC which is much higher than for ds DNA.
 SQ Sequence 2206 AA;

Query Match 1.6%; Score 7; DB 1; Length 2206;
 Best Local Similarity 100.0%; Pred. No. 2.21e+01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1271 AERKNTS 1277
 OY 106 AERKNTS 112

RESULT 23

ID W40852 standard; peptide; 9 AA.
AC W40852;
DT 09-JUN-1998 (first entry)
DE Cytotoxic Epstein-Barr T-cell epitope 25.
KW Herpes simplex virus type 4; Epstein-Barr virus; EBV; cytotoxic;
KM T-cell epitope; nuclear antigen; human leukocyte antigen; HLA; vaccine;
NM tetanus toxoid; diphtheria toxoid; Bordetella pertussis;
OS Poliovirus antigen
PN MO9745444-A1
PD 04-DEC-1997
PE 23-MAY-1997; AU0328
PR 24-MAY-1996; AU-000073.
PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (CSIC-) CSL LTD.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (UYME-) UNIV MELBOURNE.
PI Burrows SR, Kerr BM, Khanna R, Misko IS, Moss DJ;
PI WPI: 98-032576/03.
PT Cytotoxic Epstein-Barr virus T cell epitope - useful to prepare
PS vaccine to prevent and treat infection
PS Claim 3; Page 3; 41pp; English
CC This amino acid sequence is a cytotoxic Epstein-Barr virus (EBV) T-cell
CC epitope of the EBV nuclear antigen 6 (EBNA6) which binds the human
CC leukocyte antigen receptor B57 (HLA B57). It is used to prepare a
CC vaccine which may include the cytotoxic EBV T-cell epitope (W40828-
CC W40846), or a nucleic acid sequence encoding it. The vaccine produced
CC comprises or encodes at least one antigen (W40847-W40876) to which the
CC individual will mount an anamnestic response, e.g. a tetanus toxoid,
CC diphtheria toxoid, Bordetella pertussis antigen, poliovirus antigen,
CC purified protein derivative, glycoprotein 350 protein, and/or helper
CC epitope.
SQ Sequence 9 AA:

Query Match. 1.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.94e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 FRKAOI 6
|||||

OY 123 FRKAOI 128

RESULT 24
ID R80024 standard; peptide; 9 AA.
AC R80024;
DT 24-APR-1996 (first entry)
DE Cytotoxic Epstein-Barr virus T-cell epitope.
KW Epitope; EBV; cytotoxic T cell; lymphocyte; vaccine; immunisation;
KM CD8+
OS Epstein-Barr virus.
PN MO9524925-A1.
PD 21-SEP-1995.
PE 16-MAR-1994; AU0140.
PR 16-MAR-1994; AU-004465.
PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (CSIC-) CSL LTD.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (UYME-) UNIV MELBOURNE.
PI Burrows JM, Burrows SR, Kerr BM, Khanna R, Moss DJ;
PI Subrtler A;
PI WPI: 95-336817/43.
PT New cytotoxic T-cell epitopes of Epstein Barr virus - useful in
PT sub-unit vaccines to induce cytotoxic T cells
PS Claim 1; Page 15; 23pp; English.
CC New cytotoxic T-cell epitopes of Epstein-Barr virus have been
CC isolated and purified (R80017-R80028). Variants of these epitopes
CC have also been identified (R80029-R80033). The epitopes are small,
CC stable peptides whose manufacture does not involve use of any

CC Infectious material. The epitopes may be used as components of
CC subunit vaccines to induce cytotoxic T lymphocytes in a subject.
CC The vaccines are, partic. useful, against viral infections where
CC CD8+ cytotoxic T lymphocytes are protective.
SQ Sequence 9 AA;

Query Match. 1.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.94e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 FRKAOI 6
|||||

OY 123 FRKAOI 128

RESULT 25
ID R84905 standard; peptide; 9 AA.
AC R84905;
DT 25-APR-1996 (first entry)
DE Epstein-Barr virus derived cytotoxic T cell epitope.
KW Cytotoxic T cell; epitope; vaccine; antigen; tetanus; toxoid;
KM helper; poliovirus; diphtheria.
NM Epstein-Barr virus
OS Epstein-Barr virus
PN MO9524926-A1.
PD 21-SEP-1995.
PE 16-MAR-1995; AU0141.
PR 16-MAR-1994; AU-004465.
PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (CSIC-) CSL LTD.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (UYME-) UNIV MELBOURNE.
PI Cox JC, Elliott SL, Subrtler A;
PI WPI: 95-336818/43.
PT Compn. for induction of cytotoxic T cells - comprising CTL epitope
PT and at least one antigen, in a water in oil formulation
PS Claim 6; Page 23; 35pp; English.
CC A water in oil compn. comprising at least 1 antigen to which an
CC individual will mount an anamnestic response, and at least one
CC cytotoxic T cell (CTL) epitope can be used to induce CD8+ CTL.
CC cells in a vaccine, where the CTL epitope is known. The antigen is
CC a diphtheria toxoid, a pertussis or poliovirus antigen, a helper
CC epitope or esp. a tetanus toxoid, and the CTL epitope is 1 of the
CC Epstein-Barr virus derived peptides R84898-910.
SQ Sequence 9 AA:

Query Match. 1.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.94e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 FRKAOI 6
|||||

OY 123 FRKAOI 128

RESULT 26
ID R73033 standard; peptide; 19 AA.
AC R73033;
DT 18-JAN-1996 (first entry)
DE Human tyrosinase antigenic peptide.
KW Human tyrosinase; antigenic peptide; monoclonal anti-
KM pigment diseases; malignant melanoma; immunosay.
OS Homo sapiens.
PN MO9514042-A1.
PD 26-MAY-1995.
PE 14-OCT-1994; J01728.
PR 16-NOV-1993; JP-286861.
PR 31-AUG-1994; JP-207123.
PA (POK) POLA CHEM IND INC.
PI Masui S, Shibata K, Suzuki S, Tay
PI WPI: 95-200348/26.
PT Monoclonal antibody reacting with

PT tyrosinase-associated protein, is used as an immunoassay reagent for
PT melanoma diagnosis
PS Example 1: Pages 24-25; 41pp; Japanese
CC R71031-R71037 are tyrosinase antigenic peptides, with low homology
CC to the sequence of tyrosinase associated protein (TAP). The peptides
CC were used in the prepn. of an anti-tyrosinase monoclonal antibody
CC (mab), which does not react with TAP. The mab can be used in an
CC immunoassay for tyrosinase in biological samples, e.g. for the
CC diagnosis of pigment associated diseases such as malignant
CC melanoma.
SQ Sequence 19 AA;

Query Match 1.4%; Score 6; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.94e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 7 RNPGRH 12
OY 268 RNPGRH 273

RESULT 27
ID R71509 standard; Protein: 20 AA;
AC R71509;
DT 02-NOV-1995 (first entry)
DE LPIX-2.1, peptide fragment of Lol PV protein allergen.
KW Lolium perenne; Lol PV; Dactylis glomerata; Dac gV; epitope;
KW sensitivity; ryegrass pollen allergen.
OS Lolium perenne.
PN WO9506728-A.
PD 09-MAR-1995.
PE 05-AUG-1994; 009024.
PR 13-AUG-1993; US-106016.
PA (IMMU-) IMMUNOLOGIC PHARM CORP.
PI Griffith J, Kuo M, Lugman M;
DR WPI; 95-115444/15.
PT Lolium perenne Lol PV and Dactylis glomerata Dac gV epitope(s)
PT and-DNA - for treating sensitivity to ryegrass pollen allergen
PT or an immunologically cross-reactive allergen.
PS Claim 1; Fig 2; 11pp; English.
CC Lolium PV, is a major allergen of ryegrass pollen, and is encoded by the
CC cDNA sequence of clone 12R (Q85932), a full-length clone derived from
CC a lambda gt11 library. Peptides (R71508-61) comprising at least one
CC T cell-epitope derived from the Lol PV protein are claimed, and can be
CC used to treat or diagnose sensitivity to ryegrass pollen in an individual
CC or to pollen proteins that are immunologically related to Lol PV, such as
CC Dac gV (see R71507).
SQ Sequence 20 AA;

Query Match 1.4%; Score 6; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.94e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 11 AAAGK 16
OY 23 AAAGK 28

RESULT 28
ID R71510 standard; Protein: 20 AA;
AC R71510;
DT 02-NOV-1995 (first entry)
DE LPIX-3, peptide fragment of Lol PV protein allergen.
KW Lolium perenne; Lol PV; Dactylis glomerata; Dac gV; epitope;
KW sensitivity; ryegrass pollen allergen.
OS Lolium perenne.
PN WO9506728-A.
PD 09-MAR-1995.
PE 05-AUG-1994; 009024.
PR 13-AUG-1993; US-106016.
PA (IMMU-) IMMUNOLOGIC PHARM CORP.
PI Griffith J, Kuo M, Lugman M;
DR WPI; 95-115444/15.

PT Lolium perenne Lol PV and
PT and DNA - for treating se
PT or an immunologically cro
PS Claim 1; Fig 2; 11pp; Eng
CC Lol PV, is a major allerg
CC cDNA sequence of clone 12R
CC a lambda gt11 library. Pep
CC T cell epitope derived fro
CC used to treat or diagnose
CC or to pollen proteins that
CC Dac gV (see R71507).
SQ Sequence 20 AA;

Query Match 1.4%;
Best Local Similarity 100.0%;
Matches 6; Conservative

DB 1 AAAGK 6
OY 23 AAAGK 28

RESULT 29
ID R15517 standard; Protein: 23
AC R15517;
DT 09-MAR-1992 (first entry)
DE BMP-8 peptide.
KW Cartilage; wound healing; tissue repair; BMP.
OS Bos taurus.
PN WO9118098-A.
PD 28-NOV-1991.
PE 15-MAY-1991; 003388.
PR 16-MAY-1990; US-525357.
PR 15-JAN-1991; US-641204.
PA (GENE-) GENETICS INST INC.
PI Hewick RM, Wang JH;
DR WPI; 91-369252/50.
DR N-PSDB; Q15240, Q15242, Q15245, Q15246.
PT New BMP-8 protein - useful in inducing cartilage and/or bone
PT formation to treat wounds and repair fractures and tissues, e.g.
PT burns, incisions and ulcers.
PS Claim 1(d); Page 46; 50pp; English.
CC This sequence shares some homology (i.e. Asn-Glu-Leu-Pro)
CC with BMP-3 (see WO88/00205 and WO89/10409).
CC Pharmaceutical compns. contg. BMP-8, which comprises at least one
CC of the fragments represented in R15517 and R15522, can be used to aid
CC bone and/or cartilage formation or wound healing and tissue repair.
CC The proteins are not very species specific so can be used in domestic
CC and farm animals as well as humans.
CC See also Q15240-48, R15517 and R15522.
SQ Sequence 23 AA;

Query Match 1.4%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.94e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 NELPP 7
OY 227 NELPP 232

RESULT 30
ID R50181 standard; Protein: 37 AA;
AC R50181;
DT 17-OCT-1994 (first entry)
DE Fragment of excitatory amino acid receptor.
KW Excitatory amino acid receptor; EA; identification; detection;
KW CNS; Central nervous system; therapeutic; antibody; ligand;
KW screening.
OS Homo sapiens.
PN EP-368642-A.
PD 23-MAR-1994.
PF 16-SEP-1993; 307325.

Imoto H;
human tyrosinase - but not with

PR 17-SEP-1992; US-945210.
 PA (ELIOT) ELIOT C E.
 PA (KAMBOJ) KAMBOJ R.
 PI (NUTT) NUTT S L.
 PI Elliott CE, Kamboj R, Nutt SL;
 DR NPI: 94-094202/12.
 PT Nucleic acid encoding human excitatory aminoacid receptors - used
 for producing receptors and in assays for test ligands for
 binding to human CNS receptors
 PS Disclosure; Figure 3; 34pp; English.
 CC Nucleotides which encode the excitatory amino acid receptors (EAA's)
 can be used for the production of the receptors to identify
 a specimen. Recombinant cells which produce the receptors, or their
 membrane preparations, can be used for assaying a test ligand for
 binding to a human CNS receptor to develop therapeutics. The
 receptors can themselves be used in the production of antibodies for
 use in detection methods. This sequence is a fragment of an EAA
 receptor (EAA5c) which differs from EAA5a described in R50179
 (the fragment corresponds to amino acid residues 804-840 of EAA5a).
 CC EAA5c is composed of 840 amino acids whereas EAA5a is composed of 889
 amino acids (mature protein).
 SQ Sequence 37 AA;

Query Match 1.4%; Score 6; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 VLVAVG 7
 |||||
 QY 12 VLVAVG 17

RESULT 31
 ID W40091 standard; Protein; 38 AA.
 AC W40091;
 DT 29-MAY-1998 (first entry)
 DE Seq ID 99 from US5703221.
 KM Stealth virus; chronic fatigue syndrome; CFS; disease; detection;
 KM medical diagnostic; veterinary diagnostic; agricultural diagnostic;
 KM quality control.
 OS Unknown.
 PN US5703221-A.
 PD 30-DEC-1997.
 PE 05-JUN-1995; 463115.
 PR 05-JUN-1995; US-463115.
 PR 23-MAY-1991; US-704814.
 PR 20-SEP-1991; US-763039.
 PR 22-MAY-1992; US-887502.
 PR 23-NOV-1993; US-157811.
 PA (MART) MARTIN W J.
 PI Martin WJ;
 DR MPI: 98-076485/07.
 PT Stealth virus nucleic acid molecule - useful to detecting stealth
 virus, e.g. in chronic fatigue syndrome diagnosis
 PS Disclosure; Column 109-110; 82pp; English.
 CC This specification outlines the isolation and analysis of nucleic acid
 sequences obtained from a patient with a stealth virus infection, namely
 chronic fatigue syndrome (CFS). Such nucleic acid sequences can be used
 to detect the stealth virus in medical, veterinary and agricultural
 diagnostics and in industrial and pharmaceutical biological quality
 control, e.g. to diagnose a disease associated with the stealth virus.
 CC Note: This sequence does not appear in the printed patent specification.
 SQ Sequence 38 AA;

Query Match 1.4%; Score 6; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 3 SDAVCE 8
 |||||
 QY 422 SDAVCE 427

RESULT 32
 ID W59202 standard; Protein; 38 AA.
 AC W59202;
 DT 14-AUG-1998 (first entry)
 DE Seq ID 99 from US 5753486
 KM Chronic fatigue syndrome; CFS; vaccine; cytopathic effect;
 KM detection.
 OS Unknown.
 PN US5753486-A.
 PD 19-MAY-1998.
 PE 05-JUN-1995; 465388.
 PR 05-JUN-1995; US-465388.
 PR 23-MAY-1991; US-704814.
 PR 20-SEP-1991; US-763039.
 PR 22-MAY-1992; US-887502.
 PR 23-NOV-1993; US-157811.
 PA (MART) MARTIN W J.
 PI Martin WJ;
 DR MPI: 98-311405/27.
 PT Stealth virus contained in MRC-5 cell line, ATCC number VR2343 - is
 useful as a vaccine against chronic fatigue syndrome
 PS Disclosure; Column 111-112; 99pp; English.
 CC This specification describes the amplification of stealth virus fragments
 from patient D.W. Such fragments can be used as vaccine against chronic
 fatigue syndrome (CFS). This illness causes unexplained fatigue lasting
 more than 6 months and greater than 50% reduction in an infected persons
 normal level of activity. The virus causes a cytopathic effect (CPE) to
 fibroblast cells observed in culture, characterised by the appearance of
 CC rounded, slightly enlarged, refractile cells in the culture.
 CC NOTE: This sequence is given in the Seq ID listing but is not explained
 in the body of the specification
 SQ Sequence 38 AA;

Query Match 1.4%; Score 6; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 3 SDAVCE 8
 |||||
 QY 422 SDAVCE 427

RESULT 33
 ID W78223 standard; Protein; 42 AA.
 AC W78223;
 DT 13-APR-1999 (first entry)
 DE Human secreted protein.
 KM Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KM developmental abnormality; foetal deficiency; blood; allergy; renal;
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KM inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT Misc-difference 42
 PN W09856804-A1.
 FT W09856804-A1.
 PD 17-DEC-1998.
 PE 02-OCT-1997; US-061060.
 PR 13-JUN-1997; US-049547.
 PR 13-JUN-1997; US-049547.
 PR 13-JUN-1997; US-049549.
 PR 13-JUN-1997; US-049550.
 PR 13-JUN-1997; US-049606.
 PR 13-JUN-1997; US-049607.
 PR 13-JUN-1997; US-049608.
 PR 13-JUN-1997; US-049609.
 PR 13-JUN-1997; US-049610.

PR 13-JUN-1997; US-049611.
 PR 13-JUN-1997; US-050566.
 PR 13-JUN-1997; US-050901.
 PR 13-JUN-1997; US-052989.
 PR 08-JUL-1997; US-051919.
 PR 18-AUG-1997; US-055984.
 PR 12-SEP-1997; US-058668.
 PR 12-SEP-1997; US-058668.
 PR 12-SEP-1997; US-058669.
 PR 12-SEP-1997; US-058750.
 PR 12-SEP-1997; US-058971.
 PR 12-SEP-1997; US-058972.
 PR 12-SEP-1997; US-058975.
 PR 02-OCT-1997; US-060834.
 PR 02-OCT-1997; US-060841.
 PR 02-OCT-1997; US-060844.
 PR 02-OCT-1997; US-060865.
 PR 02-OCT-1997; US-061059.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Brewer LA, Ebner R, Ferrle AM, Feng P, Greene JM, Lafleur DW,
 PI Moore PA, NI J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P,
 PI Yu GL;
 DR MPI; 99-080881/07.
 DR N-PSDB; X04408.
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 PS Claim 11; Page 317; 380pp; English.
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. X04302) for increasing the stability of the fused protein
 CC as compared to the human protein only.
 CC The invention relates to 86 novel genes and their fragments (nucleic acid
 CC sequences: X04311-X04410; amino acid sequences W78126-W78225) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 86 polynucleotides, based on
 CC which tissues they are most highly expressed in (see X04311 for described
 CC uses).
 SQ Sequence 42 AA;

Query Match 1.4%; Score 6; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 14 LSNAAG 19
 111111
 QY 21 LSNAAG 26

RESULT 34
 ID W33605 standard; Protein; 45 AA.
 AC W33605;
 DT 21-MAY-1998 (first entry)
 DE Human secreted protein AK583 full-length sequence.
 KW Secreted protein; AK583; cytokine; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /Label- S1g-peptide
 FT Protein 25..45
 FT Protein /Label- Mat_protein
 PV W09739030-A2.
 PD 23-OCT-1997;
 PF 16-APR-1997; 006475.
 PR 13-JAN-1997; US-783520.
 PR 18-APR-1996; US-634325.
 PA (GENY) GENETICS INST INC.
 PI Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racle LA,
 PI Spalding V;

DR MPI; 97-526400/48.
 DR N-PSDB; V02297.
 PT New isolated secretory proteins AM340, AM282 and AK583 - possibly
 PT have cytokine, cell proliferation/differentiation regulating,
 PT immunomodulating activities, etc.
 PS Claim 19; Page 48; 59pp; English.
 CC This human secreted protein, designated AK583, is encoded by a
 CC full-length cDNA clone (see V02297), deposited in ATCC 98026, that
 CC was identified from a database search using an isolated partial
 CC AK583 clone (see V02299). AK583 protein can be used in a claimed
 CC method for preventing, treating or ameliorating a medical
 CC condition. It may exhibit cytokine, cell proliferation (either
 CC inducing or inhibiting) or cell differentiation (either inducing or
 CC inhibiting) activity or may induce production of other cytokines in
 CC certain cell populations. It may also exhibit e.g. immune
 CC stimulating or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic or chemokinetic activity, haemostatic or thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC tumour inhibition activity, or other activities. No evidence of
 CC any of these activities is given in the specification.
 SQ Sequence 45 AA;

Query Match 1.4%; Score 6; DB 1; Length 45;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 36 EKLKNS 41
 111111
 QY 413 EKLKNS 418

RESULT 35
 ID W55271 standard; Protein; 60 AA.
 AC W55271;
 DT 02-JUL-1998 (first entry)
 DE H. pylori ORF 056p1091orf3 protein.
 KW Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
 KW Identification; binding compound; bacteria; life cycle; activator;
 KW Inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
 OS Helicobacter pylori.
 PV W09737044-A1.
 PD 09-OCT-1997;
 PF 27-MAR-1997; 005223.
 PR 06-DEC-1996; US-761318.
 PR 29-MAR-1996; US-625811.
 PR 02-APR-1996; US-758731.
 PR 25-OCT-1996; US-736805.
 PR 28-OCT-1996; US-738859.
 PA (ASTR) ASTRA AB.
 PI Alm RA, Smith D;
 DR MPI; 97-503122/46.
 DR N-PSDB; V24680.
 PT Helicobacter pylori nucleic acid sequences, and encoded
 PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori
 PT infection and for diagnosis of H. pylori infection
 PS Claim 14; Page 510; 1145pp; English.
 CC This sequence is a H. pylori protein of unspecified function.
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds.
 CC useful as potential H. pylori life cycle activators or inhibitors. The
 CC DNA and probes derived from it may be used for the identification of
 CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic
 CC acid sequences complementary to the DNA act as antisense sequences and
 CC can be used to prevent the translation of H. pylori mRNA. Antibodies
 CC against the protein can be used in immunoassays to evaluate the abundance
 CC and distribution of H. pylori-specific antigens. The genomic sequence of
 CC H. pylori (ATCC 55679) was determined from overlapping contigs generated
 CC by mechanically shearing the bacterial DNA. The sequences were analysed
 CC for ORF of at least 180 nucleotides, and the predicted coding regions
 CC defined by computer evaluation. To identify likely H. pylori antigens for
 CC vaccine development, the amino acid sequences predicted from various ORF
 CC were analysed for significant homology to other known or exported

CC membrane proteins. Having identified and determined the sequences of
 CC interest, particular regions can be isolated from R. pylori by PCR
 CC amplification for recombinant polypeptide production, e.g. in E. coli
 CC hosts.
 CC Sequence 60 AA.

Query Match 1.44; Score 6; DB 1; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2,94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 52. FTKRN-57;
 QY 265. FTKRN-270

RESULT 36
 ID W74756 standard; Protein: 76 AA.
 AC W74756.
 DT 19-JAN-1999 (first entry)
 DE Human secreted protein encoded by gene 26 clone H66EH18.
 KW Human; secreted protein; testis; tumour; foetal brain tissue;
 KW fusion protein; cancer; central nervous system; seizure;
 KW diagnosis; neurodegenerative disease.
 OS Homo sapiens.
 PN WO9839448-A2.
 PD 11-SEP-1998.
 PE 06-MAR-1998; US-04493.
 PF 02-OCT-1997; US-061060.
 PR 07-MAR-1997; US-038621.
 PR 07-MAR-1997; US-040161.
 PR 07-MAR-1997; US-040162.
 PR 07-MAR-1997; US-040163.
 PR 07-MAR-1997; US-040333.
 PR 07-MAR-1997; US-040334.
 PR 07-MAR-1997; US-040336.
 PR 07-MAR-1997; US-040626.
 PR 11-APR-1997; US-043311.
 PR 11-APR-1997; US-043312.
 PR 11-APR-1997; US-043313.
 PR 11-APR-1997; US-043314.
 PR 11-APR-1997; US-043358.
 PR 11-APR-1997; US-043569.
 PR 11-APR-1997; US-043576.
 PR 11-APR-1997; US-043578.
 PR 11-APR-1997; US-043580.
 PR 11-APR-1997; US-043659.
 PR 11-APR-1997; US-043670.
 PR 11-APR-1997; US-043671.
 PR 11-APR-1997; US-043672.
 PR 11-APR-1997; US-043674.
 PR 23-MAY-1997; US-047492.
 PR 23-MAY-1997; US-047500.
 PR 23-MAY-1997; US-047501.
 PR 23-MAY-1997; US-047502.
 PR 23-MAY-1997; US-047503.
 PR 23-MAY-1997; US-047581.
 PR 23-MAY-1997; US-047582.
 PR 23-MAY-1997; US-047583.
 PR 23-MAY-1997; US-047584.
 PR 23-MAY-1997; US-047585.
 PR 23-MAY-1997; US-047586.
 PR 23-MAY-1997; US-047587.
 PR 23-MAY-1997; US-047588.
 PR 23-MAY-1997; US-047589.
 PR 23-MAY-1997; US-047590.
 PR 23-MAY-1997; US-047592.
 PR 23-MAY-1997; US-047593.
 PR 23-MAY-1997; US-047594.
 PR 23-MAY-1997; US-047595.
 PR 23-MAY-1997; US-047596.
 PR 23-MAY-1997; US-047597.
 PR 23-MAY-1997; US-047598.
 PR 23-MAY-1997; US-047599.

PR 23-MAY-1997; US-047600.
 PR 23-MAY-1997; US-047601.
 PR 23-MAY-1997; US-047612.
 PR 23-MAY-1997; US-047613.
 PR 23-MAY-1997; US-047614.
 PR 23-MAY-1997; US-047615.
 PR 23-MAY-1997; US-047617.
 PR 23-MAY-1997; US-047618.
 PR 23-MAY-1997; US-047632.
 PR 23-MAY-1997; US-047633.
 PR 06-JUN-1997; US-048964.
 PR 13-JUN-1997; US-049630.
 PR 16-JUL-1997; US-051926.
 PR 18-AUG-1997; US-052874.
 PR 22-AUG-1997; US-055724.
 PR 22-AUG-1997; US-056630.
 PR 22-AUG-1997; US-056631.
 PR 22-AUG-1997; US-056632.
 PR 22-AUG-1997; US-056636.
 PR 22-AUG-1997; US-056637.
 PR 22-AUG-1997; US-056662.
 PR 22-AUG-1997; US-056664.
 PR 22-AUG-1997; US-056845.
 PR 22-AUG-1997; US-056846.
 PR 22-AUG-1997; US-056872.
 PR 22-AUG-1997; US-056874.
 PR 22-AUG-1997; US-056875.
 PR 22-AUG-1997; US-056876.
 PR 22-AUG-1997; US-056877.
 PR 22-AUG-1997; US-056878.
 PR 22-AUG-1997; US-056879.
 PR 22-AUG-1997; US-056880.
 PR 22-AUG-1997; US-056881.
 PR 22-AUG-1997; US-056882.
 PR 22-AUG-1997; US-056884.
 PR 22-AUG-1997; US-056886.
 PR 22-AUG-1997; US-056887.
 PR 22-AUG-1997; US-056888.
 PR 22-AUG-1997; US-056889.
 PR 22-AUG-1997; US-056908.
 PR 22-AUG-1997; US-056909.
 PR 22-AUG-1997; US-056910.
 PR 22-AUG-1997; US-056911.
 PR 05-SEP-1997; US-057650.
 PR 05-SEP-1997; US-057659.
 PR 05-SEP-1997; US-057761.
 PR 12-SEP-1997; US-058785.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
 PI Feng P, Ferrite AM, Fischer CL, Florence KA, Greene JM, Hu JS,
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 DR MPI; 98-506364/43.
 DR N-PSDB; V59536.
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 PS Claim 1; page 55; 721pp; English.
 CC This sequence represents a secreted human protein encoded by the nucleic
 CC acid molecule designated Gene 26 from the human cDNA clone H66EH18
 CC (deposited as clone ATCC 97836 and ATCC 209044).
 CC The gene can be used to generate fusion proteins by linking to the gene
 CC to a human immunoglobulin Fc portion (e.g. V59502) for increasing the
 CC stability of the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which
 CC are useful for preventing, treating or ameliorating medical conditions

e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on CC which tissues they are most highly expressed in (see V59511 for described CC uses).

SO Sequence 76 AA:

Query Match 1.4%; Score 6; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.94e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 FSSUKL 8
89 FSSUKL 94

RESULT 37

ID W58848 standard; Protein; 85 AA.

AC W58848;

DT 23-JUL-1998 (first entry)

DE Human A168_4 secreted protein.

KM Secreted protein; prevention; treatment; gene therapy.

OS Homo sapiens.

PN W09801554-A2.

PD 15-JAN-1998.

PE 07-JUL-1997; 011876.

PR 09-JUL-1996; US-677231.

PA (GENY) GENETICS INST INC.

PI Bowman M, Evans C, Jacobs K, Lavallie ER, McCoy JM,

PI Weinberg D, Racle LA, Spaulding V, Treacy M;

PI WPI: 98-110230/10.

DR N-PSDB: V11431.

PT Secreted proteins and polynucleotides encoding them - useful to

PT prevent, treat and ameliorate medical conditions

PS Claim 22; Page 64; 93pp: English.

CC This sequence represents a fragment of a novel secreted protein derived

CC from clone A168_4 which was isolated from a human adult testes cDNA

CC library. The protein can be used to prevent, treat or ameliorate a

CC medical condition, while the polynucleotides can be used for gene

CC therapy.

SO Sequence 85 AA:

Query Match 1.4%; Score 6; DB 1; Length 85;

Best Local Similarity 100.0%; Pred. No. 2.94e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 25 AFLPP 30

OY 330 AFLPP 335

RESULT 38

ID W20172 standard; Protein; 92 AA.

AC W20172;

DT 08-JUL-1997 (first entry)

DE H. pylori protein.

KM Cytoplasmic; vaccine; prevention; treatment; infection; identification;

KM binding compound; bacterium; life cycle; activator; bacteria; inhibitor;

KM duodenal ulcer disease; chronic gastritis; diagnosis; envelope;

KM outer membrane; cell envelope; transporter.

OS Helicobacter pylori.

PH Key Location/Qualifiers

FT misc difference 86

FT note- "encoded by codon GSC"

PN W09640893-A1.

PD 19-DEC-1996.

PE 06-JUN-1996; 009122.

PR 07-JUN-1995; US-487032.

PR 01-APR-1996; US-630405.

PA (ASTR) ASTRA AB.

PI Berglundh OT, Smith D, Mellgaard BL;

PI WPI: 97-052306/05.

DR N-PSDB: T67408.

PT Helicobacter pylori nucleic acid sequences and related

PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori

PT infection, and to detect Helicobacter

PT disclosure; Pages 389; 1481pp; English.

CC The present sequence is a Helicobacter pylori protein of unknown

CC function. The protein may be used in a vaccine to prevent or treat

CC H. pylori infection or to identify H. pylori polypeptide binding

CC compounds, useful as potential H. pylori life cycle activators or

CC inhibitors. The genomic sequence of H. pylori (ATCC 55679) was

CC determined from overlapping contigs generated by mechanically shearing

CC the bacterial DNA. The sequences were analysed for ORF of at least 180

CC nucleotides, and the predicted coding regions defined by computer

CC evaluation. To identify likely H. pylori antigens for vaccine

CC development, the amino acid sequences predicted from various ORF were

CC analysed for significant homology to other known or exported membrane

CC proteins. Having identified and determined the sequences of interest,

CC particular regions can be isolated from H. pylori by PCR amplification

CC for recombinant polypeptide production, e.g. in E. coli hosts.

SO Sequence 92 AA:

Query Match 1.4%; Score 6; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.94e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 TTLVAV 21
9 TTLVAV 14

RESULT 39

ID W29774 standard; Protein; 102 AA.

AC W29774;

DT 23-FEB-1998 (first entry)

DE Malassezia fungus MF-7 antigenic protein.

KM Malassezia; fungus; antigenic; human; IGE; immunoglobulin E;

KM antibody; allergy; antigen.

OS Malassezia sp.

PN W09721817-A1.

PD 19-JUN-1997.

PE 10-DEC-1996; JP-257613.

PR 05-SEP-1996; JP-257613.

PR 12-DEC-1995; JP-346627.

PR 05-SEP-1996; JP-257612.

PA (TAKI) TAKARA SHUZO CO LTD.

PI Akiyama K, Kato I, Kuroda M, Okado T, Onishi Y;

PI Takesako K, Yagihara T, Yamaguchi H, Yasuda H;

PI WPI: 97-332788/30.

DR N-PSDB: T85880.

PT Antigenic proteins from the fungus Malassezia - bind to IGE

PT antibodies present in patients with Malassezia allergies, useful for

PT diagnosis, treatment and prevention of such conditions

PS Claim 44; Page 91; 162pp; Japanese.

CC The present sequence represents a specifically claimed antigenic

CC protein isolated from the fungus Malassezia. The antigenic protein

CC can bind to IGE antibodies present in patients with allergic

CC conditions. Antigenic proteins, peptides and nucleic acids from the

CC fungus Malassezia can be used in the diagnosis, treatment and

CC prevention of allergic conditions due to Malassezia organisms (such

CC as M. furfur, M. sympodialis and M. pachydermatis).

SO Sequence 102 AA:

Query Match 1.4%; Score 6; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.94e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 DSFRHY 45

OY 344 DSFRHY 349

RESULT 40

ID W20533 standard; Protein; 110 AA.

AC W20533;
 DT 15-JUN-1997 (first entry)
 DE H. pylori cytoplasmic protein 495312.aa.
 KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;
 KM binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
 OS duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
 SM Helicobacter pylori.
 FH Key Location/Qualifiers
 FT misc_difference 102
 FT /note- "encoded by ASC"
 PN M09640893-A1.
 PD 19-DEC-1996
 PE 06-JUN-1996; u09122.
 PR 07-JUN-1995; US-487032.
 PR 01-APR-1996; US-630405.
 PA (ASTR) ASTRA AB
 PI Berglundh OF, Smith D, Mellgaard BL;
 DR WPI: 97-052306/05
 DR N-PSDB: T67686.
 PT Helicobacter pylori nucleic acid sequences and related
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
 PT infection, and to detect Helicobacter
 PS Claim 61; Page 690; 1481pp; English.
 CC This sequence is a H. pylori cytoplasmic protein involved in
 CC outer membrane or cell wall biosynthesis.
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds,
 CC useful as potential H. pylori life cycle activators or inhibitors.
 CC The genomic sequence of H. pylori (ATCC 55679) was determined from
 CC overlapping contigs generated by mechanically shearing the bacterial
 CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
 CC and the predicted coding regions defined by computer evaluation. To
 CC identify likely H. pylori antigens for vaccine development, the amino
 CC acid sequences predicted from various ORF were analysed for significant
 CC homology to other known or exported membrane proteins. Having identified
 CC and determined the sequences of interest, particular regions can be
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide
 CC production, e.g. in E. coli hosts.
 CC Sequence 110 AA;
 SQ

Query Match 1.4%; Score 6; DB 1; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 IIDNF 103
 111111
 40 IIDNF 45

RESULT 41
 ID M06050 standard; Protein; 112 AA.
 AC M06050;
 DT 12-OCT-1998 (first entry)
 DE Human C-C chemokine DGMCC.
 KM DGMCC; DNA; groin wound expressed CC chemokine; cytokine; human;
 KW immune system; cancer; cell proliferation; therapy; diagnosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1; 24
 FT /label- Sig-peptide
 FT Protein 25; 112
 FT /label- Mat.protein
 FT /note- "Claim 2"
 PN M09823750-A2.
 PD 04-JUN-1998.
 PE 26-NOV-1997; U21092.
 PR 05-DEC-1996; US-761071.
 PR 27-NOV-1996; US-031805.
 PA (SCHE) SCHERING CORP.
 PI Hedrick JA, Morales J, Vilearl A, Zlotnik A;
 DR WPI: 98-322730/28.
 DR N-PSDB: V38294.
 DT DVC-1 and DGMCC chemokines - useful for developing products for

PT treating abnormal physiology or development, e.g. cancerous or
 PT degenerative conditions
 PS Claim 2; Page 62; 71pp; English.
 CC This polypeptide comprises mature human DNAX groin wound expressed
 CC CC chemokine (DGMCC), the nature portion of which is claimed. The
 CC DGMCC amino acid sequence was deduced from a cDNA clone (see V38294).
 CC Also claimed is novel human DNAX VIC-1 (DVA-1) (see W60649) mature
 CC polypeptide, as well as expression vectors and host cells. DGMCC
 CC and DVC-1 play a role in the regulation or development of neuronal
 CC or haematopoietic cells, e.g. lymphoid cells, which affect
 CC immunological responses. They can be used in the treatment of
 CC conditions associated with abnormal physiology or development,
 CC including abnormal proliferation, e.g. cancerous conditions or
 CC degenerative conditions. Abnormal proliferation, regeneration,
 CC degeneration, and atrophy may be modulated by appropriate
 CC therapeutic treatment using products of the invention. The products
 CC can also be used for detection, diagnosis and drug screening.
 CC Sequence 112 AA;
 SQ

Query Match 1.4%; Score 6; DB 1; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 AFLPP 29
 111111
 330 AFLPP 335

RESULT 42
 ID R38777 standard; peptide; 114 AA.
 AC R38777;
 DT 22-DEC-1993 (first entry)
 DE Active site peptide fragment #16.
 KM Active site; active region; prediction; secondary structure;
 KW energy value; engineering.
 OS Synthetic.
 PN J0515899-A.
 PD 22-JUN-1993.
 PE 23-AUG-1991; 212284.
 PR 23-AUG-1991; JP-212284.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 DR WPI: 93-232353/29.
 PT Prediction of the active site in physiologically active
 PT polypeptide - by determ. of sec. structure energy values of
 PT partial regions along prim. sequence of physiologically active
 PT polynucleotide, etc.
 PS Disclosure; Page 24; 43pp; Japanese.
 CC The sequences given in R38762-79 are peptides which were used to
 CC demonstrate the method of the invention. These peptides represent
 CC active sites/regions and the method of the invention may be used to
 CC predict the active site of a polypeptide by determining the energy
 CC values of the secondary structure of various partial regions of the
 CC polypeptide to be tested and the primary sequence as well. At
 CC least one partial region should show a local peak energy value
 CC significantly higher or lower than the average standard energy value.
 CC This method may be used in the elucidation of the mechanism of
 CC action of polypeptides or polynucleotides, and in the engineered
 CC improvement of such sequences.
 CC Sequence 114 AA;
 SQ

Query Match 1.4%; Score 6; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 6 RSDSV 11
 111111
 51 RSDSV 56

RESULT 43
 ID R26960 standard; Protein; 114 AA.
 AC R26960;
 DT 11-FEB-1993 (first entry)

DE Human T lymphocyte receptor V-beta w21 subfamily segment.
 KW TCR, IGR b 02; variable region; immunomodulation;
 KW polymerase chain reaction; T cell receptor.
 OS Homo sapiens.
 PN MO9213950-A.
 PD 20-AUG-1992.
 PF 12-FEB-1992; F00130.
 PR 12-FEB-1991; FR-001613.
 PR 12-APR-1991; FR-004523.
 PA (ROOS) ROOSSEL-UCIAF.
 PI Ferradini L, Herceud T, Roman-Roman S, Tritel F;
 DR MPI: 92-300036/36.
 DR N-PSDB: Q28173.
 PT Variable regions of b-chain of T-lymphocyte receptors and their
 PT DNA - useful as immuno:modulant(s) and for diagnosing immune
 PT disorders.
 PS Claim 7; Page 37; 75pp; French.
 CC RNA was isolated from peripheral lymphocytes and converted to cDNA
 CC using a C-beta-specific primer. The cDNA was amplified by anchored
 CC PCR using C-beta and polyc primers, then amplified again using a
 CC different C-beta specific primer. The amplified product was SacI-
 CC restricted, inserted into Bluescript SK+ vector and used to transform
 CC E. coli XL-1-blue. Transforms were screened with a C-beta specific
 CC probe and DNA from positive clones was sequenced in the C-beta
 CC region. The sequence designated "IGR b 02" has ca. 85% homology
 CC with the sequence H5TCRB23 (see Wilson R.K. et al., Immunogenetics
 CC 32:406, 1990) and is a member of the Vbeta w21 subfamily. The
 CC peptide encoded by it can be used to block T cell epitopes and in
 CC vaccines. See also Q28174-Q28228.
 SQ Sequence 114 AA.

Query Match 1.4%; Score 6; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 30 KIEKK 35
 111111
 383 KIEKK 388

RESULT 44
 ID R25524 standard; Protein: 117 AA.
 AC R25524.
 DT 06-JAN-1993 (first entry)
 DE Tobacco Ring spot Virus functional region.
 KW Functional site; protein modification; active site; TRSV.
 OS Tobacco Ring Spot Virus.
 PN EP-494502-A.
 PD 15-JUL-1992.
 PF 29-NOV-1991; 311129.
 PR 30-NOV-1990; JP-329895.
 PR 15-JUL-1991; JP-173690.
 PA (NITRA) NIPPON MINING CO.
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 PA (TOYJ) TOSOH CORP.
 PI Kidokoro S, Numao N;
 DR MPI: 92-235588/29.
 PT Summing functional sites in polypeptide or polynucleotide - by
 PT comparison with sequences in polypeptide(s) whose functional
 PT sites are known
 PS Example 3; Page 28; 75pp; English.
 CC The method for identifying functional sites in proteins was applied
 CC to an RNA composed of 359 nucleotides from TRSV. It is known that
 CC the catalytically active site exists in the 50 nucleotides between
 CC the thymine residues at positions 175 and 224. The nucleotide
 CC sequence was translated (the "x"s in the sequence are not defined
 CC in the specification). A "discriminant function" was derived from
 CC the amino acid sequences of known active sites in a range of other
 CC polypeptides and then used to locate the putative position of the
 CC TRSV active site.
 SQ Sequence 117 AA;

Query Match 1.4%; Score 6; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 6 RSDSV 11
 111111
 51 RSDSV 56

RESULT 45
 ID Y12709 standard; Protein: 130 AA.
 AC Y12709.
 DT 21-JUN-1999 (first entry)
 DE Human 5' EST secreted protein SEQ ID NO:299.
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; anti-inflammatory; tumour inhibition.
 OS Homo sapiens.
 PN MO9906549-A2.
 PD 11-FEB-1999.
 PF 31-JUL-1998; IB1231.
 PR 01-AUG-1997; US-905279.
 PA (GEST) GENEST.
 PA Ductert A, Dumas M, Line Edwards J, Lacroix B;
 DR MPI: 99-153779/13.
 DR N-PSDB: X51487.
 PT New nuclear acids encoding human secreted proteins - obtained from
 PT cDNA libraries derived from testis, ovary, uterus and spleen tissue
 PS Claim 34; Page 400; 522pp; English.
 CC X51459 to X51691 represent 5' expressed sequence tags (ESTs) for human
 CC secreted proteins, and encode the proteins given in Y12681 to Y12913,
 CC respectively. The proteins given represent the signal peptide and an
 CC N-terminal fragment of a secreted protein. The nucleic acid sequences
 CC can be used for producing secreted human gene products. They can also
 CC be used to develop products for diagnosis and therapy. The proteins
 CC obtained may have cytokine activity, cell proliferation/differentiation
 CC activity, haematopoiesis regulating activity, tissue growth regulating
 CC activity, reproductive hormone regulating activity, chemotactic/
 CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
 CC ligand activity, anti-inflammatory activity, tumour inhibition activity
 CC or other activities. The products can be used in forensic, gene therapy
 CC and chromosome mapping procedures. The sequences can also be used for
 CC obtaining corresponding promoter sequences. The nucleic acids encoding
 CC the signal peptide can be used for directing extracellular secretion of
 CC a polypeptide or the insertion of a polypeptide into a membrane, or
 CC importing a polypeptide into a cell.
 SQ Sequence 130 AA;

Query Match 1.4%; Score 6; DB 1; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 LSDSFH 24
 111111
 342 LSDSFH 347

Search completed: Mon Aug 21 10:30:21 2000
 Job time : 48 secs.

[illegible]

1 ATGATGGTCGTCCCTCTGGGGCGACGACCCT
1 MetMetValValLeuLeuGluValatThrThrLeu

51 CCATGGGCTGTTCGCGACCGAGGTGAAAAATCTAAATCTCCTC 100
 17 YPTOTPVAlLeuSerAlaIAlaIaGlyGlyLysAsnLeuLysSerProG 34
 101 AAAAGTAGAGTCGACATCATAGATGACAACTTATCCGAGGTGGAAC 150
 34 InlySValGIuValAspIleIleAspAspAsnPhelIleuAlaGlyTPAsn 50
 151 AGGAGGATAGTCGTGCGGAATGTGACTTTTTCATTGATTATCAAAA 200
 51 ArgSerAspIuSerValGIyAsnValThrPheSerPheAspTyrGlnly 67
 201 A 201
 67 s 67

seq_name: /cgnl_7/ptodata/1/paa/US088_COMB.pep:US-08-871-572B-9

seq_documentation_block:

Sequence 9, Application US/08871572B

GENERAL INFORMATION:

APPLICANT: Pestka, Sidney

APPLICANT: Kolenko, Serguei

APPLICANT: Soh, Jaemog

APPLICANT: Donnelly, Robert

APPLICANT: Mariano, Thomas

APPLICANT: Cook, Jeffrey

APPLICANT: Emmanuel, Stuart

APPLICANT: Schwartz, Barbara

TITLE OF INVENTION: Accessory Factor for Interferon Gamma

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard R. Muccino

STREET: 758 Springfield Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,572B

FILING DATE: 9-JUNE-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Muccino, Richard R.

REGISTRATION NUMBER: 32,538

REFERENCE/DOCKET NUMBER: UMDI-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 273-4988

TELEFAX: (908) 273-4679

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 224 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-871-572B-9

alignment_block:
 US-09-240-675-1_COPY_27_229 x US-08-871-572B-9
 Align seq 1/1 to: US-08-871-572B-9 from: 1 to: 224

51 CCATGGGCTGTTCGCGACCGAGGTGAAAAATCTAAATCTCCTC 100
 17 YPTOTPVAlLeuSerAlaIAlaIaGlyGlyLysAsnLeuLysSerProG 34
 101 AAAAGTAGAGTCGACATCATAGATGACAACTTATCCGAGGTGGAAC 150
 34 InlySValGIuValAspIleIleAspAspAsnPhelIleuAlaGlyTPAsn 50
 151 AGGAGGATAGTCGTGCGGAATGTGACTTTTTCATTGATTATCAAAA 200
 51 ArgSerAspIuSerValGIyAsnValThrPheSerPheAspTyrGlnly 67
 201 A 201
 67 s 67

seq_name: /cgnl_7/ptodata/1/paa/US07_COMB.pep:US-07-971-834-2

seq_documentation_block:

Sequence 2, Application US/07971834

GENERAL INFORMATION:

APPLICANT: Eid, Pierre

APPLICANT: GRESSER, Ion

APPLICANT: LOTFALLA, Georges

APPLICANT: MEYER, Francois

APPLICANT: MOGENSEN, Knud E.

APPLICANT: TOVEY, Michael

APPLICANT: OZE, Gilles

TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH

TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/971,834

FILING DATE: 17-FEB-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR91/00318

FILING DATE: 17-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: EID-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 436 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-971-834-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-07-971-834-2

Align seg 1/1 to: US-07-971-834-2 from: 1 to: 436

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1 ATATGTCGTCCTCCGCGCCGACACCTAGTCTGCGCCGCGG 50
|||||
1 MetetValValLeuLeuGlyAlaThrThreValLeuValAlaValG 17
|||||
51 CCCATGGGTGTGTCGCGAGCGAGTGGAATAAATCTCTCTC 100
|||||
17 YPOTRIPVAlLeuSerAlaAlaAlaGlyGlyLysAsnLeuYsSerProG 34
|||||
101 AAAAGTAGAGTCGACATCATAGATGACAACCTTATCTGAGTGAAC 150
|||||
34 IntysValGluValAlaSpilletleAspAsnPhelleLeuArgTrpAsn 50
|||||
151 AGGAGCATGAGTCTGCGGAGATGACATTTTCATTGATTAACAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTryGlnly 67
|||||
201 A 201
67 s 67
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seq_name: /cgn1_7/ptodata/1/paa/US092_COMB.pep:US-09-240-675-2

seq_documentation_block:

Sequence 2, Application US/09240675

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVEY, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSER: FOLEY & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/240,675

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17283/117/GDPL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEQ. ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 436 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-240-675-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-09-240-675-2

Align seg 1/1 to: US-09-240-675-2 from: 1 to: 436

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1 ATATGTCGTCCTCCGCGCCGACACCTAGTCTGCGCCGCGG 50
|||||
1 MetetValValLeuLeuGlyAlaThrThreValLeuValAlaValG 17
|||||
51 CCCATGGGTGTGTCGCGAGCGAGTGGAATAAATCTCTCTC 100
|||||
17 YPOTRIPVAlLeuSerAlaAlaAlaGlyGlyLysAsnLeuYsSerProG 34
|||||
101 AAAAGTAGAGTCGACATCATAGATGACAACCTTATCTGAGTGAAC 150
|||||
34 IntysValGluValAlaSpilletleAspAsnPhelleLeuArgTrpAsn 50
|||||
151 AGGAGCATGAGTCTGCGGAGATGACATTTTCATTGATTAACAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTryGlnly 67
|||||
201 A 201
67 s 67
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seq_name: /cgn1_7/ptodata/1/paa/PCTUS_COMB.pep:PCT-US99-12156-3

seq_documentation_block:

Sequence 3, Application PC/TUS9912156

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc. et al.

TITLE OF INVENTION: Interferon Receptor HKAFF92

FILE REFERENCE: PF465PCT

CURRENT APPLICATION NUMBER: PCT/US99/12156

CURRENT FILING DATE: 1999-06-03

EARLIER APPLICATION NUMBER: 60/088,185

EARLIER FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.0

SEQ. ID NO. 3

LENGTH: 557

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US99-12156-3

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x PCT-US99-12156-3

Align seg 1/1 to: PCT-US99-12156-3 from: 1 to: 557

1 ANGATGTCCTCTCGGGCGGACACCTAGTCCTGCGCGTGGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValG 17
51 CCATGGGCTGTTCGGCGCGGAGTGGAAAAATCTAAATCTCC 100
17 yProtpValLeuSerAlaAlaIaGlyGlyAsnLeuLysSerPro 34
101 AAAAAGTAGAGTCGACATCATAGATGACAACTTTATCCTGAGTGG 150
34 InLysValGluValAlaSpIleIleAspAspAsnPhelLeuArgTrpAsn 50
151 AGAGCGATGAGTCGTGCGGAATGTGACTTTTTCATTCGATTATCA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
201 A 201
67 s 67

seq_name: /cgnl_7/ptodata/1/paa/US07_COMB.pep:US-07-971-834-4

seq_documentation_block:

Sequence 4, Application US/07971834
GENERAL INFORMATION:
APPLICANT: EID, Pierre
APPLICANT: GRESSER, Ion
APPLICANT: LUTFALLA, Georges
APPLICANT: MEYER, Francois
APPLICANT: MOGENSEN, Knud E.
APPLICANT: TOVEY, Michael
TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH
TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,834
FILING DATE: 17-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR91/00318
FILING DATE: 17-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: EID-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-971-834-4

alignment_scores: Quality: 340.00

Length: 67

Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-07-971-834-4

Align seg 1/1 to: US-07-971-834-4 from: 1 to: 557

1 ANGATGTCCTCTCGGGCGGACACCTAGTCCTGCGCGTGGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValG 17
51 CCATGGGCTGTTCGGCGCGGAGTGGAAAAATCTAAATCTCC 100
17 yProtpValLeuSerAlaAlaIaGlyGlyAsnLeuLysSerPro 34
101 AAAAAGTAGAGTCGACATCATAGATGACAACTTTATCCTGAGTGG 150
34 InLysValGluValAlaSpIleIleAspAspAsnPhelLeuArgTrpAsn 50
151 AGAGCGATGAGTCGTGCGGAATGTGACTTTTTCATTCGATTATCA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
201 A 201
67 s 67

seq_name: /cgnl_7/ptodata/1/paa/US084A_COMB.pep:US-08-453-090-2

seq_documentation_block:

Sequence 2, Application US/08453090
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: cDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,090
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-090-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-453-090-2

Align seg 1/1 to: US-08-453-090-2 from: 1 to: 557

1 ATGATGTCGTCCTCTGCGCGAGACCTAGTCGTCGCGCGG 50
|||||
1 MetMetValValLeuLeuValAlaThrThrLeuValAlaValAla 17
51 CCCATGGGTGTGTCCGCGAGCCGAGGAGGAAAAATCTAATCTCTC 100
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTCCGACATCATGATGACAACTTATCTCTGAGGTGAGC 150
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGAGCGATGAGTCTGCGGAGATGACTTTTTCATTGATTCATTCACAAA 200
|||||
51 ArgSerAspGluSerValGlyLysValThrPheSerPheAspTyrGlnLys 67
201 A 201
67 s 67

seq_name: /cgnl_7/ptodata/1/paa/US092_COMB.pep:US-09-240-675-4

seq_documentation_block:
Sequence 4, Application US/09240675

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVEY, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/240,675

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:
NAME: SAYE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-675-4

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_229 x US-09-240-675-4

Align seg 1/1 to: US-09-240-675-4 from: 1 to: 557

1 ATGATGTCGTCCTCTGCGCGAGACCTAGTCGTCGCGCGG 50
|||||
1 MetMetValValLeuLeuValAlaThrThrLeuValAlaValAla 17
51 CCCATGGGTGTGTCCGCGAGCCGAGGAGGAAAAATCTAATCTCTC 100
|||||
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGTCCGACATCATGATGACAACTTATCTCTGAGGTGAGC 150
|||||
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGAGCGATGAGTCTGCGGAGATGACTTTTTCATTGATTCATTCACAAA 200
|||||
51 ArgSerAspGluSerValGlyLysValThrPheSerPheAspTyrGlnLys 67
201 A 201
67 s 67

seq_name: /cgnl_7/ptodata/1/paa/PCTUS_COMB.pep:PCT-US00-05988-1672

seq_documentation_block:
Sequence 1672, Application PC/TUS0005988

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruben

TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptid

FILE REFERENCE: P4101PCT

CURRENT APPLICATION NUMBER: PCT/US00/05988

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 60/124,270

EARLIER FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 1672

LENGTH: 575

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (186)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (555)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

PCT-US00-05988-1672

alignment_scores:

Quality: 334.00 Length: 67
Ratio: 4.985 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.507

alignment_block:

US-09-240-675-1_COPY_27_229 x PCT-US00-05988-1672

Align seg 1/1 to: PCT-US00-05988-1672 from: 1 to: 575

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1 ATGATGTCCTCCTCGGCGGAGACCCCTAGTGTCTGCGCCGGG 50
19 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValAla 35
51 CCCATGGGTGTTCGCGACCCGAGGTGAGAAAAATCTAAATCTCTC 100
35 APTPTPValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 52
101 AAAAGTAGGTGCGATCATGATGATGACACTTTTATCTGAGTGAAC 150
52 LnyValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 68
151 AGAGCGATGATGTCGCGGAGATGACTTTTTCATTCGATTATCAAAA 200
69 ArgSerAspLeuSerValGlyAsnValThrPheserPhespyrGlnly 85
201 A 201
85 s 85

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seq_name: /cgnl_7/ptodata/1/paa/US60_COMB.pep:US-60-160-202-2519

seq_documentation_block:

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Sequence 2519, Application US/60160202
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
FILE REFERENCE: CLO000114
CURRENT APPLICATION NUMBER: US/60/160,202
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 4392
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2519
LENGTH: 42
TYPE: PRT
ORGANISM: HUMAN
US-60-160-202-2519

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alignment_scores:

Quality: 222.00 Length: 42
Ratio: 5.286 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-60-160-202-2519

Align seg 1/1 to: US-60-160-202-2519 from: 1 to: 42

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76 GGTGGAAAAATCTAAATCTCTGAAAAAGTAGAGTGCATCATAGA 125
1 GlyGlyLysAsnLeuLysSerProGlnlyValGluValAspIleIleAs 17
126 TGAACATTATCTCTGAGTGAAGAGGAGCATGATGTCGGGGAAG 175
17 PAspAsnPhelIleLeuArgTrpAsnArgSerAspGluSerValGlyAsn 34
176 TGACTTTTCATTCGATTATCAAAA 201

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34 alrPheserPhespyrGlnlys 42

seq_name: /cgnl_7/ptodata/1/paa/US08_COMB.pep:US-08-871-572-13

seq_documentation_block:

Sequence 13, Application US/08871572

GENERAL INFORMATION:

```

APPLICANT: Pestka, Sidney
APPLICANT: Kotenko, Sergei
APPLICANT: Son, Jaemog
APPLICANT: Donnelly, Robert
APPLICANT: Mariano, Thomas
APPLICANT: Cook, Jeffrey
APPLICANT: Emanuel, Stuart
APPLICANT: Schwartz, Barbara
TITLE OF INVENTION: Accessory factor for Interferon Gamma
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Richard R. Muccino
STREET: 758 Springfield Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,572
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/444,134
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD1-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 273-4988
TELEFAX: (908) 273-4679
INFORMATION FOR SEQ. ID NO.: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-871-572-13

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alignment_scores:

Quality: 209.00 Length: 65
Ratio: 3.800 Gaps: 2
Percent Similarity: 84.615 Percent Identity: 69.231

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-871-572-13

Align seg 1/1 to: US-08-871-572-13 from: 1 to: 224

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4 ATGTCCTCCTCCTGCGGCGAGACCTGATGCTGCGCCGCGCC 53
1 MetLeuAlaLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyArg 16
54 ATGGGTGTTCGCGAGCCGAGGTGAGAAAAATCTAAATCTCTCAAA 103
16 gtrValLeuProAlaAlaSerGlyLysAlaAsnLeuLys...ProGln 32

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188 TCGATTATCAAAA 201
|||||
34 heaptrycrlnlys 38

seq_name: /cgnl7/ptodata/1/paa/US088_COMB.pep:US-08-888-140-22

seq_documentation_block:

Sequence 22, Application US/08888140

GENERAL INFORMATION:

APPLICANT: Chuntharapal, Anan

APPLICANT: Kim, Kyung Jin

APPLICANT: Love, Richard B.

APPLICANT: Lu, Ji

TITLE OF INVENTION: Monoclonal Antibodies to Type I Interferon Receptor

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/888,140

FILING DATE: 03-Jul-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/

FILING DATE: 16-Jul-1996

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1039R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 631 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-888-140-22

alignment_scores:

Quality: 199.00 Length: 38

Ratio: 5.237 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-888-140-22 ..

Align seg 1/1 to: US-08-888-140-22 from: 1 to: 631

88 CTAATAATCTCTCAAAAAGTAGAGTCGACATCATGATGACAACTTTAT 137

|||||

1 LeuLysSerProGlnLysValGluValAspIleIleAspAspAsnPhel 17

138 CCGAGGTGGAACAGAGCGATGAGTCTGTCGGAATGTGACTTTTCAT 187

|||||

17 eleuAgytrPaanArgSerAspIuSerValGlyAsnValThrPheserp 34

188 TCGATTATCAAAA 201

|||||

34 heaptrycrlnlys 38

seq_name: /cgnl7/ptodata/1/paa/US090_COMB.pep:US-09-056-461-22

seq_documentation_block:

Sequence 22, Application US/09056461

GENERAL INFORMATION:

APPLICANT: Chuntharapal, Anon

APPLICANT: Kim, Kyung Jin

APPLICANT: Love, Richard B.

APPLICANT: Lu, Ji

TITLE OF INVENTION: Type I Interferon Receptor Antibodies

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,461

FILING DATE: 07-Apr-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/058212

FILING DATE: 16

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1039P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 631 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-056-461-22

alignment_scores:

Quality: 199.00 Length: 38

Ratio: 5.237 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-09-056-461-22 ..

Align seg 1/1 to: US-09-056-461-22 from: 1 to: 631

88 CTAATAATCTCTCAAAAAGTAGAGTCGACATCATGATGACAACTTTAT 137

|||||

1 LeuLysSerProGlnLysValGluValAspIleIleAspAspAsnPhel 17

138 CCGAGGTGGAACAGAGCGATGAGTCTGTCGGAATGTGACTTTTCAT 187

|||||

17 eleuAgytrPaanArgSerAspIuSerValGlyAsnValThrPheserp 34

188 TCGATTATCAAAA 201

|||||

34 heaptrycrlnlys 38

Tue Aug 22 08:32:06 2000

us-09-240-675-1_copy_27_229.n2p.rap

151 AGAGGAGGAGTCTGTCGGGAGTGTGACTTTTCATTGATTATCAAAA 200
34 lnlsvAlgluValaspIlelleaspAspsnphelleuValgrtPasn 50
51 ArgSerAspIuSerValglYasnValthrPheSerPheAspTyrclnly 67

201 A 201
67 s 67

seq_name: /cgn1_7/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-2

seq_documentation_block:

Sequence 2: Application US/08307588
Patent No. 5919453

GENERAL INFORMATION:

APPLICANT: BENOTT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVER, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
RECEPTOR WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

TITLE OF INVENTION: INTERFERON

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: SAKS, Bernard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17283/117/GUPL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 436 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-307-588-2

alignment_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Length: 67

Gaps: 0

Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-307-588-2

Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436

1 ATGATGCTGCTCTGCTGGCGGACGACCTAGTGTCTGCTGCCGTGGG 50

1 MetMeValValleuValleuValatThrThrleuValleuValalValalgl 17

51 CCATGCGGTGTTCGCCGCGCGCGGTGGAAAAATCAAAATCTCCGC 100

34 lnlsvAlgluValaspIlelleaspAspsnphelleuValgrtPasn 50

17 yProtrPalluSerValalalalalYolYlYasnleuLysSerProG 34

101 AAAAGTAGAGGTGACATCATGATGACACACTTATCTCGAGTGGAGAC 150

151 AGAGCGATGAGTCTGTCGGGAGTGTGACTTTTCATTGATTATCAAAA 200

51 ArgSerAspIuSerValglYasnValthrPheSerPheAspTyrclnly 67

201 A 201
67 s 67

seq_name: /cgn1_7/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-12

seq_documentation_block:

Sequence 12: Application US/08328256

Patent No. 5643749

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

APPLICANT: RATOVITSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

PREPARATION AND USE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-328-256-12

alignment_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Length: 67

Gaps: 0

Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-328-256-12

Align seg 1/1 to: US-08-328-256-12 from: 1 to: 496

1 ATGATGCTGCTCTCTGGCGGCGAGCCCTAGTGTCTGCGCGGTGG 50
1 MetetvalleuileuenglYAlathrthreulleuvalAlaValaGl 17
51 CCCATGGGTGTGCCGAGCGCGAGGAGGAAAAATCTAAATCTCTC 100
17 YPOTRPAleuserAlaAlaIaIaGlyLysasnLeuLysSerProg 34
101 AAAAGTAGAGTCGACATCATAGTACCACTTATCTCGAGTGGAAC 150
34 InlyvalGluvalAspIlelleaspaspasnPhelleuArgTrpasn 50
151 AGGAGCATGAGTCTGTGGGAATGTGACTTTTCATTGATTAACAAA 200
51 ArgSeraspGluSerValGlyAsnValThrPheSerPheaspTrpGlnly 67
201 A 201
67 s 67

seq_name: /cgnl_7/ptodata/1/laa/5A.COMB.pep:US-08-328-256-10

seq_documentation_block:

Sequence 10, Application US/08328256
Patent No. 5643749

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

APPLICANT: RANOVITSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NETMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-328-256-10

alignment_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Percent Identity: 100.000

Length: 67

Gaps: 0

Alignment block:

US-09-240-675-1_COPY_27_229 x US-08-328-256-10

Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557

1 ATGATGCTGCTCTCTGGCGGCGAGCCCTAGTGTCTGCGCGGTGG 50
1 MetetvalleuileuenglYAlathrthreulleuvalAlaValaGl 17
51 CCCATGGGTGTGCCGAGCGCGAGGAGGAAAAATCTAAATCTCTC 100
17 YPOTRPAleuserAlaAlaIaIaGlyLysasnLeuLysSerProg 34
101 AAAAGTAGAGTCGACATCATAGTACCACTTATCTCGAGTGGAAC 150
34 InlyvalGluvalAspIlelleaspaspasnPhelleuArgTrpasn 50
151 AGGAGCATGAGTCTGTGGGAATGTGACTTTTCATTGATTAACAAA 200
51 ArgSeraspGluSerValGlyAsnValThrPheSerPheaspTrpGlnly 67
201 A 201
67 s 67

seq_name: /cgnl_7/ptodata/1/laa/5A.COMB.pep:US-08-471-454-2

seq_documentation_block:

Sequence 2, Application US/08471454

Patent No. 5731169

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LOTFALLA, Georges

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-454-2

alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-471-454-2

Align seg 1/1 to: US-08-471-454-2 from: 1 to: 557

1 ARGATGTCCTCTCTGCGCGGCGAGACCTAGTCGTCGCGCGTGGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
51 CCATGCGGTGTGTCGCGAGCCGCGAGTGAATAAATCTAATCTCTC 100
17 yProtrPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
101 AAAAGTAGAGTCGACATCATGATGACACACTTATCTGAGGTGGAAC 150
34 InlyValGluValAlaSplIleIleAspAspAsnHeIleLeuArgTrpAsn 50
151 AGAGGAGTGTCTGTCGGAATGTGACTTTTTCATTGATTATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
201 A 201
67 s 67

seq_name: /cgnl_7/ptodata/1/1aa/5B_COMB.pep:US-08-466-974-2

seq_documentation_block:

Sequence 2, Application US/08466974

Patent No. 5861258

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTERALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,974

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US-07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/33770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-466-974-2

alignment_scores:

Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-240-675-1_COPY_27_229 x US-08-466-974-2

Align seg 1/1 to: US-08-466-974-2 from: 1 to: 557

1 ARGATGTCCTCTCTGCGCGGCGAGACCTAGTCGTCGCGCGTGGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValAl 17
51 CCATGCGGTGTGTCGCGAGCCGCGAGTGAATAAATCTAATCTCTC 100
17 yProtrPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34
101 AAAAGTAGAGTCGACATCATGATGACACACTTATCTGAGGTGGAAC 150
34 InlyValGluValAlaSplIleIleAspAspAsnHeIleLeuArgTrpAsn 50
151 AGAGGAGTGTCTGTCGGAATGTGACTTTTTCATTGATTATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
201 A 201
67 s 67

seq_name: /cgnl_7/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2

seq_documentation_block:

Sequence 2, Application US/08471453

Patent No. 586153

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTERALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-453-2

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-471-453-2 ..

Align seq 1/1 to: US-08-471-453-2 from: 1 to: 557

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1 ATGATGTCGTCCTGCGGCGGCGAGACCTAGTGTGTCGCGCGTGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlaG1 17
51 CCCATGGGTGTGTCGCCGAGCCGAGGTGAAAAAATCTAAATCTCTC 100
|||||
17 yProTyrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
34 LnyLysValGluValAspLeuLeuLeuAspAsnPheLeuArgTyrPsn 50
151 AGGAGCGATGATGCTGCGGGAATGTGACTTTTCATTCGATTATCAAA 200
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51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnL 67
201 A 201
67 s 67
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seq_name: /cgn1_7/ptodata/1/laa/5B.COMB.pep:US-08-307-588-4

seq_documentation_block:
; Sequence 4, Application US/08307588
; Patent No. 5919453
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; TITLE OF INVENTION: INTERFERON

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAYE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4

alignment_scores:
Quality: 340.00 Length: 67
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-307-588-4 ..

Align seq 1/1 to: US-08-307-588-4 from: 1 to: 557

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1 ATGATGTCGTCCTGCGGCGGCGAGACCTAGTGTGTCGCGCGTGG 50
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1 MetMetValValLeuLeuGlyAlaThrThrLeuValAlaValAlaG1 17
51 CCCATGGGTGTGTCGCCGAGCCGAGGTGAAAAAATCTAAATCTCTC 100
|||||
17 yProTyrValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
34 LnyLysValGluValAspLeuLeuLeuAspAsnPheLeuArgTyrPsn 50
151 AGGAGCGATGATGCTGCGGGAATGTGACTTTTCATTCGATTATCAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnL 67
201 A 201
67 s 67
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seq_name: /cgn1_7/ptodata/1/laa/PCTUS.COMB.pep:PCT-US94-14277-3

seq_documentation_block:
; Sequence 3, Application PC/TUS9414277
; GENERAL INFORMATION:
; APPLICANT: Aguet, Michel

TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION/DOCKET NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..543
OTHER INFORMATION: /note="murine ERF amino acid sequence
OTHER INFORMATION: (first 8 amino acids from first exon not
included)"
US-08-469-412A-7
alignment_scores:
Quality: 61.00 Length: 24
Ratio: 3.389 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 45.833
alignment_block:
US-09-240-675-1_COPY_27_229/rev x US-08-469-412A-7
Align seg 1/1 to: US-08-469-412A-7 from: 1 to: 543
seq_name: /cgn1_7/ptodata/1/1aa/5A.COMB.pep:US-08-317-310A-64
seq_documentation_block:
Sequence 64, Application US/08317310A
Patent No. 5856701
GENERAL INFORMATION:
APPLICANT: WHITE, Morris F.
APPLICANT: SUN, Xiao Jian
APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,310A
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION/DOCKET NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 1321 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-317-310A-64
alignment_scores:
Quality: 61.00 Length: 29
Ratio: 2.652 Gaps: 1
Percent Similarity: 79.310 Percent Identity: 51.724
alignment_block:
US-09-240-675-1_COPY_27_229/rev x US-08-317-310A-64
Align seg 1/1 to: US-08-317-310A-64 from: 1 to: 1321
seq_name: /cgn1_7/ptodata/1/1aa/5A.COMB.pep:US-08-323-170B-2
seq_documentation_block:
Sequence 2, Application US/08323170B
Patent No. 5733772
GENERAL INFORMATION:
APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: falciiparum Transmission-Blocking Target Antigen, Pf230
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,170B
FILING DATE: 13-OCT-1994
seq_name: /cgn1_7/ptodata/1/1aa/5A.COMB.pep:US-08-323-170B-2
seq_documentation_block:
Sequence 2, Application US/08323170B
Patent No. 5733772
GENERAL INFORMATION:
APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: falciiparum Transmission-Blocking Target Antigen, Pf230
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,170B
FILING DATE: 13-OCT-1994

CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/010,409
 FILING DATE: 29-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Quine, Jonathan A.
 REGISTRATION NUMBER: 41,261
 REFERENCE/DOCKET NUMBER: 015280-113100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3135 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-323-170B-2

alignment_scores:
 Quality: 59.00 Length: 51
 Ratio: 1.844 Gaps: 3
 Percent Similarity: 62.745 Percent Identity: 37.255

alignment_block:
 US-09-240-675-1_COPY_27_229 x US-08-323-170B-2 ..

Align seg 1/1 to: US-08-323-170B-2 from: 1 to: 3135

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64 TCCTGACCCGAGGTGA.....AAAATCTAAATCTCTCA 101
||||| ||||| ||||| ||||| |||||
787 SerGlyAspIleGlyIleLeuPheProLysAsnIleLysSerThr 803
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
102 AAAAGTAGAGTGCATCATGATGACAACTTATCTGAGTGAGACA 151
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
803 rGysPheGlu..GluMetIleProTyrAsnLysGluIleLysTyrPsnL 819
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
152 GGAGCGATGAGTCTGTGCGGAAAT..GTGACTTTTCATTCATGATCA 198
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
819 yscLusnLysSerLeuGlyAsnLeuValAsnSerValValTyrAsn 835
|||||
199 AAA 201
|||
836 Lys 836

```

seq_name: /cgnl_7/ptodata/1/1aa/5A_COMB.pep:US-08-252-626A-2

seq_documentation_block:

Sequence 2, Application US/08252626A
 Patent No. 5585269
 GENERAL INFORMATION:
 APPLICANT: Baird, Henry S.
 APPLICANT: Graham, Douglas K.
 APPLICANT: Dawson, Thomas L.
 APPLICANT: Mullaney, David L.
 APPLICANT: Snodgrass, Hiram R.
 TITLE OF INVENTION: Isolated DNA Encoding C-MER
 TITLE OF INVENTION: Protooncogene
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenneth D. Sibley
 STREET: P.O. Drawer 34009
 CITY: Charlotte
 STATE: No. 5585269th Carolina
 COUNTRY: USA
 ZIP: 28234
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/252,626A
 FILING DATE: 02-JUN-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Sibley, Kenneth D.
 REGISTRATION NUMBER: 31,665
 REFERENCE/DOCKET NUMBER: 5470-81
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 881-3140
 TELEFAX: (919) 881-3175
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 999 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-252-626A-2

alignment_scores:
 Quality: 58.00 Length: 37
 Ratio: 2.417 Gaps: 1
 Percent Similarity: 64.865 Percent Identity: 35.135

alignment_block:
 US-09-240-675-1_COPY_27_229 x US-08-252-626A-2 ..

Align seg 1/1 to: US-08-252-626A-2 from: 1 to: 999

```

43 GCCGTGGCCCATGGTGTTCGCCGACGCCGAGTGAGAAAAATATAA 92
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
369 AlaValSerProTyrIleLeuAlaSerThrGluGlyAlaProSerVa 385
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
93 ACTCTCTCAAAAGTAGAGTGCATCATGATGAT.....GACAACTTAA 136
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
385 lAlaProLeuAsnValThrValPheLeuAsnGluSerSerAspAsnVal 402
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
137 TCCTGAGGTGG 147
|||||
402 splenLgTrrp 405

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seq_name: /cgnl_7/ptodata/1/1aa/5B_COMB.pep:US-08-505-218-4

seq_documentation_block:

Sequence 4, Application US/08505218

Patent No. 5914447

GENERAL INFORMATION:

APPLICANT: ARAYA, ALEJANDRO

APPLICANT: MOURAS, ARMAND

TITLE OF INVENTION: TRANSGENIC PLANTS INCLUDING A HYBRID

TITLE OF INVENTION: NUCLEIC ACID SEQUENCE, COMPRISING AN UNEDITED

TITLE OF INVENTION: MITOCHONDRIAL GENE FRAGMENT FROM HIGHER PLANTS AND PROCESS

TITLE OF INVENTION: FOR PRODUCING THEM

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER

STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/505,218

FILING DATE: 03-NOV-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: KRAUS, ERIC J

RX MEDLINE: 98288806.
 RA RUBINO D., DRIGGERS P., ARBIT D., KEMP L., MILLER B., COSO O.,
 RA PAGLIAI K., GRAY K., GUTKIND S., SEGARS J.;
 RT "Characterization of Btx, a novel Dbl family member that modulates
 RT estrogen receptor action.";
 RL Oncogene 16:2513-2526(1998).

RP [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RA RUBINO D.M., DRIGGERS P.H., MILLER B., SEGARS J.H.;
 RL SUBMITTED (FEB-1999) to the EMBL/Genbank/DBJ databases;
 DR EMBL: AF126008; AAD21311.1;
 RW Receptor
 SQ SEQUENCE 1429 AA; 161033 MW; 542BDC35 CRC32;

alignment_scores:
 Quality: 75.00 Length: 74
 Ratio: 1.923 Gaps: 5
 Percent Similarity: 52.703 Percent Identity: 41.892

alignment_block:

US-09-240-675-1_COPY_27_229 x 09Y5T6

Align seg 1/1 to: 09Y5T6 from: 1 to: 1429

3 GATGCTGCTCTCTGCGGCGGACGACCTAGTCTGCTGCGCGGCGCC 52
 1230 AAGPLAARGPProserTrp.....ProserAlaArgArgArgCysSe 1243
 53 CATGGTGTGTCGCCGACGCGGCGGAAAAATCTAAATCTCTCA 102
 1243 ranggly.....SeArghTrpArgSerArgSerSerSers 1257
 103 AAGTAGAGTCGACATCATAGTACACT..... 134
 1257 eArArgArgArgAlaHisSerGlnTrpAspGlnArgLeuArgAlaAla 1273
 135TATCTGAGCTGGAACAGGACGATGATCTGCGGATGTGA 178
 1274 GlnLysGlnLeuGlnArgGlnGlnLHis...ValArgArgLysLysL 1289
 179 CTTTTCATTCGATATCAAA 200
 1289 u.....ArgLeuSerGln 1293

seq_name: sp_invertebrate:076514

seq_documentation_block:
 ID 076514 PRELIMINARY; PRT; 365 AA.

AC 076514;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE CEF-1.
 GN CEF-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 CC Rhabditidae; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-N2;
 RA MORITA K., CHOW K.L., UENO N.;
 RT "Body length and Male Tail Ray Pattern Formation of C. elegans are
 RT Regulated by a Member of TGF Family.";
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF074395; AAC26791.1;
 DR HSSP: P18075; IAMP.
 DR PFAM: PF00019; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 SQ SEQUENCE 365 AA; 41781 MW; 54051BEE CRC32;

alignment_scores:
 Quality: 66.00 Length: 54
 Ratio: 1.941 Gaps: 2
 Percent Similarity: 62.963 Percent Identity: 31.481

alignment_block:

US-09-240-675-1_COPY_27_229 x 076514

Align seg 1/1 to: 076514 from: 1 to: 365

27 GACCCAGGCTGCTGCGCGGCGGCGGCGGCGGCGGCGGCGG 76
 228 GlnPArgSerValArgArg.....LysArgSerArgGln 239
 77 GTGGAATAAATCTAAATCTCTCAAAAGTAGAGTGCATCATAGAT 126
 239 nArGArgAsnSerGlnArgLysAsnArgLysLysGlnArgLysHis 255
 127 GACAACTTATCTGAGTGTGAGACGACGATGATGCTGCGGATGT 176
 256AsnArgGlnAlaGlnSerAsnLeuGlnArgArgTrn 267
 177 GACTTTTCAT 188
 268 AspPheTrpVal 271

seq_name: sp_human:Q13507

seq_documentation_block:
 ID Q13507 PRELIMINARY; PRT; 848 AA.

AC Q13507; 000593;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE TRANSPARENT RECEPTOR POTENTIAL RELATED CHANNEL 3 PROTEIN.
 GN TRPC3 OR HTRP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eukaryota; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96234226.
 RA ZHU X., JIANG M., PEYTON M., BOULAY G., HURST R., STEFANI E.,
 RA BIRNBAUMER L.;
 RT "trp, a novel mammalian gene family essential for agonist-activated
 RT capacitative Ca2+ entry.";
 RL Cell 85:661-671(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97358541.
 RA XU X.Z.S., LI H.S., GUCCINO W.B., MONTELL C.;
 RT "Coassembly of TRP and TRPL produces a distinct store-operated
 RT conductance.";
 RL Cell 89:1155-1164(1997).
 DR EMBL: U47050; AAC51653.1;
 DR EMBL: Y13758; CAA74083.1;
 DR PFAM: PF00023; ank; 2.
 DR PRINTS: PRO1097; TRNSRECEPTR.
 SQ SEQUENCE 848 AA; 97354 MW; 78AC2E9D CRC32;

alignment_scores:
 Quality: 63.00 Length: 75
 Ratio: 1.537 Gaps: 3
 Percent Similarity: 54.667 Percent Identity: 33.333

alignment_block:

US-09-240-675-1_COPY_27_229 x Q13507

Align seg 1/1 to: Q13507 from: 1 to: 848

4 ATGTCGCTCTCTGCGGCGGACGACCTAGTCTGCTGCGCGGCGCC 53

 111


```

:::|||||::: |||||
228 GIUPTGSSerValArgArg..... LysArgSerValArg 239
77 GTCGAAAAATCTAAATCTCTCAAAAGTAGAGTCGACATCATAGAT 126
:::|||||::: |||||
239 nfhnglyAaSerGlyArgLysAnArgLysGlyArgLysHSHLS 255
127 GACAACTTATCTGAGCGGACAGAGCATGATCTGCGGATATG 176
256 ..... |||||
177 GACTTTTCAT 188
|||||:::
268 AspPheTyrVal 271
seq_name: sp_rudent:Q60805

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```

seq_documentation_block:
ID 060805 PRELIMINARY; PRT: 994 AA.
AC 060805;
DT 01-NOV-1996 (TRENBLREL 01, Created)
DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
DT 01-NOV-1999 (TRENBLREL 12, Last annotation update)
DE C-MER PROTOONCOGENE PRECURSOR (C-MER TYROSINE KINASE RECEPTOR).
GN MER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE OF 1-315 FROM N.A.
RC STRAIN-B6; TISSUE-SPLEEN;
RX MEDLINE; 95303502.
RA GRAHAM D.K., BOWMAN G.W., DAMSON T.L., STANFORD W.L., EARP H.S.,
RA SNODGRASS H.R.;
RT "Cloning and developmental expression analysis of the murine c-met
RT tyrosine kinase."
RL Oncogene 10:2349-2359(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-B6; TISSUE-SPLEEN;
RA SNODGRASS H.R.;
RL EMBL: U21301; AAA80222.1;
DR HSP; P06213; ITRK.
DR MGD; MGI:96965; Mer.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00047; 1g; 2.
DR PFAM; PF00069; pkinase; 1.
KW signal..
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 994 C-MER TYROSINE KINASE RECEPTOR.
SQ SEQUENCE 994 AA; 110156 MW; 3C2F429D CRC32;

```

```

alignment_scores:
Quality: 60.00 Length: 39
Ratio: 2.222 Gaps: 1
Percent Similarity: 69.231 Percent Identity: 33.333

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```

alignment_block:
US-09-240-675-1_COPY_27_229 x Q60805

```

```

Align seg 1/1 to: Q60805 from: 1 to: 994

```

```

43 GCGCGGCGCCATGGGTGTCGCGAGCGCGAGGGAAGAAATCTAA 92
|||||:::|||||:::|||||
364 AATATATATATATATATATATATATATATATATATATATATAT 380
93 ATCTCTCAAAAGTAGAGCGACATCATAGATGACAACTTATCTCTG 141
|||||:::|||||:::|||||
380 AATATATATATATATATATATATATATATATATATATATATAT 397
142 .....AGTGGACACAG 153

```

```

397 spLleArgTyrThrLys 402

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```

seq_name: sp_human:Q9Y5L9
seq_documentation_block:
ID Q9Y5L9 PRELIMINARY; PRT: 2971 AA.
AC Q9Y5L9;
DT 01-NOV-1999 (TRENBLREL 12, Created)
DT 01-NOV-1999 (TRENBLREL 12, Last sequence update)
DT 01-NOV-1999 (TRENBLREL 12, Last annotation update)
DE TRANSCRIPTIONAL ACTIVATOR SRCAP.
GN SRCAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99278407.
RA JOHNSTON H., KNEER J., CHACKALAPARAMPIL I., YACIOK P., CHIRIVIA J.;
RT "Identification of a novel SNF2/SMI2 protein family member, SRCAP,
RT which interacts with CREB-binding protein."
RL J. Biol. Chem. 274:16370-16376(1999).
DR EMBL; AF143946; AAD39760.1;
SQ SEQUENCE 2971 AA; 315639 MW; 1C7B94CB CRC32;

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alignment_scores:
Quality: 60.00 Length: 25
Ratio: 3.333 Gaps: 0
Percent Similarity: 72.000 Percent Identity: 52.000

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alignment_block:
US-09-240-675-1_COPY_27_229/rev x Q9Y5L9

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Align seg 1/1 to: Q9Y5L9 from: 1 to: 2971

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```

83 TTTCCACCTGCGGTCGCGACACACCCATGGCGCGCAGCAGCAGC 34
|||||:::|||||:::|||||
942 PheProProlAlaAlaAlaThrThrThrSerThrThrAlaThrAla 958
33 TAGGTCGTCGCGCGCCAGAGCAGC 9
|:::|||||
958 rThrThrAlaValProAlaProThr 966

```

```

seq_name: sp_archaea:Q9YEB6

```

```

seq_documentation_block:
ID Q9YEB6 PRELIMINARY; PRT: 108 AA.
AC Q9YEB6;
DT 01-NOV-1999 (TRENBLREL 12, Created)
DT 01-NOV-1999 (TRENBLREL 12, Last sequence update)
DT 01-NOV-1999 (TRENBLREL 12, Last annotation update)
DE 108AA LONG HYPOTHETICAL PROTEIN.
GN APE0658.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Aeropyrum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K1;
RX MEDLINE; 99310339.
RA KAWARABAYASHI Y., HINO Y., HORIKAWA H., YANAZAKI S., HAIKAWA Y.,
RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
RA HOSOMURA A., FUKUDA S., NAGAI Y., NISHIJIMA K., NAKAYAMA H.,
RA TAKAMURA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,
RA YANAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
RA NOMURA N., SAKO Y., KIKUCHI H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999)
DR EMBL; AP000060; BA079630.1;
SQ SEQUENCE 108 AA; 11371 MW; BCB1E741 CRC32;

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alignment_scores: Quality: 59.50 Length: 35
 Ratio: 2.705 Gaps: 1
Percent Similarity: 62.857 Percent Identity: 42.857

alignment_block:
us-09-240-675-1_copy_27_229 x Q9YEB6

Align seg 1/1 to: Q9YEB6 from: 1 to: 108

```
12 CCCTCTGGGCGCGAGACCTAGTCTCGTGGCCGCGCCCATGGCTGT 61
   |||||:::||||       :::||||       :::|||||
13 ProProSerArgProSerPro.....GlnArgGlyProGlnGlyVa 26
   62 TGTCGCGAGCGCGAGGTGGAATAATCTAAATCTCTCAAAAGTAGAG 111
   |       ::: |||       ::: |||       ::: |||||
26 lPheGlyAlaCysArgGlyProGlnProLeuGlnSerArgSerArgG 43
   112 GTCGA 116
   |||||
43 lYArg 44
```

OM of: US-09-240-675-1_COPY_27_229 to: SwissProt_38: * out_format : pfs
 Date: Aug 21, 2000 7:33 PM

About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL-frame+ n2p.model -DEV-xlp
 -O-/gnl_1/USPto_spool/US09240675/runat_21082000_102213_24165/app_query.fasta_1.274
 -DB-SwissProt_38: -OFMT-fastaa -SUFFIX-n2p.rsp -GAPOP-12.000
 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPT-0.000 -LOOEXT-0.000
 -OGAPOP-4.500 -OGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
 -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPO-10.000 -YGAPEXT-0.500
 -DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
 -TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
 -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
 -NOR-ext -MINLEN-0 -MAXLEN-2000000000
 -USER-US09240675_ecgn1_1_26 -NCPD-6 -ICPD-3 -LONGLOG -NO_XLPHY
 -WAIT -THREADS-1

Search information block:

Query: US-09-240-675-1_COPY_27_229
 Query Length: 203
 Database: SwissProt_38: *
 Database sequences: 85661
 Database length: 30989116
 Search time (sec): 41.190000

Sequence	Strid	Orig	Zscore	EScore	Len	Documentation
SwissProt_38:INRL_HUMAN	340.00	742.98	1.6e-34	557	1	P17181 homo sapiens (human).
SwissProt_38:INRL_BOVIN	209.00	449.22	3.6e-18	560	1	O04790 bos taurus (bovine).
SwissProt_38:INRL_SHEEP	204.00	438.01	1.5e-17	560	1	O28589 ovis aries (sheep).
SwissProt_38:INRL_MOUSE	199.00	424.12	8.6e-17	590	1	P33896 mus musculus (mouse).
SwissProt_38:INIL3_HUMAN	65.00	118.23	3.73	1475	1	P49790 homo sapiens (human).
SwissProt_38:CONA_BETA	62.50	132.30	6.43	141	1	O01438 bacteriophage t4. contd
SwissProt_38:PHIC_PSEAE	62.00	127.06	8.39	730	1	P06200 pseudomonas aeruginos
SwissProt_38:CRF4_HUMAN	61.50	113.40	9.12	325	1	O08334 homo sapiens (human).
SwissProt_38:ERE_MOUSE	61.00	117.52	10.96	551	1	P70459 mus musculus (mouse).
SwissProt_38:IRK2_MOUSE	61.00	110.19	11.69	1321	1	P81122 mus musculus (mouse).
SwissProt_38:SF22_CHICK	60.00	122.93	13.64	221	1	P30352 gallus gallus (chicken)
SwissProt_38:CCAA_RABIT	60.00	102.86	16.31	2424	1	P27884 oryzocolagus cuniculu
SwissProt_38:CAPA_HUMAN	59.50	109.31	17.61	982	1	P28594 anabaena sp. (strain
SwissProt_38:SF22_HUMAN	59.00	120.69	18.19	221	1	O01130 homo sapiens (human).
SwissProt_38:HXA_HUMAN	59.00	113.91	19.32	496	1	P31260 homo sapiens (human).
SwissProt_38:IS230_PLAFO	59.00	98.46	22.17	3135	1	O08372 plasmodium falcipar
SwissProt_38:RPOA_STRCO	58.50	115.96	21.69	340	1	P72404 streptomyces coelicol
SwissProt_38:RPOA_STRGT	58.50	115.96	21.69	340	1	O9456 streptomyces graminic
SwissProt_38:FLIL_BACSU	58.00	122.27	23.44	140	1	P23452 bacillus subtilis. fl
SwissProt_38:Y288_METJA	58.00	120.26	23.86	178	1	O57736 methanococcus jannas
SwissProt_38:VG2_SPIR	58.00	114.91	25.03	337	1	P15893 spiroplasma virus sp
SwissProt_38:AT6_WHEAT	57.50	112.65	29.19	386	1	P20599 triticum aestivum (wh
SwissProt_38:TAP_DROME	57.50	112.39	29.26	398	1	O16867 drosophila melanogast
SwissProt_38:AK3_BACSU	57.50	111.29	29.55	454	1	P94417 bacillus subtilis. p
SwissProt_38:PERX_BMCH	57.50	108.93	30.17	602	1	P15922 erythra chrysanthem
SwissProt_38:DNL2_ZYMO	57.50	107.30	30.61	731	1	P28719 zymomonas mobilis. di
SwissProt_38:DEAD_KLEPN	57.50	107.05	35.08	659	1	P33306 klebsiella pneumoniae
SwissProt_38:RPE_BACSU	56.50	115.23	37.28	217	1	O34557 bacillus subtilis. rih
SwissProt_38:VE2_HPV20	56.50	108.29	39.66	497	1	P50766 human papillomavirus v
SwissProt_38:RRL_HPV20	56.50	108.29	39.66	2149	1	P27316 rift valley fever v
SwissProt_38:SF3_HUMAN	56.00	116.46	42.15	164	1	P23152 homo sapiens (human).
SwissProt_38:CTL_RAT	56.00	107.25	45.75	492	1	P1167 ratius norvegicus (rat).
SwissProt_38:SECT_ARCGA	56.00	107.15	45.80	498	1	O52251 mycoplasma gallisept
SwissProt_38:IRR_CAVPO	55.00	99.11	49.19	1300	1	P16617 cavia porcellus (guir
SwissProt_38:ET2_HUMAN	55.00	114.65	48.97	178	1	P20800 homo sapiens (human).
SwissProt_38:AMP_LACIC	55.50	101.60	55.00	845	1	P37897 lactococcus lactis (s
SwissProt_38:IF2_ECOLI	55.50	101.17	55.23	890	1	P02995 escherichia coli. trid
SwissProt_38:IF2_SATY	55.50	101.15	55.23	892	1	O92f31 salmonella typhimurium
SwissProt_38:IF2_KLBOX	55.50	101.11	55.25	896	1	O92f28 klebsiella oxyloca. cl
SwissProt_38:IF2_ENTCL	55.50	101.10	55.25	897	1	O92f25 enterobacter cloacae.

seq name: SwissProt_38:INRL_HUMAN

SwissProt_38:GUNZ_CLOSR	55.50	100.31	55.64	986	1	P23659 clostridium sterco
SwissProt_38:RHSB_ECOLI	55.50	97.22	57.19	1426	1	P16919 escherichia coli.
SwissProt_38:MOV2_TWATO	55.00	110.23	58.23	264	1	P03584 tobaco mosaic vir
SwissProt_38:MOV2_TOMVA	55.00	110.23	58.23	264	1	P29799 tomato mosaic viru
SwissProt_38:POOK_RHIME	55.00	99.97	63.80	898	1	O59754 rhizobium meliloti

seq documentatoin block:

ID INRL_HUMAN STANDARD: PRT: 557 AA.
 AC P17181;
 DT 01-NOV-1990 (rel. 15, Created)
 DT 01-NOV-1990 (rel. 15, Last sequence update)
 DT 15-FEB-2000 (rel. 39, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNARI OR IFNAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90124632.
 RA Uze G., Lutfalla G., Gresser I.;
 RT Genetic transfer of a functional human interferon alpha receptor
 RT into mouse cells: cloning and expression of its cDNA.
 RL Cell 60:225-234(1990).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92129376.
 RA Lutfalla G., Gardiner K., Proudhon D., Vleth E., Uze G.;
 RT The structure of the human interferon alpha/beta receptor gene.*;
 RL J. Biol. Chem. 267:2802-2809(1992).
 RN (3)
 RP PHOSPHORYLATION BY TYK2.
 RX MEDLINE: 95059042.
 RA Colamonici O., Yan H., Domanski P., Handa R., Smalley D.,
 RA Mullerstein J., Witte M., Krishnan K., Krolewski J.;
 RT Direct binding to and tyrosine phosphorylation of the alpha subunit
 RT of the type I interferon receptor by p135tyk2 tyrosine kinase.*;
 RL Mol. Cell. Biol. 14:8133-8142(1994).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
 CC EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
 CC -1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@sib-sib.ch)
 CC -----
 CC EMBL: J03171; AAA52730.1; -
 CC EMBL: X60459; CAA42992.1; -
 CC PIR: A32694; A32694;
 CC PIR: S17112; S17112.
 CC MTM: 107450; -
 CC Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 CC Phosphorylation.
 KW PHOSPHORYLATION.
 FT CHAIN 1 27
 FT SIGNAL 1 27
 FT CHAIN 28 557
 FT DOMAIN 28 436
 FT TRANSMEM 437 457
 FT DOMAIN 458 557
 FT DISULFID 79 87
 FT BY SIMILARITY.


```

CC -1- DOMAIN: CONTAINS X-E-X-F-G-REPEATS.
CC -1- SIMILARITY: THE REPEAT REGION COMPOSED OF PENTAPEPTIDE REPEATS
CC SEPARATED BY SER/THR-RICH DOMAINS IS SIMILAR TO THAT OF YEAST
CC NUP1, NUP1, POM 121 AND MAMMALIAN P2.
CC
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CC
DR EMBL: Z25535; CAA80982.1;
DR MIM: 603948;
DR PFM: PFM0041; zf-RanBP; 4
KW Nuclear Protein; Transport; Repeat; Zinc-finger; DNA-binding.
FT DOMAIN 4 14 GLY-RICH.
FT DOMAIN 4 14 POLY-GLY.
FT ZN_FING 443 447 C4-TYPE.
FT ZN_FING 662 681 C4-TYPE.
FT ZN_FING 726 745 C4-TYPE.
FT ZN_FING 797 816 C4-TYPE.
FT ZN_FING 855 874 C4-TYPE.
SQ SEQUENCE 1475 AA; 153889 MW; 3CB415A6909DF80E CRC64;

Alignment_scores:
Quality: 65.00 Length: 51
Ratio: 2.167 Gaps: 1
Percent Similarity: 58.824 Percent Identity: 39.216

Alignment_block:
US-09-240-675-1_COPY_27_229/rev x N153_HUMAN ..

Align seg 1/1 to: N153_HUMAN from: 1 to: 1475

167 AAGAGCATGATCGCTCCTGTCACCTCAGCATTAAGTCATCATGAT 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1248 ThrSerGlnSerLeuPheSerGlnAspSerLysLeuAlaThrThr 1264
117 GTGCACTCTACTTTTGTGAGAGATTATTGATTTTTCACCTCGCGCTG 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1264 rSerThrGlyThrAlaValThrProPheValPheGlyProGlyAlaSer 1281
67 CGGACACACCC.....CATGGCCCGCCGCGGAGAGAC 36
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1281 erAsnAsnThrThrThrSerGlyPheGlyPheGlyAlaThrThrThrSer 1297

35 ACT 33

1298 Ser 1298

seq_name: SwissProt_38:COMA_BPT4

seq_documentation_block:
ID COMA_BPT4 STANDARD: PRT: 141 AA.
AC 001438;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE COMC-ALPHA PROTEIN.
OS COMC OR GOF.
SC Bacteriophage T4.
CC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
CC T4-like phages.
RN [1]
RX MEDLINE: 93015705.
RA Sanson B., Uzan M.;
RT "Sequence and characterization of the bacteriophage T4 comC alpha
RL j. Bacteriol. 174:6539-6547(1992).
CC -1- FUNCTION: ACTS AS A TRANSCRIPTION ANTI-TERMINATOR.

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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M89919; AAA32485.1; -
 DR PIR; A45731; A45731.
 KW Transcription regulation.
 SQ SEQUENCE 141 AA; 16682 MW; 96C9EFA8C673C479 CRC64;

alignment_scores:
 Quality: 62.50 Length: 50
 Ratio: 2.155 Gaps: 3
 Percent Similarity: 58.000 Percent Identity: 34.000

alignment_block:

US-09-240-675-1_COPY_27_229 x COMA_BPT4

Align seg 1/1 to: COMA_BPT4 from: 1 to: 141

16 CTGGGCGGAGACCTAGTCTGCTGCGGCGGCGGCGGCGGCTTGTTC 65
 ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
 49 LcnglytrpProthrlysllemerThrsrlly...Valleuly 63
 66 CGGAGCGGCGGAGTGGAAAAATCTAAATCTCCCAAAAGTACAGTCG 115
 63 sArgcysAlaglyely.....A 69
 116 ACATCATAGATGACACTTATCTCTGAGTGAGACAGACGATGACTCT 165
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 69 spleleuaspGluasnPhelle.....TrrleuSerThrAsnGluAla 83

seq_name: SwissProt_38:PHLC_PSEAE

seq_documentation_block:

ID PHLC_PSEAE STANDARD; PRT; 730 AA.

AC P06300:

DT 01-JAN-1988 (rel. 06, Created)

DT 01-JAN-1988 (rel. 06, Last sequence update)

DT 01-MAY-1991 (rel. 18, Last annotation update)

DE HEMOLYTIC PHOSPHOLIPASE C PRECURSOR (EC 3.1.4.3) (HEAT LABILE-
 DE HEMOLYSIN) (PHOSPHATIDYLCHOLINE CHOLINEPHOSPHOHIDROLASE).

GN PLCH.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
 OC Pseudomonas.

CC [1]

RP SEQUENCE FROM N.A.

RA MEDLINE; 86250607.

RA Pritchard A.E., Vasil M.L.;

RT "Nucleotide sequence and expression of a phosphate-regulated gene
 RT encoding a secreted hemolysin of Pseudomonas aeruginosa.";

RT J. Bacteriol. 167:291-298(1986).

RL [2]

REVISIONS.

RA Pritchard A.E.;

RT Submitted (Aug-1986) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: HYDROLYSES SPHINGOMELIN IN ADDITION TO
 CC PHOSPHATIDYLCHOLINE.

CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O -> 1,2-
 CC DIACYLGLYCEROL + CHOLINE PHOSPHATE.

CC -1- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.

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 CC
 CC EMBL; M13047; AAA25966.1; -
 DR PIR; A26391; A26391.
 KW Hemolysis; Toxin; Hydrolase; Signal.
 FT SIGNAL 1 38
 FT CHAIN 39 730
 SQ SEQUENCE 730 AA; 82655 MW; F1D3695824445F8F CRC64;

alignment_scores:
 Quality: 62.00 Length: 69
 Ratio: 1.824 Gaps: 4
 Percent Similarity: 49.275 Percent Identity: 26.087

alignment_block:

US-09-240-675-1_COPY_27_229 x PHLC_PSEAE

Align seg 1/1 to: PHLC_PSEAE from: 1 to: 730

37 CTCTGCGCGGAGGCGCCATGGCTGTGTCGCGGCGGCGGAGAAAAA 86
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 404 LeuilealalieserProtrp.....Serlysglygly..... 414
 87 TCTAAATCTCTCCAAAAGTAGAGTCGACATCATGATGACACTTTA 136
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 415LysValserAlaGluValPheaspIsthrserV 426
 137 TCTGAGG..... 144
 426 alleuArgPheleuGluArgArgPheGlyLeuValGluGluAsnIleSer 442
 145 ..TGGAAGAGGAGCGATGATGTCGCGGATGTCGACTTTTCATTCGA 191
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 443 ProtrpArgArgAla.....ValCysGlyAspIsthrserLeuPheAs 457
 192 TTAACAA 198
 457 pPheGln 459

seq_name: SwissProt_38:CRF4_HUMAN

seq_documentation_block:

ID CRF4_HUMAN STANDARD; PRT; 325 AA.

AC 008334:

DT 01-FEB-1995 (rel. 31, Created)

DT 01-FEB-1995 (rel. 31, Last sequence update)

DT 01-OCT-1996 (rel. 34, Last annotation update)

DE CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.

GN CRF4.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

CC [1]

RP SEQUENCE FROM N.A.

RA MEDLINE; 96054036.

RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;

RT "A new member of the cytokine receptor gene family maps on chromosome
 RT 21 at less than 35 kb from IFNAR.";

RT Genomics 16:366-373(1993).

RL [2]

REVISIONS.

RA MEDLINE; 96054036.

RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;

RT "Structure of the human CRF4 gene: comparison with its IFNAR
 RT neighbor.";

RT J. Mol. Evol. 41:338-344(1995).

CC -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

SEQUENCE FROM N.A

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Archosauroida; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
0C Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RX MEDLINE; 92212859.
RA Vellard M., Sureau A., Soret J., Martinerie C., Perbal B.;
RT "A potential splicing factor is encoded by the opposite strand of the
trans-spliced c-myc exon.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2511-2515(1992).
CC -1 FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. IT IS REQUIRED
FOR FORMATION OF THE EARLIEST APP-DEPENDENT SPLICING COMPLEX AND
INTERACTS WITH SPliceosomal COMPONENTS BOUND TO BOTH THE 5' AND 3'
SPICE SITES DURING SPliceosome ASSEMBLY. IT ALSO IS REQUIRED FOR
APP-DEPENDENT INTERACTIONS OF BOTH U1 AND U2 SNRNP5 WITH PRE-
MNA.
CC -1 SUBCELLULAR LOCATION: NUCLEAR.
CC -1 ALTERNATIVE PRODUCTS: DIFFERENT FORMS OF THE PROTEIN MAY BE
PRODUCED BY ALTERNATIVE SPLICING.
CC -1 PPM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE RS
DOMAIN (BY SIMILARITY).
CC -1 SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
CC -1 SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
CC CC
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CC CC
CC EMBL; X62446; CAA44306.1; .
DR PIR; S17327; S17327.
DR PIR; B42701; B42701.
DR HSSP; P19339; ISXL.
DR PFAM; PF00076; Trm; 1.
DR PROSITE; PS00030; RNP_1; 1.
KW Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing;
RW Phosphorylation.
FT DOMAIN 16 21 RNA-BINDING (RNP2) (BY SIMILARITY).
FT DOMAIN 55 62 RNA-BINDING (RNP1) (BY SIMILARITY).
FT DOMAIN 111 116 GLY-RICH (HINGE REGION).
FT DOMAIN 117 221 ARG/SER-RICH (RS DOMAIN).
FT FT
SQ SEQUENCE 221 AA; 25524 MW; 75A4BFF9170F1BF CRC64;

alignment_scores:
Quality: 60.00 Length: 45
Ratio: 2.500 Gaps: 2
Percent Similarity: 53.333 Percent Identity: 40.000

alignment_block:
US-09-240-675-1.COPY-27-229 x SFR2_CHICK .. 1
Align seg 1/1 to: SFR2_CHICK from: 1 to: 221

        6 GGCGCTGCTGCT.....GGGCCGCAGACCTAGTGCTGTGCG 43
          |||||
          93 GtATgPrOpRoAsPserHshLSerArGaRGlyPrOPrOPrOAr 109
            |  ||  |||
            44 CGGTGGCCCATGGGCGTGTGTCGC.....ACCGCAGGTGA 81
              |  ||  |||
              109 gTyRglYseRserGlYtyRclYArGaRgeSerArgserrProArGaRgaRga 126
                :  |||||
                82 AAAAATCTAAATCTCTCAAAAAGTAGAGGTGCA 116
                  :::::||:::|||||
                  126 rGaRgeSerArgserrArgserrArgserrAr 137

seq_name: SwissProt_38:CCMA_RABIT
seq_documentation_block:

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ID      CCAA.RABIT STANDARD;      PART: 2424 AA.
AC      P27884; P27883;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      15-FEB-2000 (Rel. 35, Last annotation update)
DE      VOLTAGE-DEPENDENT P/O-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM
DE      CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL
DE      1) (B1)
GN      CACNL1A OR CACNL1A4 OR CAC4A OR CAC4B OR CACN3.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-BRAIN.
RK      MEDLINE; 91187110.
RA      Mori Y., Friedrich T., Kim M.-S., Mikami A., Nakai J., Ruth P.,
RA      Bosse E., Hofmann F., Blocker V., Furiuchi T., Mikoshiba K.,
RA      Imoto K., Tanabe T., Numa S.;
RT      "Primary structure and functional expression from complementary DNA
RT      of a brain calcium channel."
RL      Nature 350:398-402(1991).
RL      [2]
RP      BETA-SUBUNIT BINDING DOMAIN, AND MUTAGENESIS.
RX      MEDLINE; 94150724.
RA      Pragnell M., de Waard M., Mori Y., Tanabe T., Snutch T.P.,
RA      Campbell K.P.;
RT      "Calcium channel beta-subunit binds to a conserved motif in the I-II
RT      cytoplasmic linker of the alpha 1-subunit."
RL      Nature 368:67-70(1994).
CC      -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC      ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC      IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC      CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC      CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A
CC      GIVES RISE TO P AND/OR O-TYPE CALCIUM CURRENTS. P/O-TYPE CALCIUM
CC      CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND
CC      ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGATOXIN-
CC      IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO
CC      DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-
CC      GVIA).
CC      -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC      COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC      IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC      FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC      SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC      CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC      LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- ALTERNATIVE PRODUCTS: IN THE BRAIN, A SHORT ISOFORM BI-1/1A-1 AND
CC      A LONG ISOFORM BI-2/1A-2 (SHOWN HERE), ARE PRODUCED BY ALTERNATIVE
CC      SPLICING.
CC      -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC. PURKINJE CELLS CONTAIN
CC      PREDOMINANTLY P-TYPE VSCC, THE O-TYPE BEING A PROMINENT CALCIUM
CC      CURRENT IN CEREBELLAR GRANULE CELLS.
CC      -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC      HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC      POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC      PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC      SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EASY THIRD POSITION.
CC      -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC      FAMILY.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC      or send an email to license@isb-sib.ch).
OR      EMBL; X57477; CAA40715.1; -
OR      EMBL; X57689; CAA40872.1; -

```

DR	EMBL: X57476: CAA04714.1: -	
DR	EMBL: X57688: CAA04871.1: -	
DR	PRIM: PF00520: Ion_trans; 4	
DR	PRINTS: PR00167: CACHANNEL.	
DR	PRINTS: PR00170: NACHANNEL.	
KM	Ionic channel: Transmembrane; Ion transport; Voltage-gated channel;	
KM	Calcium channel; Glycoprotein; Repeat: Multigene family;	
KM	Calcium-binding; Phosphorylation; Alternative splicing.	
FT	REPEAT	85
FT	REPEAT	473
FT	REPEAT	717
FT	REPEAT	1240
FT	REPEAT	1523
FT	REPEAT	1560
FT	DOMAIN	1
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FT	DOMAIN	2411
FT	DOMAIN	2416
FT	DOMAIN	383
FT	DOMAIN	400
FT	DOMAIN	415
FT	DOMAIN	318
FT	DOMAIN	318

RT factor SC35.*? **Isolation of a complementary DNA that encodes the mammalian splicing**

RL SCIENCE 556:535-538(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BONE MARROW.
 RX MEDLINE: 92212859.
 RA Vellard M., Sureau A., Soret J., Martinerie C., Perbal B.:
 RT "A potential splicing factor is encoded by the opposite strand of the
 RT trans-spliced c-myp exon".
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2511-2515(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94134745.
 RA Sureau A., Perbal B.:
 RT "Several mRNAs with variable 3' untranslated regions and different
 RT stability encode the human PR264/SC35 splicing factor".
 RL Proc. Natl. Acad. Sci. U.S.A. 91:932-936(1994).
 RN [4]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE: 93101590.
 RA Sureau A., Soret J., Vellard M., Crochet J., Perbal B.:
 RT "The PR264/c-myp connection: expression of a splicing factor
 RT modulated by a nuclear protooncogene".
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11683-11687(1992).
 RN [5]
 RP SEQUENCE OF 67-83.
 RX MEDLINE: 92249775.
 RA Zahler A.M., Lane W.S., Stoik J.A., Roth M.B.:
 RT "SR proteins: a conserved family of pre-mRNA splicing factors".
 RL Genes Dev. 6:837-847(1992).
 RN [6]
 RP PROTEIN INTERACTIONS IN SPLICEOSOME ASSEMBLY.
 RX MEDLINE: 94084782.
 RA Wu J.Y., Maniatis T.:
 RT "Specific interactions between proteins implicated in splice site
 RT selection and regulated alternative splicing".
 RL Cell 75:1061-1070(1993).
 RN [7]
 RP BINDING TO U1-70K.
 RX MEDLINE: 94187841.
 RA Kohitz J.D., Jamison S.F., Will C.L., Zuo P., Lubmann R.,
 RT Garcia-Blanco M.A., Manley J.L.:
 RT "Protein-protein interactions and 5'-splice-site recognition in
 RL mammalian mRNA precursors".
 RL Nature 368:119-124(1994).
 RN [8]
 RP RNA BINDING SPECIFICITY.
 RX MEDLINE: 95354672.
 RA Tacke R., Manley J.L.:
 RT "The human splicing factors ASF/SF2 and SC35 possess distinct,
 RT functionally significant RNA binding specificities".
 RL EMBO J. 14:3540-3551(1995).
 RN [9]
 RP SPECIFICITY FOR BETA-GLOBIN MRNA.
 RX MEDLINE: 93368668.
 RA Fu X.-D.:
 RT "Specific commitment of different pre-mRNAs to splicing by single SR
 RT proteins".
 RL Nature 365:82-85(1993).
 CC -1- FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. IT IS REQUIRED
 CC FOR FORMATION OF THE EARLIEST ATP-DEPENDENT SPLICING COMPLEX AND
 CC INTERACTS WITH SPLICOSOMAL COMPONENTS BOUND TO BOTH THE 5' AND 3'
 CC SPLICE SITES DURING SPLICEOSOME ASSEMBLY. IT ALSO IS REQUIRED FOR
 CC ATP-DEPENDENT INTERACTIONS OF BOTH U1 AND U2 SNRNPs WITH PRE-
 CC MRNA. INTERACTS WITH OTHER SPLICOSOMAL COMPONENTS, VIA THE RS
 CC DOMAINS, TO FORM A BRIDGE BETWEEN THE 5' AND 3' SPLICE SITE
 CC BINDING COMPONENTS, U1 SNRP AND U2AF. IN VITRO, BINDS SF2/ASF,
 CC U1-70K AND THE 35 KDA BUT NOT THE 65 KDA SUBUNIT OF U2AF. BINDS TO
 CC PURINE-RICH RNA SEQUENCES, EITHER 5'-AGSAGAGTA-3' (S-C OR G) OR
 CC 5'-GTTCAGTA-3'. CAN BIND TO BETA-GLOBIN MRNA AND COMMIT IT TO THE
 CC SPLICING PATHWAY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: DIFFERENT FORMS OF THE PROTEIN MAY BE
 CC PRODUCED BY ALTERNATIVE SPLICING.

CC	-1	PM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE RS
CC		DOMAIN.
CC	-1	SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
CC	-1	SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
CC		-----
CC		THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (see http://www.isb-sib.ch/announce/sib-sib.ch).
CC		or send an email to license@sib-sib.ch .
CC		-----
DR	EMBL	M90104; AAA60306.1; -
DR	EMBL	X62447; CAA44307.1; -
DR	EMBL	X75755; CAA5383.1; -
DR	EMBL	L03693; AAA60162.1; -
DR	PIR	S17328; S17328.
DR	PIR	A42634; A42634.
DR	HSSP	P19339; ISXL.
DR	MIM	600813; -
DR	PFAM	PF00076; rrm; 1.
DR	PROSITE	PS00030; RNP_1; 1.
KW	Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing;	
KW	Phosphorylation.	
FT	DOMAIN	16 21 RNA-BINDING (RNP2) (BY SIMILARITY).
FT	DOMAIN	55 62 RNA-BINDING (RNP1) (BY SIMILARITY).
FT	DOMAIN	111 116 GLY-RICH (HINGE REGION).
FT	DOMAIN	117 221 ARG/SER-RICH (RS DOMAIN).
FT	CONFLICT	38 R -> G (IN REF. 2 AND 3).
SO	SEQUENCE	221 AA; 25575 MW; 921B/6BDB65701F5 CAC64;

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alignment_scores:
  Quality: 59.00      Length: 54
  Ratio: 2.185      Gaps: 2
  Percent Similarity: 50.000      Percent Identity: 35.185

alignment block:
US-09-240-675-1_COPY-27_229 x SFR2_HUMAN ..

Align seg 1/1 to: SFR2_HUMAN from: 1 to: 221

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6  GGTGTCCTCTCT .....GGGGCCGACGACCCCTAGTGGCTGCGCG 43
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93 G|YATgProtpApsSerHshISerAtgAg|g|YpProtpApsArg 105
   |||||
44 C.....CGTGGCCCAAGGGGTTC 63
   |
109 gTgYg|g|g|g|g|g|g|g|YATgArGserSerArgSerProHArgAtgAga 122
   |||||
64 TCCGCACCGCGCAGGTGGAAAAATCTAAATCTCCTCAAAAAAGTAGAGCT 113
   |||||
126 rGATgSerArGserArGserArGserArGserArGserArGserArGser 147
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114 CGACnCATATGA 125
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143 ArGyYserArg 146

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seq_documentation_block:
ID      HXAA_HUMAN      STANDARD:      PRT:      496 AA.
AC      P31260; Q15949;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      15-FEB-2000 (Rel. 39, Last annotation update)
DE      HMOEBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).
GN      HOXA10 OR HOX1H.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NN      [1]
```

RP SEQUENCE FROM N.A.
RX MEDLINE: 91288229.
RA Lowney P., Corral J.C., Detmer K., Lebeau M.M., Deaven L.,
RA Lawrence H.J., Largman C.;
RT "A human Hox 1, homeobox gene exhibits myeloid-specific expression of
RT alternative transcripts in human hematopoietic cells.";
RL Nucleic Acids Res. 19:3443-3449(1991).
RN [2]
RP SEQUENCE OF 404-486 FROM N.A.
RX MEDLINE: 90046832.
RA Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K.,
RA Hausen C.A., Simanitch T.A., Hack F.M., Lawrence H.J.;
RT " lineage-restricted expression of homeobox-containing genes in human
RT hematopoietic cell lines.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
RN [3]
RP SEQUENCE OF 422-487 FROM N.A.
RX MEDLINE: 90098876.
RA Acampora D., D'Esposito M., Patel A., Pannese M., Migliaccio E.,
RA Morell F., Stornaiolo A., Nigro V., Simeone A., Boncinelli E.;
RT "The human Hox gene family.";
RL Nucleic Acids Res. 17:10385-10402(1989).
RN [4]
RP SEQUENCE OF 435-473 FROM N.A.
RX MEDLINE: 94145486.
RA Castriovo V., Kusaka M., Chariot A., Gielen J., Sobel M.;
RT "Homeobox genes: potential candidates for the transcriptional control
RT of the transformed and invasive phenotype.";
RL Biochem. Pharmacol. 47:137-143(1994).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC BINDS TO THE DNA SEQUENCE 5'-AATATTTTATATAC-3'.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: HOX-A10-1/PL1 (SHOWN HERE) AND
CC HOX-A10-2/PL2. ARE PRODUCED BY ALTERNATIVE SPLICING
CC -1- SIMILARITY: BELONGS TO THE ADB-B FAMILY OF HOMEOBOX PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X58430. -; NOT ANNOTATED_CDS.
DR EMBL: M30599; AAA36006.1. -;
DR EMBL: S69027; AAD14030.1. -;
DR EMBL: S69029; AAD14031.1. -;
DR PIR: S14930; S14930.
DR PIR: S26402; S26402.
DR PIR: A34425; A34425.
DR HSSP: P02833; ISAN.
DR TRANSFAC: T01713. -;
DR MIM: 142957. -;
DR PFAM: PF00046; homeobox. 1.
DR PRINTS: PR00024; HOMEOBOX.
DR PROSITE: PS00027; HOMEOBOX_1. 1.
DR PROSITE: PS00071; HOMEOBOX_2. 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW transcription regulation; Alternative splicing.
FT DOMAIN 181 192 POLY-GLY.
FT DOMAIN 219 223 POLY-PRO.
FT DOMAIN 227 236 POLY-PRO.
FT DOMAIN 366 371 POLY-ALA.
FT DNA_BIND 422 481 HOMEOBOX.
FT VAAPPLIC 1 402 MISSING (IN ISOFORM HOX-A10-2).
FT VAAPPLIC 403 405 DSL -> MCQ (IN ISOFORM HOX-A10-2).
FT CONFLICT 435 435 L -> S (IN REF. 2).
FT CONFLICT 437 437 L -> F (IN REF. 2).
FT CONFLICT 473 473 R -> P (IN REF. 2).
SQ SEQUENCE 496 AA; 5473 MW; 77C6F675916552F0 CRC64;

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alignment_scores:
    Quality: 59.00
    Ratio: 3.105
    Percent Similarity: 79.167
    Percent Identity: 58.333

alignment_block:
US-09-240-675-1_COPY_27_229 x HXAA_HUMAN ..

Align seg 1/1 to: HXAA_HUMAN from: 1 to: 496

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350 ProGlyAArgserGluProSerIleArgAArgTrpProAArgTrp..LeuA 366
65 CCGGACCGCAGGCGAATA 84
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366 IaAlaAlaAlaGlyAlaArg 372

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Tue Aug 22 08:32:08 2000

us-09-240-675-1_copy_27_229.n2p.rsp

Sequence	Strid	Ord	ZScore	Escore	len	Documentation
P1R2.A13694	+	340.00	766.91	1.1e-35	557	interferon alpha/beta receptor
P1R2.S27387	+	209.00	466.35	1.0e-18	560	interferon alpha receptor type
P1R2.A42883	+	198.00	438.39	2.7e-17	590	interferon alpha/beta receptor
P1R2.T09357	+	71.00	148.74	0.7230	304	hypothetical protein F23K16.40
P1R2.JC5807	+	71.00	140.39	0.7742	828	trypsin protein - rat
P1R2.T76391	+	68.50	146.67	1.48	194	hypothetical protein Y105CB.0
P1R2.J00405	-	66.00	128.69	2.60	1106	hypothetical 119.5K protein (H
P1R2.TY4286	-	66.00	135.60	3.25	365	cat-1 protein - Caenorhabditis
P1R2.S54718	-	65.00	121.64	4.82	1475	nuclear pore complex protein
P1R2.T08930	+	63.00	124.90	8.19	571	hypothetical protein Y15N24.90
P1R2.A54731	+	62.50	125.38	8.64	541	comc-alpha protein - phase T4
P1R2.I54418	+	62.50	127.55	9.22	361	MHC class I histocompatibility
P1R2.A82691	+	62.00	120.55	11.23	730	phospholipase C (EC 3.1.4.3) -
P1R2.G01418	+	61.50	127.56	12.18	273	cytokine receptor family II, ma
P1R2.A47003	+	61.50	126.10	12.33	325	cytokine receptor family class
P1R2.T25677	+	60.00	123.40	16.66	340	hypothetical protein F0B2D1.9
P1R2.B47701	-	60.00	125.83	18.78	221	PR264 protein - chicken
P1R2.T02955	-	60.00	124.16	19.04	270	probable cytochrome P450 monoo
P1R2.T29518	-	60.00	121.34	19.49	379	hypothetical protein T25F10.2
P1R2.A14276	+	60.00	113.31	20.81	994	c-met tyrosine kinase receptor
P1R2.T45743	+	60.00	111.42	21.14	1247	hypothetical protein F24M12.18
P1R2.I16480	+	60.00	105.88	22.12	2424	calcium channel Bi-2 - rabbit
P1R2.I16479	+	60.00	105.88	22.12	2424	calcium channel Bi-2 - rabbit
P1R2.E75653	+	59.50	130.63	20.76	108	hypothetical protein APO658.8
P1R2.S11143	+	59.50	121.08	22.45	340	class I histocompatibility anti
P1R1.A48831	-	59.50	112.24	24.14	982	phosphoenolpyruvate carboxylase
P1R2.A42701	+	59.00	123.51	25.30	221	PR264/SC35 protein - human
P1R2.A42634	+	59.00	123.51	25.30	221	PR264/SC35 protein - human
P1R2.S24169	-	59.00	121.19	25.79	292	splicing factor SC35 - human
P1R2.J01733	+	59.00	117.68	26.54	445	self-incompatibility locus glyco
P1R2.S42881	+	59.00	116.77	26.74	445	S-locus glycoprotein type II pr
P1R2.S26402	+	59.00	116.77	26.74	496	homeotic protein Hox A10 - huma
P1R2.T25131	+	59.00	116.27	26.85	527	hypothetical protein T22H2.2 -
P1R2.D81125	+	59.00	101.41	27.62	796	DNA gyrase chain B NMB0212 (imp
P1R2.A48584	+	59.00	101.41	30.33	3135	transmission blocking target a
P1R2.T35558	-	58.50	118.76	30.25	340	DNA-directed RNA polymerase al
P1R2.A38845	-	58.00	124.96	33.04	140	flagellar protein required for
P1R2.A64336	+	58.00	122.98	33.59	178	hypothetical protein M02088 - M
P1R2.S08459	-	58.00	117.67	35.09	337	hypothetical protein 2 - spiro
P1R2.T14516	+	58.00	114.48	36.02	494	S-locus-specific glycoprotein 5

seq_documentation_block

Interferon alpha receptor type 1 precursor - bovine

C:Species: Bos primigenius taurus (cattle)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S27387; S33770
 R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
 FEBS Lett. 313, 255-259, 1992
 A:Title: Specific antiviral activities of the human alpha interferons are determined at
 A:Reference number: S27387; MIMD:93076908
 A:Accession: S27387
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-560 <MOU>
 A:Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; PID:g432
 A:Experimental source: MDK cells
 R:Lim, J.K.; Langer, J.A.
 Blochim. Biophys. Acta 1173, 314-319, 1993
 A:Title: Cloning and characterization of a bovine alpha interferon receptor.
 A:Reference number: S33770; MIMD:93305725
 A:Accession: S33770
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-421, 'V', 423-560 <LIM>
 A:Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
 A:Experimental source: Lung
 C:Keywords: antiviral; cytokine receptor; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

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Quality:	209.00	Length:	65
Ratio:	3.800	Gaps:	2
Percent Similarity:	84.615	Percent Identity:	69.231

alignment_block:

US-09-240-675-1_COPY_27_229 x S27387

Align seg 1/1 to: S27387 from: 1 to: 560

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1 MetLeuAlaValValGlyAlaIleThrIleuMetLeuValAla...GlyAr 16
54 ATGGGTGTGTCGCGAGCCGAGGTGAGAAAAATCTAAATCTCTCAAA 103
  |||.....|.....|.....|.....|.....|.....|
16 GTrValLeuProAlaIleSerGlyAlaIleAsnLeuYs...ProGluA 32
104 AAGGATGAGTGTGCGGAGATGATGACAACTTATCCCTAGGTGAGACAG 153
  |||.....|.....|.....|.....|.....|.....|
32 snValGluIleHisIleIleAspAspAspAspAspAspAspAspAsp 48
154 AGCGATGAGTGTGCGGAGATGATGACAACTTATCCCTAGGTATCAAA 198
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49 SerSerGluSerValIleValAsnValIleThrPheSerAlaAspTyrGln 63

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seq_name: p1r2:A45283

seq_documentation_block:

Interferon alpha/beta receptor - mouse

C:Species: Mus musculus (house mouse)
 C>Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
 R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proud'homme, D.; Mogensen, K.E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
 A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homospo
 A:Reference number: A45283; MIMD:92262522
 A:Accession: A45283
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-590 <UZE>
 A:Cross-references: GB:M89641; NID:g194111; PIDN:AAA7890.1; PID:g194112
 A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIP:102357)
 R:Lutfalla, G.; Uze, G.

Gene 148, 343-346, 1994

A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: h1c
 A:Reference number: I48423; MIMD:95047447
 A:Accession: I48423
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 118-125 <RES>
 A:Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA5003.1; PID:g755810
 A:Accession: I48424
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 127-224 <RE2>
 A:Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
 A:Accession: I48425
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 243-264 <RE3>
 A:Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA5004.1; PID:g510261
 A:Accession: I48426
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 265-375 <RE4>
 A:Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA5005.1; PID:g510262
 A:Accession: I48427
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 397-424 <RE5>
 A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA5006.1; PID:g55812
 A:Accession: I48428
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 426-445 <RE6>
 A:Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA5007.1; PID:g55813
 A:Accession: I48429
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 473-590 <RE7>
 A:Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA5008.1; PID:g510265
 C:Genetics:
 A:Gene: IFNAR
 A:Introns: 177/3; 331/1
 C:Keywords: cytokine receptor; transmembrane protein

alignment_scores:

Quality:	198.00	Length:	65
Ratio: <td>3.536 <td>Gaps: <td>0 </td></td></td>	3.536 <td>Gaps: <td>0 </td></td>	Gaps: <td>0 </td>	0
Percent Similarity: <td>86.154 <td>Percent Identity: <td>55.385</td> </td></td>	86.154 <td>Percent Identity: <td>55.385</td> </td>	Percent Identity: <td>55.385</td>	55.385

alignment_block:

US-09-240-675-1_COPY_27_229 x A45283

Align seg 1/1 to: A45283 from: 1 to: 590

```

4 ATGGTCGCTCTGCGGCGGCGAGCCCTAGTGTCTGCGCGGCGGCC 53
  |||.....|.....|.....|.....|.....|.....|
1 MetLeuAlaValValGlyAlaIleThrIleuMetLeuValAlaIleGlyAlaPr 17
54 ATGGGTGTGTCGCGAGCCGAGGTGAGAAAAATCTAAATCTCTCAAA 103
  |||.....|.....|.....|.....|.....|.....|
17 GTrValLeuProSerAlaIleGlyGlyAlaIleAsnLeuYsProGluA 34
104 AAGGATGAGTGTGCGGAGATGATGACAACTTATCCCTAGGTGAGACAG 153
  |||.....|.....|.....|.....|.....|.....|
34 snIleAspValIleIleIleAspAspAspAspAspAspAspAspAsp 50
154 AGCGATGAGTGTGCGGAGATGATGACAACTTATCCCTAGGTATCAAA 198
  |||.....|.....|.....|.....|.....|.....|
51 HisGlyGluSerMetGlySerValIleThrPheSerAlaGluTyrGln 65

```

seq_name: p1r2:A09357

seq_documentation_block:

A:Cross-references: GB:M13047; NID:g151492; PIDN:AAA25966.1; PID:g151493
C:Keywords: phosphoric diester hydrolase

alignment_scores:
Quality: 62.00 Length: 69
Ratio: 1.824 Gaps: 4
Percent Similarity: 49.275 Percent Identity: 26.087

alignment_block:
US-09-240-675-1_COPY_27_229 x A26391 ..

Align seg 1/1 to: A26391 from: 1 to: 730

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37 CTGCTGCGCGTGGCCGATGGCTGTTCCGCGCAGCGTGAAGAAA 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
404 Leu11Ala11IleSerProTyr.....SerLysGlyGly..... 414
87 TCTAAATATCTCCCAAAAGTAGAGTCGACATCATAGATGACACTT 136
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
415 .....LysValSerAlaGluValPheAspHisThrSerV 426
137 TCCTGAGG..... 144
426 alleuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer 442
145 ...TGCACACGAGCGCATGAGTCTGCGGGAATGACATTTTCATTGA 191
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
443 ProTyrArgArgGala.....ValCysGlyAspLeuThrSerLeuPheAs 457
192 TTTATCAA 198
457 PheGln 459

```

seq_name: p1r2:G01418

seq_documentation_block:

Cytokine receptor family II, member 4 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C:Accession: G01418
R:Luftalla, G.
Submitted to the EMBL Data Library, April 1994
A:Reference number: G06935
A:Accession: G01418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <LUT>
A:Cross-references: EMBL:U08988; NID:g571295; PID:g571296
C:Genetics:
A:Gene: GDB:CRFB4; CRF2-4
A:Cross-references: GDB:138168; OMIM:123889
A:Map position: 21q22.1-21q22.2
A:Introns: 17/1; 58/2; 111/1; 166/3; 216/1

alignment_scores:
Quality: 61.50 Length: 54
Ratio: 1.922 Gaps: 1
Percent Similarity: 59.259 Percent Identity: 29.630

alignment_block:
US-09-240-675-1_COPY_27_229 x G01418

Align seg 1/1 to: G01418 from: 1 to: 273

```

55 TGGGCTGTGTCGCGAGCCGAGTGAATAATCTAAATCT..... 96
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
3 tripSerLeuGlySerTrpLeuGlyCysLeuLeuValSerAlaLeuG1 19
97 .....CCTCAAAAAGTAGAGCTGCACATCATAGATGACAACT 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
19 yMetValProProGluAsnValArgMetAsnSerValAsnPheIysA 36

```

```

134 TTTATCTGAGTGGACACAGACGATGACTCTGCGGAATGTGACTTT 183
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
184 TCATTGATTAAT 195
53 ThrAlaGlnTyr 56

```

seq_name: p1r2:A47003

seq_documentation_block:

Cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
C:Accession: A47003
R:Luftalla, G.; Gardiner, R.; Uze, G.
Genomics 16, 366-373, 1993
A:Title: A new member of the cytokine receptor gene family maps on chromosome 21
A:Reference number: A47003; MUID:93300510
A:Accession: A47003
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-325 <LUT>
A:Cross-references: GB:217227; NID:g393378; PID:g393379
C:Genetics:
A:Map position: 21q
C:Keywords: transmembrane protein

alignment_scores:
Quality: 61.50 Length: 54
Ratio: 1.922 Gaps: 1
Percent Similarity: 59.259 Percent Identity: 29.630

alignment_block:
US-09-240-675-1_COPY_27_229 x A47003

Align seg 1/1 to: A47003 from: 1 to: 325

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55 TGGGCTGTGTCGCGAGCCGAGTGAATAATCTAAATCT..... 96
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
3 tripSerLeuGlySerTrpLeuGlyCysLeuLeuValSerAlaLeuG1 19
97 .....CCTCAAAAAGTAGAGCTGCACATCATAGATGACAACT 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
19 yMetValProProGluAsnValArgMetAsnSerValAsnPheIysA 36
134 TTTATCTGAGTGGACACAGACGATGACTCTGCGGAATGTGACTTT 183
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
184 TCATTGATTAAT 195
53 ThrAlaGlnTyr 56

```

 MIPROTEIN (TM)

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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 10:34:37 2000; MasPar time 9.36 Seconds
 713,960 Million cell updates/sec

Tabular output not generated.

Title: >US-09-240-675-2
 Description: (1-436) from US09240675.pep
 Perfect Score: 436
 Sequence: 1 MMVVLGATTLVLVAVGPMV.....KSYFSDAVCEKTPGNTSK 436

Scoring table: TABLE uniprottable
 Gap 60

Searched: 152433 segs, 15329240 residues

Post-processing: Minimum Match 0%
 Listing first 1000 summaries

Database: a-issued
 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfile1

Statistics: Mean 2.820; Variance 0.722; scale 3.904

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	436	100.0	436	2	US-08-307-Sequence 2, Applicatio	0.00e+00
2	436	100.0	557	1	US-08-471-Sequence 2, Applicatio	0.00e+00
3	436	100.0	557	2	US-08-466-Sequence 2, Applicatio	0.00e+00
4	436	100.0	557	1	US-08-471-Sequence 2, Applicatio	0.00e+00
5	436	100.0	557	2	US-08-328-Sequence 10, Applicati	0.00e+00
6	436	100.0	557	1	US-08-307-Sequence 4, Applicatio	0.00e+00
7	427	97.9	434	1	US-08-328-Sequence 11, Applicati	0.00e+00
8	413	94.7	496	1	US-08-328-Sequence 12, Applicati	0.00e+00
9	413	94.7	17	2	US-08-488-Sequence 243, Applicat	1.24e-12
10	39	3.9	17	4	PCT-US93-0 Sequence 243, Applicat	1.24e-12
11	39	3.9	17	2	US-08-480-Sequence 243, Applicat	1.24e-12
12	39	3.9	17	2	US-08-328-Sequence 9, Applicati	3.39e-11
13	39	3.9	56	1	PCT-US94-1 Sequence 4, Applicatio	2.61e-04
14	39	3.9	200	4	US-08-943-Sequence 4, Applicatio	2.03e+01
15	39	3.9	7	1	US-08-328-Sequence 9, Applicatio	2.03e+01
16	39	3.9	153	1	US-07-695-Sequence 9, Applicatio	2.03e+01
17	39	3.9	153	1	US-07-695-Sequence 9, Applicatio	2.03e+01
18	39	3.9	202	4	PCT-US94-1 Sequence 3, Applicatio	2.03e+01
19	39	3.9	221	2	US-08-943-Sequence 50, Applicati	2.03e+01
20	39	3.9	221	2	US-08-943-Sequence 54, Applicati	2.03e+01
21	39	3.9	221	2	US-08-943-Sequence 58, Applicati	2.03e+01
22	39	3.9	221	2	US-08-943-Sequence 56, Applicati	2.03e+01
23	39	3.9	258	3	US-08-961-Sequence 3, Applicatio	2.03e+01

24	7	1.6	258	2	US-08-602-Sequence 3, Applicatio	2.03e+01
25	7	1.6	327	4	PCT-US94-1 Sequence 8, Applicatio	2.03e+01
26	7	1.6	337	2	US-08-943-Sequence 20, Applicati	2.03e+01
27	7	1.6	553	2	US-08-943-Sequence 40, Applicati	2.03e+01
28	7	1.6	553	2	US-08-943-Sequence 16, Applicati	2.03e+01
29	7	1.6	553	2	US-08-943-Sequence 22, Applicati	2.03e+01
30	7	1.6	553	2	US-08-943-Sequence 42, Applicati	2.03e+01
31	7	1.6	553	2	US-08-943-Sequence 28, Applicati	2.03e+01
32	7	1.6	553	2	US-08-943-Sequence 30, Applicati	2.03e+01
33	7	1.6	553	2	US-08-943-Sequence 48, Applicati	2.03e+01
34	7	1.6	553	2	US-08-943-Sequence 32, Applicati	2.03e+01
35	7	1.6	553	2	US-08-943-Sequence 44, Applicati	2.03e+01
36	7	1.6	553	2	US-08-943-Sequence 2, Applicatio	2.03e+01
37	7	1.6	553	2	US-08-943-Sequence 18, Applicati	2.03e+01
38	7	1.6	553	2	US-08-943-Sequence 36, Applicati	2.03e+01
39	7	1.6	553	2	US-08-943-Sequence 44, Applicati	2.03e+01
40	7	1.6	553	2	US-08-943-Sequence 38, Applicati	2.03e+01
41	7	1.6	553	2	US-08-943-Sequence 26, Applicati	2.03e+01
42	7	1.6	553	2	US-08-943-Sequence 14, Applicati	2.03e+01
43	7	1.6	553	2	US-08-943-Sequence 36, Applicati	2.03e+01
44	7	1.6	553	2	US-08-943-Sequence 24, Applicati	2.03e+01
45	7	1.6	688	2	US-09-016-Sequence 2, Applicatio	2.03e+01
46	7	1.6	2206	1	US-07-852-Sequence 2, Applicatio	2.03e+01
47	7	1.6	2206	2	US-08-461-Sequence 9, Applicatio	2.03e+01
48	6	1.4	12	2	US-08-704-Sequence 3, Applicatio	2.35e+02
49	6	1.4	12	2	US-08-433-Sequence 15, Applicati	2.35e+02
50	6	1.4	12	1	US-08-433-Sequence 15, Applicati	2.35e+02
51	6	1.4	12	1	US-08-174-Sequence 15, Applicati	2.35e+02
52	6	1.4	12	2	US-08-195-Sequence 15, Applicati	2.35e+02
53	6	1.4	12	2	US-08-433-Sequence 15, Applicati	2.35e+02
54	6	1.4	17	1	US-08-149-Sequence 16, Applicati	2.35e+02
55	6	1.4	19	2	US-08-504-Sequence 5, Applicatio	2.35e+02
56	6	1.4	20	1	US-08-440-Sequence 4, Applicatio	2.35e+02
57	6	1.4	21	2	US-08-433-Sequence 11, Applicati	2.35e+02
58	6	1.4	21	2	US-08-433-Sequence 11, Applicati	2.35e+02
59	6	1.4	21	1	US-08-174-Sequence 11, Applicati	2.35e+02
60	6	1.4	21	1	US-08-433-Sequence 11, Applicati	2.35e+02
61	6	1.4	21	2	US-08-195-Sequence 11, Applicati	2.35e+02
62	6	1.4	23	1	US-07-800-Sequence 4, Applicatio	2.35e+02
63	6	1.4	23	4	PCT-US91-0 Sequence 4, Applicatio	2.35e+02
64	6	1.4	33	1	US-08-440-Sequence 54, Applicati	2.35e+02
65	6	1.4	33	2	US-08-433-Sequence 7, Applicatio	2.35e+02
66	6	1.4	34	1	US-08-433-Sequence 7, Applicatio	2.35e+02
67	6	1.4	34	1	US-08-195-Sequence 7, Applicatio	2.35e+02
68	6	1.4	34	2	US-08-433-Sequence 7, Applicatio	2.35e+02
69	6	1.4	34	2	US-08-174-Sequence 7, Applicatio	2.35e+02
70	6	1.4	38	1	US-08-463-Sequence 99, Applicati	2.35e+02
71	6	1.4	38	1	US-08-465-Sequence 99, Applicati	2.35e+02
72	6	1.4	46	2	US-08-248-Sequence 14, Applicati	2.35e+02
73	6	1.4	63	3	US-09-061-Sequence 5, Applicatio	2.35e+02
74	6	1.4	70	1	US-08-482-Sequence 5, Applicatio	2.35e+02
75	6	1.4	70	1	US-08-330-Sequence 5, Applicatio	2.35e+02
76	6	1.4	106	2	US-08-785-Sequence 11, Applicati	2.35e+02
77	6	1.4	132	1	US-07-893-Sequence 5, Applicatio	2.35e+02
78	6	1.4	132	1	PCT-US92-1 Sequence 5, Applicatio	2.35e+02
79	6	1.4	132	2	US-08-675-Sequence 5, Applicatio	2.35e+02
80	6	1.4	148	3	US-08-946-Sequence 60, Applicati	2.35e+02
81	6	1.4	152	2	US-08-606-Sequence 5, Applicatio	2.35e+02
82	6	1.4	152	2	US-08-606-Sequence 4, Applicatio	2.35e+02
83	6	1.4	152	2	US-08-606-Sequence 16, Applicati	2.35e+02
84	6	1.4	152	2	US-08-606-Sequence 30, Applicati	2.35e+02
85	6	1.4	152	2	US-08-606-Sequence 7, Applicatio	2.35e+02
86	6	1.4	152	2	US-08-606-Sequence 3, Applicatio	2.35e+02
87	6	1.4	221	2	US-08-883-Sequence 60, Applicati	2.35e+02
88	6	1.4	222	2	5223425-6 atent, No. 5223425	2.35e+02
89	6	1.4	222	2	US-08-351-Sequence 2, Applicatio	2.35e+02
90	6	1.4	232	2	US-08-897-Sequence 31, Applicati	2.35e+02
91	6	1.4	232	5	5223425-5 atent No. 5223425	2.35e+02
92	6	1.4	246	4	PCT-US93-0 Sequence 8, Applicatio	2.35e+02
93	6	1.4	246	4	US-08-295-Sequence 8, Applicatio	2.35e+02
94	6	1.4	248	2	US-08-102-Sequence 1, Applicatio	2.35e+02
95	6	1.4	248	2	US-08-744-Sequence 1, Applicatio	2.35e+02
96	6	1.4	248	1		

97	1.4	250	5	5223425-4	atent No. 5223425	2.35e+02	170	6	1.4	607	3	US-08-685-	Sequence 6, Applicatio	2.35e+02
98	1.4	253	5	5223425-8	atent No. 5223425	2.35e+02	171	6	1.4	607	1	US-08-409-	Sequence 6, Applicatio	2.35e+02
99	1.4	259	5	5223425-2	atent No. 5223425	2.35e+02	172	6	1.4	608	1	US-08-766-	Sequence 3, Applicatio	2.35e+02
100	1.4	260	5	5223425-10	atent No. 5223425	2.35e+02	173	6	1.4	638	2	US-08-681-	Sequence 3, Applicatio	2.35e+02
101	1.4	269	4	US-08-118-	Sequence 64, Applicati	2.35e+02	174	6	1.4	648	3	US-08-286-	Sequence 4, Applicatio	2.35e+02
102	1.4	269	4	PCR-US93-0	Sequence 64, Applicati	2.35e+02	175	6	1.4	654	1	US-08-083-	Sequence 16, Applicati	2.35e+02
103	1.4	274	4	PCR-US93-0	Sequence 69, Applicati	2.35e+02	176	6	1.4	654	2	US-08-446-	Sequence 35, Applicati	2.35e+02
104	1.4	274	4	US-08-118-	Sequence 69, Applicati	2.35e+02	177	6	1.4	657	2	US-08-508-	Sequence 35, Applicati	2.35e+02
105	1.4	284	1	US-08-118-	Sequence 67, Applicati	2.35e+02	178	6	1.4	664	3	5240838-5	atent No. 5240838	2.35e+02
106	1.4	284	4	PCR-US93-0	Sequence 67, Applicati	2.35e+02	179	6	1.4	670	2	US-08-473-	Sequence 11, Applicati	2.35e+02
107	1.4	285	1	US-08-149-	Sequence 24, Applicati	2.35e+02	180	6	1.4	670	2	US-08-477-	Sequence 11, Applicati	2.35e+02
108	1.4	286	4	PCR-US96-0	Sequence 9, Applicatio	2.35e+02	181	6	1.4	693	2	US-08-380-	Sequence 2, Applicatio	2.35e+02
109	1.4	286	4	US-08-628-	Sequence 9, Applicatio	2.35e+02	182	6	1.4	693	2	US-08-895-	Sequence 5, Applicatio	2.35e+02
110	1.4	286	1	US-08-467-	Sequence 9, Applicatio	2.35e+02	183	6	1.4	693	2	US-08-895-	Sequence 5, Applicatio	2.35e+02
111	1.4	301	2	US-08-433-	Sequence 2, Applicatio	2.35e+02	184	6	1.4	693	2	US-08-895-	Sequence 5, Applicatio	2.35e+02
112	1.4	301	1	US-08-174-	Sequence 2, Applicatio	2.35e+02	185	6	1.4	719	3	US-08-286-	Sequence 8, Applicatio	2.35e+02
113	1.4	301	1	US-08-440-	Sequence 2, Applicatio	2.35e+02	186	6	1.4	719	3	US-09-003-	Sequence 2, Applicatio	2.35e+02
114	1.4	301	2	US-08-195-	Sequence 2, Applicatio	2.35e+02	187	6	1.4	742	1	US-07-921-	Sequence 2, Applicatio	2.35e+02
115	1.4	301	1	US-08-433-	Sequence 2, Applicatio	2.35e+02	188	6	1.4	742	1	US-08-441-	Sequence 2, Applicatio	2.35e+02
116	1.4	301	2	US-08-433-	Sequence 2, Applicatio	2.35e+02	189	6	1.4	760	1	US-08-195-	Sequence 2, Applicatio	2.35e+02
117	1.4	313	2	US-08-284-	Sequence 5, Applicatio	2.35e+02	190	6	1.4	830	3	US-08-804-	Sequence 20, Applicati	2.35e+02
118	1.4	322	1	US-08-136-	Sequence 2, Applicatio	2.35e+02	191	6	1.4	830	3	US-08-720-	Sequence 20, Applicati	2.35e+02
119	1.4	324	3	US-08-508-	Sequence 31, Applicati	2.35e+02	192	6	1.4	831	2	US-09-047-	Sequence 4, Applicatio	2.35e+02
120	1.4	337	2	US-08-784-	Sequence 8, Applicatio	2.35e+02	193	6	1.4	855	2	US-08-619-	Sequence 6, Applicatio	2.35e+02
121	1.4	338	2	US-08-784-	Sequence 6, Applicatio	2.35e+02	194	6	1.4	864	2	US-08-209-	Sequence 29, Applicati	2.35e+02
122	1.4	338	2	US-08-784-	Sequence 10, Applicati	2.35e+02	195	6	1.4	872	1	US-08-766-	Sequence 2, Applicatio	2.35e+02
123	1.4	341	1	US-08-118-	Sequence 48, Applicati	2.35e+02	196	6	1.4	909	3	US-08-936-	Sequence 8, Applicatio	2.35e+02
124	1.4	341	4	PCR-US93-0	Sequence 48, Applicati	2.35e+02	197	6	1.4	909	3	US-08-936-	Sequence 10, Applicati	2.35e+02
125	1.4	341	2	US-08-209-	Sequence 11, Applicati	2.35e+02	198	6	1.4	914	3	US-08-936-	Sequence 18, Applicati	2.35e+02
126	1.4	351	1	US-08-700-	Sequence 2, Applicatio	2.35e+02	199	6	1.4	914	3	US-08-936-	Sequence 18, Applicati	2.35e+02
127	1.4	351	1	US-08-402-	Sequence 2, Applicatio	2.35e+02	200	6	1.4	921	1	US-08-481-	Sequence 14, Applicati	2.35e+02
128	1.4	351	1	US-08-993-	Sequence 2, Applicatio	2.35e+02	201	6	1.4	921	1	US-08-486-	Sequence 14, Applicati	2.35e+02
129	1.4	359	1	US-07-937-	Sequence 19, Applicati	2.35e+02	202	6	1.4	921	1	US-07-718-	Sequence 14, Applicati	2.35e+02
130	1.4	384	2	US-08-103-	Sequence 10, Applicati	2.35e+02	203	6	1.4	925	1	US-08-252-	Sequence 4, Applicatio	2.35e+02
131	1.4	387	1	US-08-196-	Sequence 14, Applicati	2.35e+02	204	6	1.4	925	1	US-08-834-	Sequence 4, Applicatio	2.35e+02
132	1.4	387	1	US-08-760-	Sequence 14, Applicati	2.35e+02	205	6	1.4	926	3	US-08-936-	Sequence 11, Applicati	2.35e+02
133	1.4	390	1	US-08-568-	Sequence 2, Applicatio	2.35e+02	206	6	1.4	926	3	US-08-936-	Sequence 20, Applicati	2.35e+02
134	1.4	412	1	US-08-208-	Sequence 12, Applicati	2.35e+02	207	6	1.4	931	3	US-08-936-	Sequence 16, Applicati	2.35e+02
135	1.4	415	1	US-08-602-	Sequence 10, Applicati	2.35e+02	208	6	1.4	956	1	US-08-185-	Sequence 2, Applicatio	2.35e+02
136	1.4	415	1	US-08-680-	Sequence 10, Applicati	2.35e+02	209	6	1.4	956	1	US-08-185-	Sequence 2, Applicatio	2.35e+02
137	1.4	433	1	US-08-700-	Sequence 20, Applicati	2.35e+02	210	6	1.4	956	3	US-08-789-	Sequence 2, Applicatio	2.35e+02
138	1.4	437	2	US-08-473-	Sequence 9, Applicatio	2.35e+02	211	6	1.4	971	2	US-09-066-	Sequence 19, Applicati	2.35e+02
139	1.4	437	2	US-08-477-	Sequence 6, Applicatio	2.35e+02	212	6	1.4	971	2	US-08-805-	Sequence 19, Applicati	2.35e+02
140	1.4	437	2	US-08-477-	Sequence 5, Applicatio	2.35e+02	213	6	1.4	971	1	US-08-446-	Sequence 19, Applicati	2.35e+02
141	1.4	438	1	US-08-440-	Sequence 5, Applicatio	2.35e+02	214	6	1.4	971	1	US-08-064-	Sequence 19, Applicati	2.35e+02
142	1.4	438	1	US-08-439-	Sequence 2, Applicatio	2.35e+02	215	6	1.4	971	1	US-08-742-	Sequence 23, Applicati	2.35e+02
143	1.4	459	1	US-08-403-	Sequence 5, Applicatio	2.35e+02	216	6	1.4	993	1	US-08-446-	Sequence 19, Applicati	2.35e+02
144	1.4	465	1	US-08-447-	Sequence 2, Applicatio	2.35e+02	217	6	1.4	1026	2	US-08-614-	Sequence 7, Applicatio	2.35e+02
145	1.4	473	1	US-08-439-	Sequence 4, Applicatio	2.35e+02	218	6	1.4	1026	1	US-08-194-	Sequence 7, Applicatio	2.35e+02
146	1.4	473	1	US-08-440-	Sequence 4, Applicatio	2.35e+02	219	6	1.4	1064	1	US-08-537-	Sequence 3, Applicatio	2.35e+02
147	1.4	483	3	US-09-027-	Sequence 7, Applicatio	2.35e+02	220	6	1.4	1088	2	US-08-742-	Sequence 23, Applicati	2.35e+02
148	1.4	483	3	US-09-027-	Sequence 9, Applicatio	2.35e+02	221	6	1.4	1088	2	US-08-742-	Sequence 23, Applicati	2.35e+02
149	1.4	488	1	US-08-448-	Sequence 10, Applicati	2.35e+02	222	6	1.4	1132	2	US-08-567-	Sequence 2, Applicatio	2.35e+02
150	1.4	495	2	US-08-749-	Sequence 3, Applicatio	2.35e+02	223	6	1.4	1132	2	US-09-196-	Sequence 2, Applicatio	2.35e+02
151	1.4	508	2	US-08-861-	Sequence 10, Applicati	2.35e+02	224	6	1.4	1138	1	US-08-404-	Sequence 4, Applicatio	2.35e+02
152	1.4	508	1	US-07-891-	Sequence 10, Applicati	2.35e+02	225	6	1.4	1358	1	US-08-404-	Sequence 4, Applicatio	2.35e+02
153	1.4	508	2	US-08-396-	Sequence 10, Applicati	2.35e+02	226	6	1.4	1358	1	US-08-404-	Sequence 4, Applicatio	2.35e+02
154	1.4	529	2	US-08-504-	Sequence 8, Applicatio	2.35e+02	227	6	1.4	1390	1	US-08-770-	Sequence 9, Applicatio	2.35e+02
155	1.4	529	2	US-07-891-	Sequence 8, Applicatio	2.35e+02	228	6	1.4	1398	2	US-08-750-	Sequence 9, Applicatio	2.35e+02
156	1.4	535	3	US-08-370-	Sequence 19, Applicati	2.35e+02	229	6	1.4	1437	3	US-09-061-	Sequence 2, Applicatio	2.35e+02
157	1.4	535	3	US-08-286-	Sequence 8, Applicatio	2.35e+02	230	6	1.4	1453	2	US-09-001-	Sequence 2, Applicatio	2.35e+02
158	1.4	539	1	US-08-173-	Sequence 8, Applicatio	2.35e+02	231	6	1.4	1548	1	US-08-460-	Sequence 7, Applicatio	2.35e+02
159	1.4	539	2	US-08-265-	Sequence 8, Applicatio	2.35e+02	232	6	1.4	1891	2	US-08-804-	Sequence 12, Applicati	2.35e+02
160	1.4	548	2	US-08-452-	Sequence 8, Applicatio	2.35e+02	233	6	1.4	1891	2	US-08-804-	Sequence 12, Applicati	2.35e+02
161	1.4	552	1	US-08-588-	Sequence 2, Applicatio	2.35e+02	234	6	1.4	1891	2	US-08-804-	Sequence 6, Applicatio	2.35e+02
162	1.4	552	2	US-09-005-	Sequence 2, Applicatio	2.35e+02	235	6	1.4	1912	3	US-08-685-	Sequence 6, Applicatio	2.35e+02
163	1.4	552	3	US-08-701-	Sequence 14, Applicati	2.35e+02	236	6	1.4	1912	1	US-08-409-	Sequence 4, Applicatio	2.35e+02
164	1.4	552	2	US-07-915-	Sequence 2, Applicatio	2.35e+02	237	6	1.4	2366	1	US-08-480-	Sequence 10, Applicati	2.35e+02
165	1.4	560	1	US-07-891-	Sequence 5, Applicatio	2.35e+02	238	6	1.4	2366	1	US-08-480-	Sequence 10, Applicati	2.35e+02
166	1.4	563	1	US-08-442-	Sequence 4, Applicatio	2.35e+02	239	6	1.4	2523	1	US-08-185-	Sequence 18, Applicati	2.35e+02
167	1.4	578	1	US-08-766-	Sequence 4, Applicatio	2.35e+02	240	6	1.4	3491	2	US-07-642-	Sequence 2, Applicatio	2.35e+02
168	1.4	602	4	PCR-US93-0	Sequence 2, Applicatio	2.35e+02	241	5	1.1	7	2	US-08-442-	Sequence 3, Applicati	2.13e+03
169	1.4	602	1	US-08-295-	Sequence 2, Applicatio	2.35e+02	242	5	1.1	7	3	US-08-944-	Sequence 9, Applicatio	2.13e+03

243	5	1.1	11	5	5177060-27	atent No. 5177060	2.13e+03	316	1.1	73	4	PCT-US94-0	Sequence 3, Applicatio	2.13e+03
244	5	1.1	11	5	5178861-16	atent No. 5178861	2.13e+03	317	1.1	73	4	PCT-US94-0	Sequence 2, Applicatio	2.13e+03
245	5	1.1	11	4	PCT-US96-0	Sequence 8, Applicatio	2.13e+03	318	1.1	73	1	US-08-330	Sequence 2, Applicatio	2.13e+03
246	5	1.1	12	4	PCT-US96-1	Sequence 46, Applicatio	2.13e+03	319	1.1	73	1	US-08-340	Sequence 19, Applicatio	2.13e+03
247	5	1.1	13	2	US-08-195	Sequence 1, Applicatio	2.13e+03	320	1.1	76	2	US-08-722	Sequence 7, Applicatio	2.13e+03
248	5	1.1	15	1	US-08-542	Sequence 19, Applicatio	2.13e+03	321	1.1	77	5	5466783-4	atent No. 5466783	2.13e+03
249	5	1.1	15	2	US-08-156	Sequence 70, Applicatio	2.13e+03	322	1.1	77	4	PCT-US95-1	Sequence 7, Applicatio	2.13e+03
250	5	1.1	15	2	US-08-332	Sequence 15, Applicatio	2.13e+03	323	1.1	77	4	PCT-US92-0	Sequence 5, Applicatio	2.13e+03
251	5	1.1	17	4	PCT-US95-1	Sequence 11, Applicatio	2.13e+03	324	1.1	81	2	US-08-460	Sequence 10, Applicatio	2.13e+03
252	5	1.1	18	3	US-08-788	Sequence 44, Applicatio	2.13e+03	325	1.1	82	5	5498694-2	atent No. 5498694	2.13e+03
253	5	1.1	19	3	US-08-920	Sequence 3, Applicatio	2.13e+03	326	1.1	85	2	US-08-468	Sequence 9, Applicatio	2.13e+03
254	5	1.1	19	3	US-08-871	Sequence 6, Applicatio	2.13e+03	327	1.1	86	5	5179196-2	atent No. 5179196	2.13e+03
255	5	1.1	19	3	US-08-788	Sequence 1, Applicatio	2.13e+03	328	1.1	86	5	5164304-2	atent No. 5164304	2.13e+03
256	5	1.1	19	2	US-08-719	Sequence 18, Applicatio	2.13e+03	329	1.1	86	5	5514582-41	Sequence 20, Applicatio	2.13e+03
257	5	1.1	20	5	5225193-7	atent No. 5225193	2.13e+03	330	1.1	88	1	US-08-469	Sequence 21, Applicatio	2.13e+03
258	5	1.1	20	5	5225193-2	atent No. 5225193	2.13e+03	331	1.1	88	1	US-08-203	Sequence 21, Applicatio	2.13e+03
259	5	1.1	20	5	5225193-7	Sequence 1, Applicatio	2.13e+03	332	1.1	93	2	US-08-467	Sequence 36, Applicatio	2.13e+03
260	5	1.1	23	4	PCT-US93-1	Sequence 15, Applicatio	2.13e+03	333	1.1	96	2	US-08-482	Sequence 21, Applicatio	2.13e+03
261	5	1.1	23	1	US-08-086	Sequence 18, Applicatio	2.13e+03	334	1.1	96	2	US-08-485	Sequence 53, Applicatio	2.13e+03
262	5	1.1	23	3	US-08-484	Sequence 19, Applicatio	2.13e+03	335	1.1	96	2	US-08-464	Sequence 18, Applicatio	2.13e+03
263	5	1.1	23	2	US-08-332	Sequence 2, Applicatio	2.13e+03	336	1.1	97	4	PCT-US94-0	Sequence 29, Applicatio	2.13e+03
264	5	1.1	24	2	US-08-470	Sequence 17, Applicatio	2.13e+03	337	1.1	100	2	US-08-474	Sequence 11, Applicatio	2.13e+03
265	5	1.1	24	2	US-08-761	Sequence 1, Applicatio	2.13e+03	338	1.1	101	2	US-08-468	Sequence 2, Applicatio	2.13e+03
266	5	1.1	25	4	PCT-US95-1	Sequence 38, Applicatio	2.13e+03	339	1.1	105	3	US-09-120	Sequence 63, Applicatio	2.13e+03
267	5	1.1	25	4	PCT-US93-0	Sequence 47, Applicatio	2.13e+03	340	1.1	105	3	US-08-466	Sequence 14, Applicatio	2.13e+03
268	5	1.1	25	1	US-08-425	Sequence 59, Applicatio	2.13e+03	341	1.1	106	4	PCT-US95-1	Sequence 5, Applicatio	2.13e+03
269	5	1.1	26	1	US-07-879	Sequence 43, Applicatio	2.13e+03	342	1.1	106	2	US-09-203	Sequence 7, Applicatio	2.13e+03
270	5	1.1	27	2	US-08-317	Sequence 48, Applicatio	2.13e+03	343	1.1	107	4	PCT-US95-1	Sequence 7, Applicatio	2.13e+03
271	5	1.1	27	1	US-08-425	Sequence 61, Applicatio	2.13e+03	344	1.1	107	4	PCT-US95-1	Sequence 4, Applicatio	2.13e+03
272	5	1.1	28	2	US-08-317	Sequence 10, Applicatio	2.13e+03	345	1.1	107	2	US-08-446	Sequence 4, Applicatio	2.13e+03
273	5	1.1	30	2	US-08-317	Sequence 46, Applicatio	2.13e+03	346	1.1	107	2	US-08-446	Sequence 7, Applicatio	2.13e+03
274	5	1.1	30	2	US-08-317	Sequence 61, Applicatio	2.13e+03	347	1.1	107	4	PCT-US95-1	Sequence 4, Applicatio	2.13e+03
275	5	1.1	30	2	US-08-317	Sequence 10, Applicatio	2.13e+03	348	1.1	107	2	US-08-446	Sequence 4, Applicatio	2.13e+03
276	5	1.1	30	2	US-08-280	Sequence 46, Applicatio	2.13e+03	349	1.1	107	2	US-08-446	Sequence 4, Applicatio	2.13e+03
277	5	1.1	31	2	US-08-317	Sequence 46, Applicatio	2.13e+03	350	1.1	107	2	US-08-446	Sequence 4, Applicatio	2.13e+03
278	5	1.1	34	5	5200327-16	atent No. 5200327	2.13e+03	351	1.1	107	2	US-08-446	Sequence 4, Applicatio	2.13e+03
279	5	1.1	34	1	US-08-318	Sequence 5, Applicatio	2.13e+03	352	1.1	107	2	US-08-446	Sequence 4, Applicatio	2.13e+03
280	5	1.1	38	5	5185441-1	atent No. 5185441	2.13e+03	353	1.1	107	2	US-08-446	Sequence 4, Applicatio	2.13e+03
281	5	1.1	39	2	US-08-488	Sequence 58, Applicatio	2.13e+03	354	1.1	108	2	US-08-446	Sequence 4, Applicatio	2.13e+03
282	5	1.1	39	2	US-08-488	Sequence 26, Applicatio	2.13e+03	355	1.1	113	2	US-08-446	Sequence 4, Applicatio	2.13e+03
283	5	1.1	39	1	US-08-446	Sequence 64, Applicatio	2.13e+03	356	1.1	116	1	US-08-446	Sequence 4, Applicatio	2.13e+03
284	5	1.1	41	5	5200327-15	atent No. 5200327	2.13e+03	357	1.1	121	4	PCT-US96-0	Sequence 32, Applicatio	2.13e+03
285	5	1.1	41	1	US-08-318	Sequence 4, Applicatio	2.13e+03	358	1.1	121	2	US-08-446	Sequence 32, Applicatio	2.13e+03
286	5	1.1	42	4	PCT-US93-0	Sequence 33, Applicatio	2.13e+03	359	1.1	122	1	US-08-446	Sequence 14, Applicatio	2.13e+03
287	5	1.1	42	4	PCT-US93-0	Sequence 33, Applicatio	2.13e+03	360	1.1	123	2	US-08-446	Sequence 14, Applicatio	2.13e+03
288	5	1.1	43	1	US-08-453	Sequence 73, Applicatio	2.13e+03	361	1.1	123	2	US-08-446	Sequence 14, Applicatio	2.13e+03
289	5	1.1	43	1	US-08-453	Sequence 73, Applicatio	2.13e+03	362	1.1	123	2	US-08-446	Sequence 14, Applicatio	2.13e+03
290	5	1.1	43	4	PCT-US95-0	Sequence 85, Applicatio	2.13e+03	363	1.1	125	2	US-08-553	Sequence 55, Applicatio	2.13e+03
291	5	1.1	43	4	PCT-US93-1	Sequence 85, Applicatio	2.13e+03	364	1.1	131	2	US-08-553	Sequence 55, Applicatio	2.13e+03
292	5	1.1	43	1	US-07-998	Sequence 73, Applicatio	2.13e+03	365	1.1	135	5	5164304-7	atent No. 5164304	2.13e+03
293	5	1.1	43	3	US-08-488	Sequence 60, Applicatio	2.13e+03	366	1.1	135	5	5219996-19	atent No. 5219996	2.13e+03
294	5	1.1	43	3	US-09-273	Sequence 2, Applicatio	2.13e+03	367	1.1	138	4	PCT-US95-1	Sequence 4, Applicatio	2.13e+03
295	5	1.1	44	1	US-08-479	Sequence 6, Applicatio	2.13e+03	368	1.1	138	4	PCT-US95-1	Sequence 4, Applicatio	2.13e+03
296	5	1.1	44	4	PCT-US93-0	Sequence 1, Applicatio	2.13e+03	369	1.1	138	4	PCT-US95-1	Sequence 4, Applicatio	2.13e+03
297	5	1.1	45	1	US-08-407	Sequence 23, Applicatio	2.13e+03	370	1.1	138	2	US-08-449	Sequence 12, Applicatio	2.13e+03
298	5	1.1	48	4	PCT-US95-1	Sequence 13, Applicatio	2.13e+03	371	1.1	142	1	US-08-476	Sequence 31, Applicatio	2.13e+03
299	5	1.1	48	4	PCT-US95-1	Sequence 13, Applicatio	2.13e+03	372	1.1	142	1	US-08-476	Sequence 31, Applicatio	2.13e+03
300	5	1.1	49	2	US-08-488	Sequence 36, Applicatio	2.13e+03	373	1.1	142	5	5180813-2	atent No. 5180813	2.13e+03
301	5	1.1	50	1	US-07-040	Sequence 2, Applicatio	2.13e+03	374	1.1	148	2	US-08-445	Sequence 13, Applicatio	2.13e+03
302	5	1.1	50	1	US-08-459	Sequence 2, Applicatio	2.13e+03	375	1.1	148	2	US-08-445	Sequence 13, Applicatio	2.13e+03
303	5	1.1	52	2	US-08-874	Sequence 9, Applicatio	2.13e+03	376	1.1	150	1	US-08-378	Sequence 6, Applicatio	2.13e+03
304	5	1.1	54	1	US-08-164	Sequence 6, Applicatio	2.13e+03	377	1.1	152	5	5187153-4	atent No. 5187153	2.13e+03
305	5	1.1	54	1	US-08-209	Sequence 11, Applicatio	2.13e+03	378	1.1	152	1	US-08-471	Sequence 22, Applicatio	2.13e+03
306	5	1.1	60	1	US-08-197	Sequence 11, Applicatio	2.13e+03	379	1.1	156	4	PCT-US95-0	Sequence 2, Applicatio	2.13e+03
307	5	1.1	60	1	US-08-459	Sequence 11, Applicatio	2.13e+03	380	1.1	156	2	US-08-508	Sequence 2, Applicatio	2.13e+03
308	5	1.1	63	3	US-08-871	Sequence 18, Applicatio	2.13e+03	381	1.1	156	2	US-08-508	Sequence 2, Applicatio	2.13e+03
309	5	1.1	63	3	US-09-061	Sequence 10, Applicatio	2.13e+03	382	1.1	157	4	PCT-US96-0	Sequence 5, Applicatio	2.13e+03
310	5	1.1	70	2	US-08-468	Sequence 11, Applicatio	2.13e+03	383	1.1	158	2	US-08-403	Sequence 29, Applicatio	2.13e+03
311	5	1.1	70	1	US-08-329	Sequence 17, Applicatio	2.13e+03	384	1.1	162	5	5220013-4	atent No. 5220013	2.13e+03
312	5	1.1	70	1	US-08-329	Sequence 17, Applicatio	2.13e+03	385	1.1	162	5	5220013-4	atent No. 5220013	2.13e+03
313	5	1.1	71	3	US-08-943	Sequence 2, Applicatio	2.13e+03	386	1.1	166	2	US-08-483	Sequence 3, Applicatio	2.13e+03
314	5	1.1	71	3	US-08-943	Sequence 2, Applicatio	2.13e+03	387	1.1	166	2	US-08-483	Sequence 3, Applicatio	2.13e+03
315	5	1.1	73	2	US-08-637	Sequence 406, Applicatio	2.13e+03	388	1.1	166	2	US-07-965	Sequence 3, Applicatio	2.13e+03

389	5	1.1	167	2	US-08-993-	Sequence 8, Applicatio	2.13e+03	462	5	1.1	280	4	PCT-US92-0	Sequence 3, Applicatio	2.13e+03
390	5	1.1	170	3	US-09-186-	Sequence 8, Applicatio	2.13e+03	463	5	1.1	284	2	US-08-767-	Sequence 3, Applicatio	2.13e+03
391	5	1.1	172	1	US-08-471-	Sequence 16, Applicati	2.13e+03	464	5	1.1	287	1	US-08-342-2	Sequence 3, Applicatio	2.13e+03
392	5	1.1	172	3	US-09-113-	Sequence 3, Applicatio	2.13e+03	465	5	1.1	288	1	US-08-781-	Sequence 4, Applicatio	2.13e+03
393	5	1.1	174	2	US-08-709-	Sequence 2, Applicatio	2.13e+03	466	5	1.1	289	2	US-08-475-	Sequence 4, Applicatio	2.13e+03
394	5	1.1	177	2	US-08-737-	Sequence 2, Applicatio	2.13e+03	467	5	1.1	290	1	US-08-457-	Sequence 7, Applicatio	2.13e+03
395	5	1.1	178	1	US-08-271-	Sequence 7, Applicatio	2.13e+03	468	5	1.1	292	2	US-08-688-	Sequence 7, Applicatio	2.13e+03
396	5	1.1	185	2	US-08-463-	Sequence 3, Applicatio	2.13e+03	469	5	1.1	293	3	US-08-701-	Sequence 16, Applicati	2.13e+03
397	5	1.1	190	4	PCT-US95-0	Sequence 29, Applicati	2.13e+03	470	5	1.1	293	2	US-08-701-	Sequence 20, Applicati	2.13e+03
398	5	1.1	192	2	US-08-468-	Sequence 93, Applicati	2.13e+03	471	5	1.1	295	4	PCT-US93-0	Sequence 2, Applicatio	2.13e+03
399	5	1.1	192	2	US-08-468-	Sequence 94, Applicati	2.13e+03	472	5	1.1	296	4	PCT-US95-0	Sequence 3, Applicatio	2.13e+03
400	5	1.1	192	1	US-08-086-	Sequence 102, Applicat	2.13e+03	473	5	1.1	298	2	US-09-006-	Sequence 2, Applicatio	2.13e+03
401	5	1.1	192	2	US-08-468-	Sequence 95, Applicati	2.13e+03	474	5	1.1	303	1	US-07-917-	Sequence 3, Applicatio	2.13e+03
402	5	1.1	192	2	US-08-290-	Sequence 7, Applicatio	2.13e+03	475	5	1.1	303	1	US-07-917-	Sequence 2, Applicatio	2.13e+03
403	5	1.1	196	4	PCT-US93-0	Sequence 7, Applicatio	2.13e+03	476	5	1.1	303	2	US-08-294-	Sequence 42, Applicati	2.13e+03
404	5	1.1	201	5	US-08-801-	Sequence 7, Applicatio	2.13e+03	477	5	1.1	303	2	US-08-294-	Sequence 54, Applicati	2.13e+03
405	5	1.1	201	2	US-08-801-	Sequence 7, Applicatio	2.13e+03	478	5	1.1	303	2	US-08-294-	Sequence 36, Applicati	2.13e+03
406	5	1.1	202	1	US-08-274-	Sequence 2, Applicatio	2.13e+03	479	5	1.1	303	2	US-08-294-	Sequence 26, Applicati	2.13e+03
407	5	1.1	202	2	US-08-462-	Sequence 2, Applicatio	2.13e+03	480	5	1.1	303	2	US-08-294-	Sequence 10, Applicati	2.13e+03
408	5	1.1	206	1	US-08-494-	Sequence 7, Applicatio	2.13e+03	481	5	1.1	303	2	US-08-294-	Sequence 6, Applicatio	2.13e+03
409	5	1.1	206	1	US-08-097-	Sequence 7, Applicatio	2.13e+03	482	5	1.1	303	2	US-08-294-	Sequence 44, Applicati	2.13e+03
410	5	1.1	210	3	US-08-471-	Sequence 22, Applicati	2.13e+03	483	5	1.1	304	2	US-08-415-	Sequence 5, Applicatio	2.13e+03
411	5	1.1	212	2	US-08-924-	Sequence 14, Applicati	2.13e+03	484	5	1.1	306	1	US-08-328-	Sequence 2, Applicatio	2.13e+03
412	5	1.1	213	3	US-09-186-	Sequence 6, Applicatio	2.13e+03	485	5	1.1	308	1	US-08-093-	Sequence 6, Applicatio	2.13e+03
413	5	1.1	219	1	US-08-461-	Sequence 13, Applicati	2.13e+03	486	5	1.1	308	2	US-08-468-	Sequence 16, Applicati	2.13e+03
414	5	1.1	221	3	US-08-484-	Sequence 96, Applicati	2.13e+03	487	5	1.1	309	4	PCT-US95-1	Sequence 2, Applicatio	2.13e+03
415	5	1.1	221	3	US-08-360-	Sequence 106, Applicat	2.13e+03	488	5	1.1	310	2	US-08-705-	Sequence 3, Applicatio	2.13e+03
416	5	1.1	222	1	US-08-328-	Sequence 8, Applicatio	2.13e+03	489	5	1.1	312	2	PCT-US95-1	Sequence 11, Applicati	2.13e+03
417	5	1.1	222	2	US-08-756-	Sequence 1, Applicatio	2.13e+03	490	5	1.1	312	2	US-08-510-	Sequence 2, Applicatio	2.13e+03
418	5	1.1	223	1	US-08-615-	Sequence 13, Applicati	2.13e+03	491	5	1.1	312	1	US-08-420-	Sequence 11, Applicati	2.13e+03
419	5	1.1	223	2	US-08-472-	Sequence 13, Applicati	2.13e+03	492	5	1.1	313	2	US-08-809-	Sequence 2, Applicatio	2.13e+03
420	5	1.1	227	5	US-08-499-2	Sequence 13, Applicati	2.13e+03	493	5	1.1	317	3	US-08-605-	Sequence 12, Applicati	2.13e+03
421	5	1.1	233	5	US-08-425-2	Sequence 10, Applicati	2.13e+03	494	5	1.1	318	2	US-08-695-	Sequence 17, Applicati	2.13e+03
422	5	1.1	233	4	PCT-US95-1	Sequence 10, Applicati	2.13e+03	495	5	1.1	319	3	US-09-100-	Sequence 10, Applicati	2.13e+03
423	5	1.1	233	1	US-08-607-	Sequence 6, Applicatio	2.13e+03	496	5	1.1	320	2	US-09-053-	Sequence 2, Applicatio	2.13e+03
424	5	1.1	233	1	US-08-081-	Sequence 6, Applicatio	2.13e+03	497	5	1.1	320	1	US-08-465-	Sequence 2, Applicatio	2.13e+03
425	5	1.1	233	4	PCT-US95-0	Sequence 14, Applicati	2.13e+03	498	5	1.1	321	2	US-08-813-	Sequence 2, Applicatio	2.13e+03
426	5	1.1	233	1	US-08-471-	Sequence 24, Applicati	2.13e+03	499	5	1.1	323	5	US-08-223-4	Sequence 10, Applicati	2.13e+03
427	5	1.1	240	5	US-08-394-6	Sequence 10, Applicati	2.13e+03	500	5	1.1	323	4	PCT-US93-0	Sequence 1, Applicatio	2.13e+03
428	5	1.1	240	5	US-08-394-4	Sequence 10, Applicati	2.13e+03	501	5	1.1	324	1	US-08-746-	Sequence 10, Applicati	2.13e+03
429	5	1.1	241	5	US-08-441-36	Sequence 10, Applicati	2.13e+03	502	5	1.1	324	2	US-08-671-	Sequence 11, Applicati	2.13e+03
430	5	1.1	241	5	US-08-912-	Sequence 48, Applicati	2.13e+03	503	5	1.1	324	2	PCT-US95-1	Sequence 13, Applicati	2.13e+03
431	5	1.1	245	2	US-08-989-	Sequence 5, Applicatio	2.13e+03	504	5	1.1	327	4	PCT-US95-1	Sequence 18, Applicati	2.13e+03
432	5	1.1	249	2	US-08-989-	Sequence 5, Applicatio	2.13e+03	505	5	1.1	327	4	PCT-US93-0	Sequence 15, Applicati	2.13e+03
433	5	1.1	250	5	US-08-989-	Sequence 10, Applicati	2.13e+03	506	5	1.1	329	2	US-08-606-	Sequence 2, Applicatio	2.13e+03
434	5	1.1	250	4	PCT-US92-0	Sequence 8, Applicatio	2.13e+03	507	5	1.1	330	2	US-08-827-	Sequence 2, Applicatio	2.13e+03
435	5	1.1	250	2	US-08-646-	Sequence 8, Applicatio	2.13e+03	508	5	1.1	330	2	PCT-US95-1	Sequence 3, Applicatio	2.13e+03
436	5	1.1	251	2	US-08-441-38	Sequence 15, Applicati	2.13e+03	509	5	1.1	331	1	US-08-319-	Sequence 2, Applicatio	2.13e+03
437	5	1.1	251	5	US-08-468-	Sequence 15, Applicati	2.13e+03	510	5	1.1	331	1	US-08-356-	Sequence 3, Applicatio	2.13e+03
438	5	1.1	253	2	US-08-468-	Sequence 15, Applicati	2.13e+03	511	5	1.1	331	1	US-08-630-	Sequence 3, Applicatio	2.13e+03
439	5	1.1	253	2	US-09-193-	Sequence 9, Applicatio	2.13e+03	512	5	1.1	332	1	US-08-442-	Sequence 7, Applicatio	2.13e+03
440	5	1.1	254	2	PCT-US96-0	Sequence 8, Applicatio	2.13e+03	513	5	1.1	332	1	US-08-530-	Sequence 4, Applicatio	2.13e+03
441	5	1.1	255	4	US-08-816-	Sequence 36, Applicati	2.13e+03	514	5	1.1	334	1	US-08-474-	Sequence 8, Applicati	2.13e+03
442	5	1.1	255	2	US-08-152-	Sequence 5, Applicatio	2.13e+03	515	5	1.1	336	2	US-09-032-	Sequence 2, Applicatio	2.13e+03
443	5	1.1	256	4	PCT-US96-0	Sequence 6, Applicatio	2.13e+03	516	5	1.1	336	3	US-08-784-	Sequence 2, Applicatio	2.13e+03
444	5	1.1	259	3	US-09-097-	Sequence 6, Applicatio	2.13e+03	517	5	1.1	337	3	US-09-032-	Sequence 17, Applicati	2.13e+03
445	5	1.1	263	1	US-08-441-	Sequence 4, Applicatio	2.13e+03	518	5	1.1	338	1	US-08-442-	Sequence 17, Applicati	2.13e+03
446	5	1.1	263	1	US-08-245-	Sequence 6, Applicatio	2.13e+03	519	5	1.1	338	1	US-08-606-	Sequence 17, Applicati	2.13e+03
447	5	1.1	264	4	PCT-US96-1	Sequence 6, Applicatio	2.13e+03	520	5	1.1	344	5	US-08-606-	Sequence 17, Applicati	2.13e+03
448	5	1.1	264	4	US-08-605-	Sequence 93, Applicati	2.13e+03	521	5	1.1	344	5	US-08-606-	Sequence 17, Applicati	2.13e+03
449	5	1.1	264	1	US-07-990-	Sequence 5, Applicatio	2.13e+03	522	5	1.1	345	1	US-08-446-	Sequence 10, Applicati	2.13e+03
450	5	1.1	264	1	US-08-155-	Sequence 41, Applicati	2.13e+03	523	5	1.1	347	1	US-08-630-	Sequence 58, Applicati	2.13e+03
451	5	1.1	265	1	US-08-155-	Sequence 41, Applicati	2.13e+03	524	5	1.1	347	1	US-08-630-	Sequence 2, Applicatio	2.13e+03
452	5	1.1	266	5	US-08-610-5	Sequence 41, Applicati	2.13e+03	525	5	1.1	350	3	US-09-211-	Sequence 2, Applicatio	2.13e+03
453	5	1.1	266	5	US-08-610-5	Sequence 41, Applicati	2.13e+03	526	5	1.1	351	2	US-08-468-	Sequence 46, Applicati	2.13e+03
454	5	1.1	269	5	US-08-887-	Sequence 2, Applicatio	2.13e+03	527	5	1.1	355	2	US-08-846-	Sequence 12, Applicati	2.13e+03
455	5	1.1	272	2	US-08-446-	Sequence 2, Applicatio	2.13e+03	528	5	1.1	356	1	US-08-602-	Sequence 93, Applicati	2.13e+03
456	5	1.1	273	1	US-08-446-	Sequence 2, Applicatio	2.13e+03	529	5	1.1	357	1	US-08-356-	Sequence 2, Applicatio	2.13e+03
457	5	1.1	274	5	US-08-602-	Sequence 2, Applicatio	2.13e+03	530	5	1.1	364	1	US-08-459-	Sequence 29, Applicati	2.13e+03
458	5	1.1	274	5	US-08-602-	Sequence 2, Applicatio	2.13e+03	531	5	1.1	364	1	US-08-459-	Sequence 29, Applicati	2.13e+03
459	5	1.1	278	1	US-08-201-	Sequence 16, Applicati	2.13e+03	532	5	1.1	366	3	US-08-860-	Sequence 20, Applicati	2.13e+03
460	5	1.1	280	1	US-08-477-	Sequence 128, Applicati	2.13e+03	533	5	1.1	367	3	US-08-630-	Sequence 19, Applicati	2.13e+03
461	5	1.1	280	2	US-08-646-	Sequence 128, Applicati	2.13e+03	534	5	1.1	370	3	US-09-150-	Sequence 1, Applicatio	2.13e+03

535	5	1.1	370	3	US-09-150-	Sequence 3, Applicatio	2.13e+03	608	5	1.1	439	1	US-08-694-	Sequence 10, Applicati	2.13e+03
536	5	1.1	371	5	US-08-050-3	Sequence 2, Applicatio	2.13e+03	609	5	1.1	445	2	US-08-912-	Sequence 25, Applicati	2.13e+03
537	5	1.1	372	3	US-08-685-	Sequence 2, Applicatio	2.13e+03	610	5	1.1	455	4	US-08-406-	Sequence 25, Applicati	2.13e+03
538	5	1.1	373	2	US-08-535-	Sequence 2, Applicatio	2.13e+03	611	5	1.1	455	4	PCT-US93-0	Sequence 25, Applicati	2.13e+03
539	5	1.1	375	1	US-08-542-	Sequence 5, Applicatio	2.13e+03	612	5	1.1	455	4	PCT-US93-0	Sequence 25, Applicati	2.13e+03
540	5	1.1	375	4	PCT-US94-1	Sequence 28, Applicati	2.13e+03	613	5	1.1	455	3	US-09-038-	Sequence 18, Applicati	2.13e+03
541	5	1.1	376	5	US-08-10-1	Sequence 28, Applicati	2.13e+03	614	5	1.1	455	1	US-08-462-	Sequence 25, Applicati	2.13e+03
542	5	1.1	376	5	US-08-385-	Sequence 4, Applicatio	2.13e+03	615	5	1.1	455	1	US-08-278-	Sequence 25, Applicati	2.13e+03
543	5	1.1	376	2	US-08-737-	Sequence 6, Applicatio	2.13e+03	616	5	1.1	456	5	US-08-882-	Sequence 6, Applicatio	2.13e+03
544	5	1.1	376	2	US-08-666-	Sequence 8, Applicatio	2.13e+03	617	5	1.1	457	2	US-08-882-	Sequence 6, Applicatio	2.13e+03
545	5	1.1	377	4	PCT-US95-0	Sequence 6, Applicatio	2.13e+03	618	5	1.1	457	2	US-08-882-	Sequence 6, Applicatio	2.13e+03
546	5	1.1	380	1	US-08-073-	Sequence 18, Applicati	2.13e+03	619	5	1.1	464	1	US-07-951-	Sequence 22, Applicati	2.13e+03
547	5	1.1	380	1	US-08-120-	Sequence 51, Applicati	2.13e+03	620	5	1.1	464	3	US-08-459-	Sequence 22, Applicati	2.13e+03
548	5	1.1	384	2	US-08-474-	Sequence 40, Applicati	2.13e+03	621	5	1.1	465	3	US-08-788-	Sequence 2, Applicatio	2.13e+03
549	5	1.1	385	1	US-08-329-	Sequence 4, Applicatio	2.13e+03	622	5	1.1	467	1	US-08-146-	Sequence 30, Applicati	2.13e+03
550	5	1.1	385	1	US-08-539-	Sequence 4, Applicatio	2.13e+03	623	5	1.1	467	1	US-08-151-	Sequence 32, Applicati	2.13e+03
551	5	1.1	388	1	US-08-261-	Sequence 4, Applicatio	2.13e+03	624	5	1.1	467	1	US-07-923-	Sequence 8, Applicatio	2.13e+03
552	5	1.1	396	5	US-08-058-2	Sequence 4, Applicatio	2.13e+03	625	5	1.1	467	2	US-08-374-	Sequence 8, Applicatio	2.13e+03
553	5	1.1	396	5	US-08-058-4	Sequence 4, Applicatio	2.13e+03	626	5	1.1	467	2	US-08-374-	Sequence 8, Applicatio	2.13e+03
554	5	1.1	396	5	US-08-449-	Sequence 5, Applicatio	2.13e+03	627	5	1.1	474	3	US-08-022-	Sequence 2, Applicatio	2.13e+03
555	5	1.1	396	2	US-08-939-	Sequence 14, Applicati	2.13e+03	628	5	1.1	475	2	US-08-861-	Sequence 3, Applicatio	2.13e+03
556	5	1.1	396	2	US-08-459-	Sequence 10, Applicati	2.13e+03	629	5	1.1	477	1	US-08-700-	Sequence 3, Applicatio	2.13e+03
557	5	1.1	397	2	US-08-098-	Sequence 2, Applicatio	2.13e+03	630	5	1.1	480	3	US-08-306-	Sequence 49, Applicati	2.13e+03
558	5	1.1	397	1	US-07-956-	Sequence 5, Applicatio	2.13e+03	631	5	1.1	485	3	US-08-445-	Sequence 4, Applicatio	2.13e+03
559	5	1.1	400	5	US-08-050-5	Sequence 5, Applicatio	2.13e+03	632	5	1.1	487	2	US-08-541-	Sequence 24, Applicati	2.13e+03
560	5	1.1	400	4	PCT-US91-0	Sequence 10, Applicati	2.13e+03	633	5	1.1	489	5	US-08-124-	Sequence 2, Applicatio	2.13e+03
561	5	1.1	405	2	US-08-483-	Sequence 4, Applicatio	2.13e+03	634	5	1.1	489	1	US-09-020-	Sequence 18, Applicati	2.13e+03
562	5	1.1	405	2	US-08-393-	Sequence 8, Applicatio	2.13e+03	635	5	1.1	489	2	US-09-020-	Sequence 12, Applicati	2.13e+03
563	5	1.1	406	2	US-09-203-	Sequence 5, Applicatio	2.13e+03	636	5	1.1	489	2	US-09-020-	Sequence 16, Applicati	2.13e+03
564	5	1.1	407	2	US-08-765-	Sequence 6, Applicatio	2.13e+03	637	5	1.1	489	2	US-09-020-	Sequence 8, Applicatio	2.13e+03
565	5	1.1	407	3	US-08-795-	Sequence 6, Applicatio	2.13e+03	638	5	1.1	489	2	US-09-020-	Sequence 22, Applicati	2.13e+03
566	5	1.1	407	3	US-08-481-	Sequence 2, Applicatio	2.13e+03	639	5	1.1	489	2	US-09-020-	Sequence 20, Applicati	2.13e+03
567	5	1.1	407	2	US-08-203-	Sequence 2, Applicatio	2.13e+03	640	5	1.1	489	2	US-09-062-	Sequence 8, Applicatio	2.13e+03
568	5	1.1	408	5	US-08-459-	Sequence 11, Applicati	2.13e+03	641	5	1.1	489	2	US-09-062-	Sequence 6, Applicatio	2.13e+03
569	5	1.1	408	3	US-08-459-	Sequence 21, Applicati	2.13e+03	642	5	1.1	490	1	US-08-201-	Sequence 7, Applicatio	2.13e+03
570	5	1.1	408	3	US-08-459-	Sequence 21, Applicati	2.13e+03	643	5	1.1	490	2	US-08-912-	Sequence 50, Applicati	2.13e+03
571	5	1.1	408	1	US-08-147-	Sequence 7, Applicatio	2.13e+03	644	5	1.1	495	5	US-08-897-	Sequence 4, Applicatio	2.13e+03
572	5	1.1	408	3	US-08-750-	Sequence 4, Applicatio	2.13e+03	645	5	1.1	496	2	US-08-897-	Sequence 4, Applicatio	2.13e+03
573	5	1.1	408	3	US-08-815-	Sequence 4, Applicatio	2.13e+03	646	5	1.1	497	4	PCT-US94-0	Sequence 3, Applicatio	2.13e+03
574	5	1.1	409	5	US-08-050-4	Sequence 4, Applicatio	2.13e+03	647	5	1.1	497	4	PCT-US94-0	Sequence 4, Applicatio	2.13e+03
575	5	1.1	409	2	US-08-743-	Sequence 2, Applicatio	2.13e+03	648	5	1.1	497	3	US-08-898-	Sequence 2, Applicatio	2.13e+03
576	5	1.1	410	3	US-08-630-	Sequence 17, Applicati	2.13e+03	649	5	1.1	498	2	US-08-474-	Sequence 20, Applicati	2.13e+03
577	5	1.1	410	3	US-09-083-	Sequence 2, Applicatio	2.13e+03	650	5	1.1	500	5	US-08-474-	Sequence 20, Applicati	2.13e+03
578	5	1.1	412	5	US-08-395-	Sequence 3, Applicatio	2.13e+03	651	5	1.1	500	1	US-08-454-	Sequence 15, Applicati	2.13e+03
579	5	1.1	412	2	US-08-878-	Sequence 6, Applicatio	2.13e+03	652	5	1.1	500	1	US-08-307-	Sequence 20, Applicati	2.13e+03
580	5	1.1	412	2	US-08-605-	Sequence 10, Applicati	2.13e+03	653	5	1.1	502	2	US-08-700-	Sequence 8, Applicatio	2.13e+03
581	5	1.1	413	2	US-08-943-	Sequence 10, Applicati	2.13e+03	654	5	1.1	502	3	US-08-464-	Sequence 7, Applicatio	2.13e+03
582	5	1.1	413	2	US-08-295-	Sequence 2, Applicatio	2.13e+03	655	5	1.1	503	3	US-08-389-	Sequence 8, Applicatio	2.13e+03
583	5	1.1	415	1	US-07-757-	Sequence 5, Applicatio	2.13e+03	656	5	1.1	503	3	US-08-700-	Sequence 6, Applicatio	2.13e+03
584	5	1.1	416	1	US-08-117-	Sequence 61, Applicati	2.13e+03	657	5	1.1	507	1	US-08-484-	Sequence 12, Applicati	2.13e+03
585	5	1.1	420	2	US-08-845-	Sequence 8, Applicatio	2.13e+03	658	5	1.1	508	1	US-08-435-	Sequence 6, Applicatio	2.13e+03
586	5	1.1	420	4	PCT-US96-0	Sequence 40, Applicati	2.13e+03	659	5	1.1	513	5	US-08-676-	Sequence 7, Applicatio	2.13e+03
587	5	1.1	420	1	US-08-487-	Sequence 4, Applicatio	2.13e+03	660	5	1.1	513	2	US-07-989-	Sequence 8, Applicatio	2.13e+03
588	5	1.1	420	1	US-07-847-	Sequence 29, Applicati	2.13e+03	661	5	1.1	513	3	US-08-889-	Sequence 19, Applicati	2.13e+03
589	5	1.1	423	4	PCT-US96-1	Sequence 13, Applicati	2.13e+03	662	5	1.1	513	2	US-08-459-	Sequence 19, Applicati	2.13e+03
590	5	1.1	423	4	US-08-494-	Sequence 14, Applicati	2.13e+03	663	5	1.1	516	1	US-08-638-	Sequence 41, Applicati	2.13e+03
591	5	1.1	423	3	US-08-105-	Sequence 2, Applicatio	2.13e+03	664	5	1.1	516	1	US-08-577-	Sequence 4, Applicatio	2.13e+03
592	5	1.1	425	3	US-08-484-	Sequence 14, Applicati	2.13e+03	665	5	1.1	516	2	US-08-676-	Sequence 7, Applicatio	2.13e+03
593	5	1.1	425	3	US-08-484-	Sequence 14, Applicati	2.13e+03	666	5	1.1	517	2	US-08-485-	Sequence 7, Applicatio	2.13e+03
594	5	1.1	426	5	US-08-633-8	Sequence 12, Applicati	2.13e+03	667	5	1.1	520	4	PCT-US95-0	Sequence 5, Applicatio	2.13e+03
595	5	1.1	426	1	US-08-833-	Sequence 63, Applicati	2.13e+03	668	5	1.1	525	4	PCT-US95-1	Sequence 28, Applicati	2.13e+03
596	5	1.1	426	1	US-08-459-	Sequence 41, Applicati	2.13e+03	669	5	1.1	525	4	PCT-US95-1	Sequence 27, Applicati	2.13e+03
597	5	1.1	428	5	US-07-816-	Sequence 12, Applicati	2.13e+03	670	5	1.1	525	4	US-08-681-	Sequence 2, Applicatio	2.13e+03
598	5	1.1	428	1	US-08-417-	Sequence 12, Applicati	2.13e+03	671	5	1.1	528	1	US-08-368-	Sequence 13, Applicati	2.13e+03
599	5	1.1	428	1	US-08-301-	Sequence 18, Applicati	2.13e+03	672	5	1.1	528	4	PCT-US93-0	Sequence 13, Applicati	2.13e+03
600	5	1.1	429	5	US-08-301-	Sequence 18, Applicati	2.13e+03	673	5	1.1	531	2	US-08-789-	Sequence 13, Applicati	2.13e+03
601	5	1.1	430	1	US-08-535-	Sequence 8, Applicatio	2.13e+03	674	5	1.1	531	4	PCT-US95-0	Sequence 3, Applicatio	2.13e+03
602	5	1.1	430	1	US-08-677-	Sequence 8, Applicatio	2.13e+03	675	5	1.1	532	3	US-08-933-	Sequence 3, Applicatio	2.13e+03
603	5	1.1	433	1	US-08-522-	Sequence 7, Applicatio	2.13e+03	676	5	1.1	533	3	US-08-484-	Sequence 13, Applicati	2.13e+03
604	5	1.1	433	1	US-08-484-	Sequence 18, Applicati	2.13e+03	677	5	1.1	533	1	US-08-484-	Sequence 13, Applicati	2.13e+03
605	5	1.1	437	1	US-08-764-	Sequence 1, Applicatio	2.13e+03	678	5	1.1	533	1	US-08-220-	Sequence 15, Applicati	2.13e+03
606	5	1.1	437	1	US-08-764-	Sequence 1, Applicatio	2.13e+03	679	5	1.1	533	1	US-08-220-	Sequence 15, Applicati	2.13e+03
607	5	1.1	438	1	US-08-494-	Sequence 11, Applicati	2.13e+03	680	5	1.1	540	4	PCT-US95-1	Sequence 25, Applicati	2.13e+03

681	5	1.1	540.4	US-08-604-	Sequence 26, Applicati	2.13e+03	754	5	1.1	694.2	US-08-689-	Sequence 5, Applicatio	2.13e+03
682	5	1.1	541.1	US-08-604-	Sequence 2, Applicatio	2.13e+03	755	5	1.1	695.5	5218100-2	Sequence 5, Applicatio	2.13e+03
683	5	1.1	543.3	US-08-808-	Sequence 12, Applicati	2.13e+03	756	5	1.1	695.2	US-08-104-	Sequence 1, Applicatio	2.13e+03
684	5	1.1	543.2	US-08-808-	Sequence 12, Applicati	2.13e+03	757	5	1.1	696.3	US-08-906-	Sequence 4, Applicatio	2.13e+03
685	5	1.1	548.2	US-08-676-	Sequence 50, Applicati	2.13e+03	758	5	1.1	705.2	US-08-170-	Sequence 7, Applicatio	2.13e+03
686	5	1.1	548.2	US-08-782-	Sequence 2, Applicatio	2.13e+03	759	5	1.1	713.3	US-08-149-	Sequence 2, Applicatio	2.13e+03
687	5	1.1	548.3	US-09-111-	Sequence 14, Applicati	2.13e+03	760	5	1.1	714.4	US-08-149-	Sequence 2, Applicatio	2.13e+03
688	5	1.1	548.1	US-08-463-	Sequence 2, Applicatio	2.13e+03	761	5	1.1	714.4	US-08-149-	Sequence 2, Applicatio	2.13e+03
689	5	1.1	549.4	US-08-463-	Sequence 2, Applicatio	2.13e+03	762	5	1.1	718.1	US-08-425-	Sequence 2, Applicatio	2.13e+03
690	5	1.1	549.2	US-08-463-	Sequence 2, Applicatio	2.13e+03	763	5	1.1	722.1	US-08-158-	Sequence 5, Applicatio	2.13e+03
691	5	1.1	549.2	US-08-676-	Sequence 59, Applicati	2.13e+03	764	5	1.1	724.1	US-08-121-	Sequence 6, Applicatio	2.13e+03
692	5	1.1	552.3	US-09-111-	Sequence 10, Applicati	2.13e+03	765	5	1.1	729.2	US-08-835-	Sequence 6, Applicatio	2.13e+03
693	5	1.1	553.3	US-09-082-	Sequence 2, Applicatio	2.13e+03	766	5	1.1	732.2	US-08-459-	Sequence 14, Applicati	2.13e+03
694	5	1.1	555.4	US-08-458-	Sequence 2, Applicatio	2.13e+03	767	5	1.1	732.2	US-08-456-	Sequence 2, Applicatio	2.13e+03
695	5	1.1	559.4	US-08-458-	Sequence 12, Applicati	2.13e+03	768	5	1.1	732.1	US-08-456-	Sequence 9, Applicatio	2.13e+03
696	5	1.1	562.4	US-08-191-	Sequence 81, Applicati	2.13e+03	769	5	1.1	738.2	US-08-456-	Sequence 9, Applicatio	2.13e+03
697	5	1.1	572.1	US-08-191-	Sequence 81, Applicati	2.13e+03	770	5	1.1	745.2	US-08-484-	Sequence 43, Applicati	2.13e+03
698	5	1.1	576.4	US-08-261-	Sequence 6, Applicatio	2.13e+03	771	5	1.1	745.2	US-08-862-	Sequence 5, Applicatio	2.13e+03
699	5	1.1	582.1	US-08-261-	Sequence 6, Applicatio	2.13e+03	772	5	1.1	745.2	US-08-862-	Sequence 5, Applicatio	2.13e+03
700	5	1.1	583.2	US-08-616-	Sequence 6, Applicatio	2.13e+03	773	5	1.1	746.2	US-08-838-	Sequence 6, Applicatio	2.13e+03
701	5	1.1	585.2	US-08-869-	Sequence 6, Applicatio	2.13e+03	774	5	1.1	751.5	5187153-2	Sequence 5, Applicatio	2.13e+03
702	5	1.1	587.4	US-08-179-	Sequence 5, Applicatio	2.13e+03	775	5	1.1	751.5	5223482-2	Sequence 5, Applicatio	2.13e+03
703	5	1.1	591.2	US-08-628-	Sequence 10, Applicati	2.13e+03	776	5	1.1	751.5	5220013-2	Sequence 5, Applicatio	2.13e+03
704	5	1.1	591.2	US-08-628-	Sequence 10, Applicati	2.13e+03	777	5	1.1	751.1	US-08-123-	Sequence 4, Applicatio	2.13e+03
705	5	1.1	595.3	US-08-628-	Sequence 10, Applicati	2.13e+03	778	5	1.1	751.2	US-08-104-	Sequence 2, Applicatio	2.13e+03
706	5	1.1	595.3	US-08-478-	Sequence 8, Applicatio	2.13e+03	779	5	1.1	751.2	US-08-422-	Sequence 2, Applicatio	2.13e+03
707	5	1.1	603.2	US-08-687-	Sequence 8, Applicatio	2.13e+03	780	5	1.1	761.1	US-08-192-	Sequence 4, Applicatio	2.13e+03
708	5	1.1	604.4	US-08-687-	Sequence 8, Applicatio	2.13e+03	781	5	1.1	764.4	US-08-192-	Sequence 4, Applicatio	2.13e+03
709	5	1.1	607.1	US-07-879-	Sequence 12, Applicati	2.13e+03	782	5	1.1	764.3	US-09-177-	Sequence 4, Applicatio	2.13e+03
710	5	1.1	610.1	US-08-410-	Sequence 1, Applicatio	2.13e+03	783	5	1.1	765.2	US-08-825-	Sequence 19, Applicatio	2.13e+03
711	5	1.1	610.3	US-08-970-	Sequence 2, Applicatio	2.13e+03	784	5	1.1	769.4	US-08-825-	Sequence 19, Applicatio	2.13e+03
712	5	1.1	610.3	US-08-455-	Sequence 2, Applicatio	2.13e+03	785	5	1.1	769.2	US-08-789-	Sequence 1, Applicatio	2.13e+03
713	5	1.1	612.4	US-08-240-	Sequence 3, Applicatio	2.13e+03	786	5	1.1	770.2	US-08-752-	Sequence 1, Applicatio	2.13e+03
714	5	1.1	617.4	US-08-240-	Sequence 3, Applicatio	2.13e+03	787	5	1.1	783.2	US-08-545-	Sequence 3, Applicatio	2.13e+03
715	5	1.1	618.2	US-08-770-	Sequence 3, Applicatio	2.13e+03	788	5	1.1	787.4	US-08-545-	Sequence 3, Applicatio	2.13e+03
716	5	1.1	619.4	US-08-770-	Sequence 3, Applicatio	2.13e+03	789	5	1.1	790.2	US-08-572-	Sequence 11, Applicati	2.13e+03
717	5	1.1	619.4	US-09-156-	Sequence 4, Applicatio	2.13e+03	790	5	1.1	791.2	US-08-728-	Sequence 3, Applicatio	2.13e+03
718	5	1.1	620.4	US-08-462-	Sequence 2, Applicatio	2.13e+03	791	5	1.1	789.2	US-08-838-	Sequence 4, Applicatio	2.13e+03
719	5	1.1	621.1	US-08-462-	Sequence 2, Applicatio	2.13e+03	792	5	1.1	793.2	US-08-469-	Sequence 2, Applicatio	2.13e+03
720	5	1.1	624.2	US-08-596-	Sequence 9, Applicatio	2.13e+03	793	5	1.1	794.2	US-08-359-	Sequence 9, Applicatio	2.13e+03
721	5	1.1	624.2	US-08-596-	Sequence 9, Applicatio	2.13e+03	794	5	1.1	794.2	US-07-885-	Sequence 9, Applicatio	2.13e+03
722	5	1.1	626.2	US-08-596-	Sequence 9, Applicatio	2.13e+03	795	5	1.1	797.2	US-08-453-	Sequence 11, Applicati	2.13e+03
723	5	1.1	636.2	US-08-460-	Sequence 3, Applicatio	2.13e+03	796	5	1.1	797.2	US-08-453-	Sequence 11, Applicati	2.13e+03
724	5	1.1	638.2	US-07-888-	Sequence 22, Applicati	2.13e+03	797	5	1.1	797.2	US-08-453-	Sequence 11, Applicati	2.13e+03
725	5	1.1	649.4	US-08-472-	Sequence 2, Applicatio	2.13e+03	798	5	1.1	800.2	US-08-913-	Sequence 4, Applicatio	2.13e+03
726	5	1.1	649.4	US-08-472-	Sequence 2, Applicatio	2.13e+03	799	5	1.1	807.4	US-08-913-	Sequence 4, Applicatio	2.13e+03
727	5	1.1	649.4	US-08-472-	Sequence 2, Applicatio	2.13e+03	800	5	1.1	811.2	US-08-935-	Sequence 4, Applicatio	2.13e+03
728	5	1.1	659.2	US-08-484-	Sequence 20, Applicati	2.13e+03	801	5	1.1	821.1	US-07-928-	Sequence 2, Applicatio	2.13e+03
729	5	1.1	659.2	US-08-484-	Sequence 20, Applicati	2.13e+03	802	5	1.1	821.1	US-08-261-	Sequence 2, Applicatio	2.13e+03
730	5	1.1	660.4	US-08-484-	Sequence 20, Applicati	2.13e+03	803	5	1.1	821.1	US-08-261-	Sequence 2, Applicatio	2.13e+03
731	5	1.1	660.4	US-08-484-	Sequence 20, Applicati	2.13e+03	804	5	1.1	831.1	US-08-405-	Sequence 5, Applicatio	2.13e+03
732	5	1.1	660.4	US-08-484-	Sequence 20, Applicati	2.13e+03	805	5	1.1	831.1	US-08-405-	Sequence 5, Applicatio	2.13e+03
733	5	1.1	660.4	US-08-484-	Sequence 20, Applicati	2.13e+03	806	5	1.1	832.1	US-08-463-	Sequence 1, Applicatio	2.13e+03
734	5	1.1	660.4	US-08-484-	Sequence 20, Applicati	2.13e+03	807	5	1.1	836.1	US-07-998-	Sequence 1, Applicatio	2.13e+03
735	5	1.1	660.4	US-08-484-	Sequence 20, Applicati	2.13e+03	808	5	1.1	836.1	US-08-453-	Sequence 1, Applicatio	2.13e+03
736	5	1.1	660.4	US-08-484-	Sequence 20, Applicati	2.13e+03	809	5	1.1	837.1	US-08-268-	Sequence 1, Applicatio	2.13e+03
737	5	1.1	661.2	US-08-833-	Sequence 4, Applicatio	2.13e+03	810	5	1.1	837.1	US-07-923-	Sequence 1, Applicatio	2.13e+03
738	5	1.1	667.2	US-08-718-	Sequence 7, Applicatio	2.13e+03	811	5	1.1	842.4	US-07-923-	Sequence 1, Applicatio	2.13e+03
739	5	1.1	667.2	US-08-718-	Sequence 7, Applicatio	2.13e+03	812	5	1.1	844.4	US-07-923-	Sequence 1, Applicatio	2.13e+03
740	5	1.1	669.2	US-08-300-	Sequence 8, Applicatio	2.13e+03	813	5	1.1	845.3	US-08-804-	Sequence 1, Applicatio	2.13e+03
741	5	1.1	669.2	US-08-300-	Sequence 8, Applicatio	2.13e+03	814	5	1.1	846.1	US-08-451-	Sequence 1, Applicatio	2.13e+03
742	5	1.1	669.2	US-08-300-	Sequence 8, Applicatio	2.13e+03	815	5	1.1	856.3	5196526-1	Sequence 4, Applicatio	2.13e+03
743	5	1.1	669.2	US-08-300-	Sequence 8, Applicatio	2.13e+03	816	5	1.1	857.3	5196526-1	Sequence 4, Applicatio	2.13e+03
744	5	1.1	675.4	US-08-456-	Sequence 10, Applicati	2.13e+03	817	5	1.1	857.3	US-08-804-	Sequence 10, Applicati	2.13e+03
745	5	1.1	680.2	US-08-436-	Sequence 2, Applicatio	2.13e+03	818	5	1.1	857.3	US-08-804-	Sequence 10, Applicati	2.13e+03
746	5	1.1	681.3	US-09-183-	Sequence 4, Applicatio	2.13e+03	819	5	1.1	868.1	US-08-251-	Sequence 11, Applicati	2.13e+03
747	5	1.1	681.3	US-09-183-	Sequence 4, Applicatio	2.13e+03	820	5	1.1	868.1	US-08-413-	Sequence 7, Applicatio	2.13e+03
748	5	1.1	682.1	US-07-998-	Sequence 107, Applicat	2.13e+03	821	5	1.1	873.3	US-09-187-	Sequence 6, Applicatio	2.13e+03
749	5	1.1	682.1	US-07-998-	Sequence 107, Applicat	2.13e+03	822	5	1.1	880.1	US-08-445-	Sequence 10, Applicati	2.13e+03
750	5	1.1	682.4	US-08-453-	Sequence 107, Applicat	2.13e+03	823	5	1.1	883.2	US-08-596-	Sequence 2, Applicatio	2.13e+03
751	5	1.1	682.4	US-08-453-	Sequence 107, Applicat	2.13e+03	824	5	1.1	884.5	5208144-8	Sequence 2, Applicatio	2.13e+03
752	5	1.1	683.5	US-08-453-	Sequence 107, Applicat	2.13e+03	825	5	1.1	884.2	US-08-471-	Sequence 2, Applicatio	2.13e+03
753	5	1.1	689.1	US-08-454-	Sequence 18, Applicati	2.13e+03	826	5	1.1	886.2	US-08-474-	Sequence 65, Applicati	2.13e+03

827	1.1	888	1	US-08-445-	Sequence 35, Applicant	2.13e+03	900	1.1	1184	2	US-08-639-	Sequence 32, Applicant	2.13e+03
828	1.1	890	1	US-08-445-	Sequence 2, Applicant	2.13e+03	901	1.1	1188	5	5254799-7	Sequence 32, Applicant	2.13e+03
829	1.1	898	1	US-08-036-	Sequence 22, Applicant	2.13e+03	902	1.1	1189	5	5188960-6	Sequence 8, Applicant	2.13e+03
830	1.1	904	1	US-08-453-	Sequence 97, Applicant	2.13e+03	903	1.1	1189	5	5188960-6	Sequence 6, Applicant	2.13e+03
831	1.1	904	4	US-08-453-	Sequence 19, Applicant	2.13e+03	904	1.1	1189	1	US-08-356-	Sequence 4, Applicant	2.13e+03
832	1.1	912	4	US-08-425-	Sequence 21, Applicant	2.13e+03	905	1.1	1189	2	US-08-980-	Sequence 5, Applicant	2.13e+03
833	1.1	915	1	US-08-328-	Sequence 2, Applicant	2.13e+03	906	1.1	1189	2	US-08-980-	Sequence 6, Applicant	2.13e+03
834	1.1	915	2	US-08-723-	Sequence 2, Applicant	2.13e+03	907	1.1	1189	2	US-08-980-	Sequence 6, Applicant	2.13e+03
835	1.1	915	2	US-08-839-	Sequence 16, Applicant	2.13e+03	908	1.1	1189	2	US-08-980-	Sequence 6, Applicant	2.13e+03
836	1.1	917	4	US-08-839-	Sequence 14, Applicant	2.13e+03	909	1.1	1189	2	US-08-980-	Sequence 6, Applicant	2.13e+03
837	1.1	948	2	US-08-162-	Sequence 2, Applicant	2.13e+03	910	1.1	1189	2	US-08-980-	Sequence 6, Applicant	2.13e+03
838	1.1	951	1	US-08-162-	Sequence 2, Applicant	2.13e+03	911	1.1	1189	2	US-08-980-	Sequence 6, Applicant	2.13e+03
839	1.1	969	4	US-08-752-	Sequence 7, Applicant	2.13e+03	912	1.1	1190	1	US-08-317-	Sequence 12, Applicant	2.13e+03
840	1.1	970	1	US-08-449-	Sequence 18, Applicant	2.13e+03	913	1.1	1193	1	US-08-825-	Sequence 22, Applicant	2.13e+03
841	1.1	976	4	US-08-058-	Sequence 6, Applicant	2.13e+03	914	1.1	1205	2	US-08-819-	Sequence 10, Applicant	2.13e+03
842	1.1	979	4	US-08-058-	Sequence 6, Applicant	2.13e+03	915	1.1	1213	2	US-08-937-	Sequence 2, Applicant	2.13e+03
843	1.1	985	4	US-08-058-	Sequence 6, Applicant	2.13e+03	916	1.1	1220	1	US-08-158-	Sequence 4, Applicant	2.13e+03
844	1.1	985	4	US-08-058-	Sequence 6, Applicant	2.13e+03	917	1.1	1226	1	US-08-555-	Sequence 2, Applicant	2.13e+03
845	1.1	985	4	US-08-058-	Sequence 6, Applicant	2.13e+03	918	1.1	1229	1	US-08-474-	Sequence 4, Applicant	2.13e+03
846	1.1	985	4	US-08-058-	Sequence 6, Applicant	2.13e+03	919	1.1	1245	2	US-08-801-	Sequence 6, Applicant	2.13e+03
847	1.1	997	2	US-08-384-	Sequence 50, Applicant	2.13e+03	920	1.1	1245	2	US-08-801-	Sequence 6, Applicant	2.13e+03
848	1.1	997	2	US-08-384-	Sequence 50, Applicant	2.13e+03	921	1.1	1248	2	US-08-801-	Sequence 6, Applicant	2.13e+03
849	1.1	997	2	US-08-384-	Sequence 50, Applicant	2.13e+03	922	1.1	1255	2	US-08-801-	Sequence 6, Applicant	2.13e+03
850	1.1	1018	1	US-08-072-	Sequence 2, Applicant	2.13e+03	923	1.1	1271	3	US-08-095-	Sequence 2, Applicant	2.13e+03
851	1.1	1022	3	US-08-072-	Sequence 2, Applicant	2.13e+03	924	1.1	1271	3	US-08-095-	Sequence 2, Applicant	2.13e+03
852	1.1	1025	4	US-08-304-	Sequence 2, Applicant	2.13e+03	925	1.1	1280	5	5206352-4	Sequence 2, Applicant	2.13e+03
853	1.1	1055	2	US-08-304-	Sequence 2, Applicant	2.13e+03	926	1.1	1280	5	5206352-4	Sequence 2, Applicant	2.13e+03
854	1.1	1089	4	US-08-180-	Sequence 36, Applicant	2.13e+03	927	1.1	1289	5	5426049-4	Sequence 2, Applicant	2.13e+03
855	1.1	1089	4	US-08-180-	Sequence 36, Applicant	2.13e+03	928	1.1	1289	5	5426049-4	Sequence 2, Applicant	2.13e+03
856	1.1	1089	4	US-08-180-	Sequence 36, Applicant	2.13e+03	929	1.1	1289	5	5426049-4	Sequence 2, Applicant	2.13e+03
857	1.1	1089	4	US-08-180-	Sequence 36, Applicant	2.13e+03	930	1.1	1289	5	5426049-4	Sequence 2, Applicant	2.13e+03
858	1.1	1089	4	US-08-180-	Sequence 36, Applicant	2.13e+03	931	1.1	1289	5	5426049-4	Sequence 2, Applicant	2.13e+03
859	1.1	1089	4	US-08-180-	Sequence 36, Applicant	2.13e+03	932	1.1	1289	5	5426049-4	Sequence 2, Applicant	2.13e+03
860	1.1	1091	2	US-08-311-	Sequence 25, Applicant	2.13e+03	933	1.1	1334	4	US-08-996-	Sequence 2, Applicant	2.13e+03
861	1.1	1091	2	US-08-311-	Sequence 25, Applicant	2.13e+03	934	1.1	1334	4	US-08-996-	Sequence 2, Applicant	2.13e+03
862	1.1	1104	2	US-08-327-	Sequence 5, Applicant	2.13e+03	935	1.1	1334	4	US-08-996-	Sequence 2, Applicant	2.13e+03
863	1.1	1104	2	US-08-327-	Sequence 5, Applicant	2.13e+03	936	1.1	1338	2	US-08-996-	Sequence 2, Applicant	2.13e+03
864	1.1	1118	1	US-08-278-	Sequence 2, Applicant	2.13e+03	937	1.1	1338	2	US-08-996-	Sequence 2, Applicant	2.13e+03
865	1.1	1138	1	US-08-220-	Sequence 5, Applicant	2.13e+03	938	1.1	1362	2	US-08-874-	Sequence 3, Applicant	2.13e+03
866	1.1	1148	1	US-08-239-	Sequence 23, Applicant	2.13e+03	939	1.1	1362	2	US-08-874-	Sequence 3, Applicant	2.13e+03
867	1.1	1148	2	US-08-239-	Sequence 27, Applicant	2.13e+03	940	1.1	1368	2	US-08-874-	Sequence 3, Applicant	2.13e+03
868	1.1	1148	2	US-08-239-	Sequence 27, Applicant	2.13e+03	941	1.1	1385	5	5426049-1	Sequence 34, Applicant	2.13e+03
869	1.1	1148	2	US-08-239-	Sequence 27, Applicant	2.13e+03	942	1.1	1385	5	5426049-1	Sequence 34, Applicant	2.13e+03
870	1.1	1148	2	US-08-239-	Sequence 27, Applicant	2.13e+03	943	1.1	1385	5	5426049-1	Sequence 34, Applicant	2.13e+03
871	1.1	1148	2	US-08-239-	Sequence 27, Applicant	2.13e+03	944	1.1	1385	5	5426049-1	Sequence 34, Applicant	2.13e+03
872	1.1	1148	2	US-08-239-	Sequence 27, Applicant	2.13e+03	945	1.1	1385	5	5426049-1	Sequence 34, Applicant	2.13e+03
873	1.1	1150	1	US-08-349-	Sequence 21, Applicant	2.13e+03	946	1.1	1403	1	US-08-699-	Sequence 17, Applicant	2.13e+03
874	1.1	1150	1	US-08-349-	Sequence 21, Applicant	2.13e+03	947	1.1	1403	1	US-08-699-	Sequence 17, Applicant	2.13e+03
875	1.1	1155	3	US-08-453-	Sequence 9, Applicant	2.13e+03	948	1.1	1456	1	US-08-026-	Sequence 4, Applicant	2.13e+03
876	1.1	1155	3	US-08-453-	Sequence 9, Applicant	2.13e+03	949	1.1	1456	1	US-08-026-	Sequence 4, Applicant	2.13e+03
877	1.1	1155	3	US-08-453-	Sequence 9, Applicant	2.13e+03	950	1.1	1477	2	US-08-530-	Sequence 4, Applicant	2.13e+03
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879	1.1	1162	2	US-08-021-	Sequence 2, Applicant	2.13e+03	952	1.1	1477	2	US-08-530-	Sequence 4, Applicant	2.13e+03
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881	1.1	1165	1	US-08-728-	Sequence 2, Applicant	2.13e+03	954	1.1	1477	2	US-08-530-	Sequence 4, Applicant	2.13e+03
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883	1.1	1167	2	US-08-881-	Sequence 4, Applicant	2.13e+03	956	1.1	1481	3	US-08-944-	Sequence 40, Applicant	2.13e+03
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885	1.1	1174	5	5188960-8	Sequence 2, Applicant	2.13e+03	958	1.1	1507	5	526870-2	Sequence 2, Applicant	2.13e+03
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897	1.1	1181	3	US-08-459-	Sequence 15, Applicant	2.13e+03	970	1.1	1863	4	US-08-825-	Sequence 6, Applicant	2.13e+03
898	1.1	1184	5	5254799-6	Sequence 17, Applicant	2.13e+03	971	1.1	1863	4	US-08-825-	Sequence 6, Applicant	2.13e+03
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975	5	1.1	2050	2	US-08-347-Sequence 2, Applicatio
976	5	1.1	2257	2	US-08-422-Sequence 10, Applicatio
977	5	1.1	2335	3	US-08-417-Sequence 6, Applicatio
978	5	1.1	2332	1	US-08-276-Sequence 2, Applicatio
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981	5	1.1	2549	4	PCT-US95-0-Sequence 12, Applicatio
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985	5	1.1	2813	3	US-08-896-Sequence 2, Applicatio
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988	5	1.1	3010	2	US-08-904-Sequence 2, Applicatio
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991	5	1.1	3011	1	PCT-US93-0-Sequence 2, Applicatio
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994	5	1.1	3165	5	5223423-4-Sequence 3, Applicatio
995	5	1.1	3224	2	US-08-705-Sequence 34, Applicatio
996	5	1.1	3248	4	PCT-US95-1-Sequence 1, Applicatio
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998	5	1.1	3778	2	US-08-222-Sequence 2, Applicatio
999	5	1.1	3959	2	US-08-970-Sequence 30, Applicatio
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ALIGNMENTS

PRT: 436 AA.

Sequence 2, Application US/08307588

Sequence 2, Application US/08307588
Patent No. 5919453

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVER, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patenting Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 11283/117/GUPL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 436 AA: 49723 MW, 1061275 CN;

Query Match 100.0%; Score 436; DB 2; Length 436;

Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY	121	TPFRKAGPPPVHLEAEKATVIRHSPTKDSVMALDGLSPTYSLLTKNKSQVEEI	180
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OY	361	VIQDPLIYEIIFWENTSNAERKIEKTDVVPNLKPLTVYCVARATHDEKLNKSSV	420
DB	421	FSDVCEKTKPKNTSK 436	
OY	421	FSDVCEKTKPKNTSK 436	

Sequence 2, Application US/08471454
Patent No. 5731169.1

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTPALA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

RESULT 3
ID US-08-466-974-2 STANDARD; PRT: 557 AA.
XX xxxxxx
XX
XX
DT
XX
DE Sequence 2, Application US/08466974
XX
CC Sequence 2, Application US/08466974
CC Patent No. 5861258;
CC GENERAL INFORMATION:
CC APPLICANT: MOGENSEN, Knud E.
CC APPLICANT: UZE, Gilles
CC APPLICANT: LUTFALLA, Georges
CC APPLICANT: GRESSER, Ion
CC TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
CC TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
CC TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: NIXON & VANDERHAYE, P.C.
CC STREET: 1100 NORTH GLEBE ROAD
CC CITY: ARLINGTON
CC STATE: VIRGINIA
CC COUNTRY: U.S.A.
CC ZIP: 22201-4714
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/466,974
CC FILING DATE: 06-JUN-1995

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CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: US 07/900,642
CC CC FILING DATE: 15-JUN-1992
CC CC APPLICATION NUMBER: FR 89/13770
CC CC FILING DATE: 20-OCT-1989
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: BYRNE, THOMAS E.
CC CC REGISTRATION NUMBER: 32,205
CC CC REFERENCE/DOCKET NUMBER: 960-7
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: (703) 816-4000
CC CC TELEFAX: (703) 816-4100
CC CC TELEX: 200797 NIXN UR
CC CC INFORMATION FOR SEQ ID NO: 2:
CC CC     SEQUENCE CHARACTERISTICS:
CC CC         LENGTH: 557 amino acids
CC CC         TYPE: amino acid
CC CC         STRANDEDNESS: single
CC CC         TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
CC CC QUANTITY: 1
SQ    SEQUENCE 557 AA; 63525 MW; 1717510 CN;
Query Match      100.0%   Score 436, DB 2, Length 557;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MAVVLLGATTVLYLVAVGFWVLSSAAGGNLNLSPOKVEVDIIDNFILRMNSDESQVNT 60
Db 1 FSPFYOKTGDMNWIKISGCCNITSTKCNFSFLAKLNYEELRLIRAREKENTSMYEDSF 120
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OY 301 GYLLARVQASDGNNTSPWSEIKFDEIOAFLLPVPVNIISLSDSFHIIYGAPQSGNTP 360
DB 361 VIQDYPLIYEIIFWENTSNMERKIIKKTDTVPNKLPLVYCYKAAHPTMDEKLNSV 420
OY 361 VIQDYPLIYEIIFWENTSNMERKIIKKTDTVPNKLPLVYCYKAAHPTMDEKLNSV 420
DB 421 FSDAVCEKTRPGNTSK 436
OY 421 FSDAVCEKTRPGNTSK 436

RESULT

4 US-08-471-453-2 STANDARD; PRT: 557 AA.

AC XXXXXX

DE Sequence 2, Application US/08471453

CC Sequence 2, Application US/08471453
CC Patent No. 5886153
CC GENERAL INFORMATION:
CC APPLICANT: MOGENSEN, Knud E.
CC APPLICANT: UZE, Gilles
CC APPLICANT: LOTFALLA, Georges
CC APPLICANT: GRESSER, Ion
CC TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
CC TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
CC TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: NIXON & VANDERHAYE P. C.
CC STREET: 1100 NORTH GLEBE ROAD
CC CITY: ARLINGTON
CC STATE: VIRGINIA
CC COUNTRY: U.S.A.
CC ZIP: 22201-4714

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/471.453
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/900,642
CC FILING DATE: 15-JUN-1992
CC APPLICATION NUMBER: FR 89/13770
CC FILING DATE: 20-OCT-1989
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BYRNE, THOMAS E.
CC REGISTRATION NUMBER: 32,205
CC REFERENCE/DOCKET NUMBER: 960-7
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (703) 816-4000
CC TELEFAX: (703) 816-4100
CC TELEX: 200797 NIKX UR
CC INFORMATION FOR SEQ ID NO: 2:

CC INFORMATION FOR SEQ ID NO: 2:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 557 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 557 AA; 63525 MW; 1717510 CN;

Query Match 100.0%; Score 436; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMYVLGATTLVLYAVGPWVLSAAGKRNLSKPKYEVVDIIDDFFILRNRSDSVGNVT 60
OY 1 MMYVLGATTLVLYAVGPWVLSAAGKRNLSKPKYEVVDIIDDFFILRNRSDSVGNVT 60
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OY 361 VIQDYPLIYEIIFWENTSNMERKIIKKTDTVPNKLPLVYCYKAAHPTMDEKLNSV 420
DB 421 FSDAVCEKTRPGNTSK 436
OY 421 FSDAVCEKTRPGNTSK 436

RESULT

5 US-08-328-256-10 STANDARD; PRT: 557 AA.

AC XXXXXX

DE Sequence 10, Application US/08328256

CC Sequence 10, Application US/08328256
CC Patent No. 5643749
CC GENERAL INFORMATION:
CC APPLICANT: REVEL, Michel
CC APPLICANT: ABRAMOVICH, Carolina
CC APPLICANT: RATOYITSKI, Edward
CC TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BROWDY AND NETMARK
CC STREET: 419 Seventh Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20004
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible

Query Match	100.0%;	Score 436;	DB 1;	Length 557;
Best Local Similarity	100.0%;	Pred. No. 0.00e+00;		
Matches 436; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Sequence 4, Application US/08307588
Sequence 4, Application US/08307588
Patent No. 5919453

Query Match	100.0%	Score 436	DB 2	Length 557
Best Local Similarity	100.0%	Pred. No. 0.00e+00		
Matches	436	Conservative	0	Mismatches 0
			Indels	0
			Gaps	0

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301 GYLLRVQASDGNNTSFMSSEIKFETLEIQAEFLPPVFNIRSLSDSFHYICAPQSGNTP 366c
|||||

Db 361 VIODYPLIYEIEMENTSNAERKIIIEKTDVTPNKLPLTVYCYKARAHMDEKLNSSV 420
OY 361 VIODYPLIYEIEMENTSNAERKIIIEKTDVTPNKLPLTVYCYKARAHMDEKLNSSV 420
Db 421 FSDAVCEKTRKGNJSK 436
OY 421 FSDAVCEKTRKGNJSK 436

RESULT 7
ID US-08-328-256-11 STANDARD: PRT: 434 AA.
XX xxxxxx

Sequence 11, Application US/08328256

CC Sequence 11, Application US/08328256
CC Patent No. 5643749
CC GENERAL INFORMATION:
CC APPLICANT: REVEL, Michel
CC APPLICANT: ABRAMOVICH, Carolina
CC APPLICANT: RATOVIJSKI, Edward
CC TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
CC TITLE OF INVENTION: PREPARATION AND USE
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BROMDY AND NEIMARK
CC STREET: 419 Seventh Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20004
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/328,256
CC FILING DATE: 24-OCT-1994
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: IL 107378
CC FILING DATE: 24-OCT-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BROMDY, Roger L.
CC REGISTRATION NUMBER: REVEL-13
CC REFERENCE/DOCKET NUMBER: 25,618
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-628-5197
CC TELEFAX: 202-737-3528
CC TELEX: 248633
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 434 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 434 AA: 49546 MW: 1042221 CN:

Query Match 97.9%; Score 427; DB 1; Length 434;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMYVLLGATTLVAVGPMVLSAAGGKNLSKSPQKVEVDIIDNFILRNRSDESNGVNT 60
OY 1 MMYVLLGATTLVAVGPMVLSAAGGKNLSKSPQKVEVDIIDNFILRNRSDESNGVNT 60
Db 61 FSDYOKTGADNNIKLSGCONITSTKCNFSSKLNLVYEEIKLRIRAKENTSSMYEDSF 120
OY 61 FSDYOKTGADNNIKLSGCONITSTKCNFSSKLNLVYEEIKLRIRAKENTSSMYEDSF 120

Db 121 TPERKAOIGPPEVHLEEDAAIVIHISPGTRDSYMAALDGLSFYSLILMKNSSGVEERI 180
OY 121 TPERKAOIGPPEVHLEEDAAIVIHISPGTRDSYMAALDGLSFYSLILMKNSSGVEERI 180
Db 181 ENIYSRKIKYLSPEYTYCKVKAALLTSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
OY 181 ENIYSRKIKYLSPEYTYCKVKAALLTSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
Db 241 NONYVLKMDYTYANMFQVOVOMLAFLKRNNGNHLKKKQIPDCENVYTCQVPONFQK 300
OY 241 NONYVLKMDYTYANMFQVOVOMLAFLKRNNGNHLKKKQIPDCENVYTCQVPONFQK 300
Db 301 GYLLRVOASDGNNSTFSWESEIKFDEIQAFLPPVFNISLSDSFHIYIGAPQSGNTP 360
OY 301 GYLLRVOASDGNNSTFSWESEIKFDEIQAFLPPVFNISLSDSFHIYIGAPQSGNTP 360
Db 361 VIODYPLIYEIEMENTSNAERKIIIEKTDVTPNKLPLTVYCYKARAHMDEKLNSSV 420
OY 361 VIODYPLIYEIEMENTSNAERKIIIEKTDVTPNKLPLTVYCYKARAHMDEKLNSSV 420
Db 421 FSDAVCE 427
OY 421 FSDAVCE 427

RESULT 8
ID US-08-328-256-12 STANDARD: PRT: 496 AA.
XX xxxxxx

Sequence 12, Application US/08328256

CC Sequence 12, Application US/08328256
CC Patent No. 5643749
CC GENERAL INFORMATION:
CC APPLICANT: REVEL, Michel
CC APPLICANT: ABRAMOVICH, Carolina
CC APPLICANT: RATOVIJSKI, Edward
CC TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
CC TITLE OF INVENTION: PREPARATION AND USE
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BROMDY AND NEIMARK
CC STREET: 419 Seventh Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20004
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/328,256
CC FILING DATE: 24-OCT-1994
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: IL 107378
CC FILING DATE: 24-OCT-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BROMDY, Roger L.
CC REGISTRATION NUMBER: REVEL-13
CC REFERENCE/DOCKET NUMBER: 25,618
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-628-5197
CC TELEFAX: 202-737-3528
CC TELEX: 248633
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 496 amino acids

CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 496 AA; 56718 MM; 1344690 CN;
Query Match 94.7%; Score 413; DB 1; Length 496;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MMVLLGATLVLYAVAVPMTLSAAGKRLKSPQKVEVDIIDNFILRMNRSDSYCVNT 60
1 MMVLLGATLVLYAVAVPMTLSAAGKRLKSPQKVEVDIIDNFILRMNRSDSYCVNT 60
DB 61 FSDYQKGTGMDNWKISGCONITSTKCNFSSLKLVYEEIKRLIRAKENTSSMYEVSF 120
61 FSDYQKGTGMDNWKISGCONITSTKCNFSSLKLVYEEIKRLIRAKENTSSMYEVSF 120
QY 61 FSDYQKGTGMDNWKISGCONITSTKCNFSSLKLVYEEIKRLIRAKENTSSMYEVSF 120
DB 121 TPRKQIGPPEVHLEEDAKIYHISPGTKDSYMAALDGLSTFYSLIKNNSGVEERI 180
121 TPRKQIGPPEVHLEEDAKIYHISPGTKDSYMAALDGLSTFYSLIKNNSGVEERI 180
QY 181 ENIYSRHKIKLSPETTYCKLVKRAALTSMKIGVSPVHCIKTVENELPPEXIEVSQ 240
181 ENIYSRHKIKLSPETTYCKLVKRAALTSMKIGVSPVHCIKTVENELPPEXIEVSQ 240
DB 241 NQNVYLMKYDYANMTFQVOMLHAFKRNPNHLYKWKQIPDCENVTTCCVFPQNVFK 300
241 NQNVYLMKYDYANMTFQVOMLHAFKRNPNHLYKWKQIPDCENVTTCCVFPQNVFK 300
QY 241 NQNVYLMKYDYANMTFQVOMLHAFKRNPNHLYKWKQIPDCENVTTCCVFPQNVFK 300
DB 301 GYLLRVQASDGNNTSWSEIKFDTETIOAFLLPVPVNISSLSDFIYIGAPKQSGNTP 360
301 GYLLRVQASDGNNTSWSEIKFDTETIOAFLLPVPVNISSLSDFIYIGAPKQSGNTP 360
QY 301 GYLLRVQASDGNNTSWSEIKFDTETIOAFLLPVPVNISSLSDFIYIGAPKQSGNTP 360
DB 361 VIQDYPLIYIIFEMTSMNAEKIIEKTDVTPNKLPLVYCVKARAHMTDE 413
361 VIQDYPLIYIIFEMTSMNAEKIIEKTDVTPNKLPLVYCVKARAHMTDE 413
QY 361 VIQDYPLIYIIFEMTSMNAEKIIEKTDVTPNKLPLVYCVKARAHMTDE 413
RESULT 9
ID US-08-488-379-243 STANDARD; PRT; 17 AA.
XX xxxxxx
DE Sequence 243, Application US/08488379
CC Sequence 243, Application US/08488379
CC Patent No. 5580103
CC GENERAL INFORMATION:
CC APPLICANT: Robert G. Urban
CC APPLICANT: Roman M. Chicz
CC APPLICANT: Dario A. A. Vignali
CC APPLICANT: Mary L. Hedley
CC APPLICANT: Lawrence J. Stern
CC APPLICANT: Jack L. Strominger
CC TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
CC NUMBER OF SEQUENCES: 274
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson
CC STREET: 225 Franklin Street
CC CITY: Boston
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02110-2804
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB
CC COMPUTER: IBM PS/2 Model 502 or 55SX
CC OPERATING SYSTEM: MS-DOS (Version 5.0)
CC SOFTWARE: WordPerfect (Version 5.1)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/488-379

CC FILING DATE: 514
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/077,255
CC FILING DATE: June 15, 1993
CC APPLICATION NUMBER: 07/925,460
CC FILING DATE: August 11, 1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clark, Paul T.
CC REGISTRATION NUMBER: 30,162
CC REFERENCE/DOCKET NUMBER: 00246/168001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 542-8970
CC TELEFAX: (617) 542-8906
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 243:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 17
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
SQ SEQUENCE 17 AA; 2072 MM; 1573 CN;
Query Match 3.9%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.24e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 GNLHYKWKQIPDCENVK 17
271 GNLHYKWKQIPDCENVK 287
QY 271 GNLHYKWKQIPDCENVK 287
RESULT 10
ID PCT-US93-07545-243 STANDARD; PRT; 17 AA.
XX xxxxxx
DE Sequence 243, Application PC/TUS9307545
CC Sequence 243, Application PC/TUS9307545
CC GENERAL INFORMATION:
CC APPLICANT: Robert G. Urban
CC APPLICANT: Roman M. Chicz
CC APPLICANT: Dario A. A. Vignali
CC APPLICANT: Mary L. Hedley
CC APPLICANT: Lawrence J. Stern
CC APPLICANT: Jack L. Strominger
CC TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
CC NUMBER OF SEQUENCES: 273
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Fish & Richardson
CC STREET: 225 Franklin Street
CC CITY: Boston
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02110-2804
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB
CC COMPUTER: IBM PS/2 Model 502 or 55SX
CC OPERATING SYSTEM: MS-DOS (Version 5.0)
CC SOFTWARE: WordPerfect (Version 5.1)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/07545
CC FILING DATE: 19930811
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/925,460
CC FILING DATE: August 11, 1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clark, Paul T.
CC REGISTRATION NUMBER: 30,162

CC REFERENCE/DOCKET NUMBER: 00246/168001
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 542-5070
CC TELEFAX: (617) 542-8906
CC TELEX: 200154
CC INFORMATION FOR SEQ ID NO: 243:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 17
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC SEQUENCE 17 AA: 2072 MM; 1573 CN;
SO
Query Match 3.9%; Score 17; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.24e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 GNHLTKMKRQIPDCENVK 17
QY 271 GNHLTKMKRQIPDCENVK 287
RESULT 11
ID US-08-480-190-243 STANDARD; PRT: 17 AA.
XX xxxxxx
DT
XX
DE Sequence 243, Application US/08480190
Sequence 243, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignall
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480.190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:

CC LENGTH: 17
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC SEQUENCE 17 AA: 2072 MM; 1573 CN;
SO
Query Match 3.9%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.24e-12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 GNHLTKMKRQIPDCENVK 17
QY 271 GNHLTKMKRQIPDCENVK 287
RESULT 12
ID US-08-328-256-9 STANDARD; PRT: 56 AA.
XX xxxxxx
DT
XX
DE Sequence 9, Application US/08328256
Sequence 9, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVIITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328.256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 56 AA: 6323 MM; 16937 CN;
SO
Query Match 3.7%; Score 16; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.39e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 PLTYTCVARRAHYMD 16
IIIIIIIIIIIIIIIIIIII

Sequence 4, Application US/08328256

STATE: CA

CC COUNTRY: US
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/241,387
 CC FILING DATE: 10-MAY-1994
 CC CLASSIFICATION: 530
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER: USSN 07/695,564
 CC FILING DATE: 03-MAY-1004
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: TSR241.001
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 9:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 153 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: unknown
 CC MOLECULE TYPE: protein
 CC HYPOTHEICAL: YES
 CC ANTI-SENSE: NO
 CC FRAGMENT TYPE: Internal
 CC FEATURE:
 CC NAME/KEY: Region
 CC LOCATION: 1..153
 CC OTHER INFORMATION: /note- "SEQ ID NO:9 is the 153
 CC OTHER INFORMATION: amino acid sequence predicted from the product
 CC OTHER INFORMATION: which results from amplification of the mouse
 CC FEATURE:
 CC NAME/KEY: Domain
 CC LOCATION: 108..112
 CC OTHER INFORMATION: /note- "The cytoplasmic sequence
 CC OTHER INFORMATION: CDEPK begins at amino acid position 108."
 CC SEQUENCE 153 AA; 17843 MW; 134354 CN;
 CC
 CC Query Match 1.6%; Score 7; DB 1; Length 153;
 CC Best Local Similarity 100.0%; Pred. No. 2.03e+01;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 86 LVLVAVG 92
 11 LVLVAVG 17
 QY
 RESULT 16
 ID US-07-695-564-9 STANDARD; PRT; 153 AA.
 AC xxxxxx
 DE Sequence 9, Application US/07695564
 CC Patent No. 5310874
 CC GENERAL INFORMATION:
 CC APPLICANT: Tamura, Richard N.
 CC TITLE OF INVENTION: INTEGRIN ALPHA SUBUNIT CYTOPLASMIC
 CC TITLE OF INVENTION: DOMAIN POLYPEPTIDES, ANTIBODIES AND METHODS
 CC NUMBER OF SEQUENCES: 16
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Thomas Fitting
 CC STREET: 11300 Sorrento Valley Road, Suite 200
 CC CITY: San Diego

CC STATE: California
 CC COUNTRY: United States
 CC ZIP: 92121
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patentin Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/695,564
 CC FILING DATE: 19910503
 CC CLASSIFICATION: 435
 CC PRIORITY APPLICATION DATA:
 CC APPLICATION NUMBER:
 CC FILING DATE:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCRO377P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-546-1555
 CC INFORMATION FOR SEQ ID NO: 9:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 153 amino acids
 CC TYPE: AMINO ACID
 CC TOPOLOGY: unknown
 CC MOLECULE TYPE: protein
 CC HYPOTHEICAL: YES
 CC ANTI-SENSE: NO
 CC FRAGMENT TYPE: Internal
 CC FEATURE:
 CC NAME/KEY: Region
 CC LOCATION: 1..153
 CC OTHER INFORMATION: /note- "SRD ID NO:9 is the 153
 CC OTHER INFORMATION: amino acid sequence predicted from the product
 CC OTHER INFORMATION: which results from amplification of the mouse
 CC OTHER INFORMATION: ALPHA 3B CDNA with primers 2032/2033."
 CC FEATURE:
 CC NAME/KEY: Domain
 CC LOCATION: 108..112
 CC OTHER INFORMATION: /note- "The cytoplasmic sequence
 CC OTHER INFORMATION: CDEPK begins at amino acid position 108."
 CC SEQUENCE 153 AA; 17843 MW; 134354 CN;
 CC
 CC Query Match 1.6%; Score 7; DB 1; Length 153;
 CC Best Local Similarity 100.0%; Pred. No. 2.03e+01;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 86 LVLVAVG 92
 11 LVLVAVG 17
 QY
 RESULT 17
 ID PCT-US94-14277-3 STANDARD; PRT; 202 AA.
 AC xxxxxx
 DE Sequence 3, Application PC/TUS9414277
 CC Patent No. 5310874
 CC GENERAL INFORMATION:
 CC APPLICANT: Aguet, Michel
 CC TITLE OF INVENTION: INTEGRIN ALPHA SUBUNIT CYTOPLASMIC
 CC TITLE OF INVENTION: RECEPTOR SUBUNIT POLYPEPTIDES
 CC NUMBER OF SEQUENCES: 8
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Genentech, Inc.
 CC STREET: 460 Point San Bruno Blvd
 CC CITY: South San Francisco

CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PC7/US94/14277
CC FILING DATE: 07-DEC-1994
CC CLASSIFICATION:
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: 08/164596
CC FILING DATE: 09-DEC-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Love, Richard B.
CC REGISTRATION NUMBER: 34,659
CC REFERENCE/DOCKET NUMBER: 866PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-5530
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 202 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SO SEQUENCE 202 AA; 23375 MW; 241129 CN;

Query Match 1.6%; Score 7; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 168 PETTYCL 174
1111111
QY 194 PETTYCL 200

RESULT 18
ID US-08-943-087-50 STANDARD; PRT; 221 AA.
XX xxxxxx

Sequence 50, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
CC APPLICANT: Lok, SI
CC APPLICANT: rho, Choon J.
CC APPLICANT: jelmeberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Fairish, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943.087

CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 50:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 221 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SO SEQUENCE 221 AA; 25263 MW; 276613 CN;

Query Match 1.6%; Score 7; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 QIGPPEV 113
1111111
QY 127 QIGPPEV 133

RESULT 19
ID US-08-943-087-54 STANDARD; PRT; 221 AA.
XX xxxxxx

Sequence 54, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
CC APPLICANT: Lok, SI
CC APPLICANT: rho, Choon J.
CC APPLICANT: jelmeberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Fairish, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943.087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G

CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 54:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 221 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SEQUENCE 221 AA; 25263 MW; 276805 CN;
SQ
Query Match 1.6%; Score 7; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 107 QIGPPEV 113
QY 127 QIGPPEV 133
DB 107 QIGPPEV 113
QY 127 QIGPPEV 133
RESULT 20
ID US-08-943-087-58 STANDARD; PRT; 221 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 58, Application US/08943087
XX
CC Sequence 58, Application US/08943087
CC Patent No. 5945511
CC GENERAL INFORMATION:
CC APPLICANT: Lok, SI
CC APPLICANT: Kho, Choon J.
CC APPLICANT: Jelmeberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Parrish, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943,087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G.
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 58:
CC INFORMATION FOR SEQ ID NO: 58:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 221 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SEQUENCE 221 AA; 25179 MW; 274987 CN;
SQ
Query Match 1.6%; Score 7; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 107 QIGPPEV 113
QY 127 QIGPPEV 133
DB 107 QIGPPEV 113
QY 127 QIGPPEV 133
RESULT 21
ID US-08-943-087-52 STANDARD; PRT; 221 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 52, Application US/08943087
XX
CC Sequence 52, Application US/08943087
CC Patent No. 5945511
CC GENERAL INFORMATION:
CC APPLICANT: Lok, SI
CC APPLICANT: Kho, Choon J.
CC APPLICANT: Jelmeberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Parrish, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943,087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G.
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 52:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 221 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal

SO SEQUENCE 221 AA: 25235 MW: 277495 CN;

Query Match 1.6%; Score 7; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 107 QIGPPEV 113

OY 127 QIGPPEV 133

RESULT 22
ID US-08-943-087-56 STANDARD; PRT: 221 AA.

AC xxxxxx

1

Sequence 56, Application US/08943087

Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kno, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Robyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Farrah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,087

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24CI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 221 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE 221 AA: 25207 MW: 276174 CN;

Query Match 1.6%; Score 7; DB 2; Length 221;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 107 QIGPPEV 113

OY 127 QIGPPEV 133

RESULT 23
ID US-08-961-264-3 STANDARD; PRT: 258 AA.

AC xxxxxx

Sequence 3, Application US/08961264

Patent No. 6025331

GENERAL INFORMATION:

APPLICANT: Moses, Marsha A.

APPLICANT: Langer, Robert S.

APPLICANT: Wiederschain, Dimitri G.

APPLICANT: Wu, Imiin

APPLICANT: Sytkowski, Arthur

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: COMPRISING TROPONIN SUBUNITS, FRAGMENTS AND ANALOGS

TITLE OF INVENTION: THEREOF AND METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,264

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/602,941

FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,452

REFERENCE/DOCKET NUMBER: 8657-021-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-869-8864/9741

TELEFAX: 212-790-9090

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 258 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6025331e

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..258

OTHER INFORMATION: //Label- Human Fast Skeletal Beta

OTHER INFORMATION: Troponin T

SEQUENCE 258 AA: 30596 MW: 286474 CN;

Query Match 1.6%; Score 7; DB 3; Length 258;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 108 RIRAEKE 114

OY 103 RIRAEKE 109


```

DE XX      Sequence 8, Application PC/TUS9414277
CC XX      .GENERAL INFORMATION:
CC          APPLICANT: Aguet, Michel
CC          APPLICANT: Bohml, Ruth
CC          APPLICANT: Hemmi, Silvio
CC          TITLE OF INVENTION: Receptor Subunit Polypeptides
CC          NUMBER OF SEQUENCES: 8
CC          CORRESPONDENCE ADDRESS:
CC              ADDRESSEE: Genentech, Inc.
CC              STREET: 460 Point San Bruno Blvd
CC              CITY: South San Francisco
CC              STATE: California
CC              COUNTRY: USA
CC              ZIP: 94080
CC          COMPUTER READABLE FORM:
CC              MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC              COMPUTER: IBM PC compatible
CC              OPERATING SYSTEM: PC-DOS/MS-DOS
CC              SOFTWARE: patin (Genentech)
CC          CURRENT APPLICATION DATA:
CC              APPLICATION NUMBER: PCT/US94/14277
CC              FILING DATE: 07-DEC-1994
CC          CLASSIFICATION:
CC              PRIOR APPLICATION DATA:
CC                  APPLICATION NUMBER: 08/164596
CC                  FILING DATE: 09-DEC-1993
CC              ATTORNEY/AGENT INFORMATION:
CC                  NAME: Love, Richard B.
CC                  REGISTRATION NUMBER: 34,659
CC                  REFERENCE/DOCKET NUMBER: 866PCT
CC                  TELECOMMUNICATION INFORMATION:
CC                      TELEPHONE: 415/225-5530
CC                      TELEFAX: 415/952-9881
CC                      TELEX: 910/371-7168
CC              INFORMATION FOR SEQ ID NO: 8:
CC                  SEQUENCE CHARACTERISTICS:
CC                      LENGTH: 337 amino acids
CC                      TYPE: amino acid
CC                      TOPOLOGY: linear
CC          SEQUENCE 337 AA; 37820 MW; 633736 CN;
SO DB       142 PENIEV 148
OY QY       231 PENIEV 237
           |||||
Query Match 1.6%; Score 7; DB 4; Length 337;
Best Local Similarity 100.0%; Pred.No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
RESULT 26
ID US-08-943-087-20 STANDARD; PRT.: 553 AA.
AC xxxxxx
XX
DT
XX
DE XX      Sequence 20, Application US/08943087
CC XX      Patent No. 594511
CC          GENERAL INFORMATION:
CC              APPLICANT: Lok, Si
CC              APPLICANT: Kho, Choon J.
CC              APPLICANT: Jelmeberg, Anna C.
CC              APPLICANT: Adams, Robyn L.
CC              APPLICANT: Whitmore, Theodore E.
CC              APPLICANT: Farrah, Theresa M.
CC              TITLE OF INVENTION: CYTOKINE RECEPTOR

```

CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943.087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/803.305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G.
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 553 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SEQUENCE: 553 AA; 62533 MW; 1648042 CN;
SQ

Query Match: 1.6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 136 QIGPPEV 142
OY 127 QIGPPEV 133

RESULT 27
ID US-08-943-087-40 STANDARD; PRT; 553 AA.
AC xxxxxx
DT
XX
XX
DE Sequence 40, Application US/08943087
XX
XX Patent No. 5945511
CC
CC GENERAL INFORMATION:
CC APPLICANT: LOK, SI
CC APPLICANT: Kuo, Choon J.
CC APPLICANT: Jelmeberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Parrish, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA

CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943.087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/803.305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G.
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 40:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 553 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SEQUENCE: 553 AA; 62533 MW; 1648042 CN;
SQ

Query Match: 1.6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 136 QIGPPEV 142
OY 127 QIGPPEV 133

RESULT 28
ID US-08-943-087-16 STANDARD; PRT; 553 AA.
AC xxxxxx
DT
XX
XX
DE Sequence 16, Application US/08943087
XX
XX Patent No. 5945511
CC
CC GENERAL INFORMATION:
CC APPLICANT: LOK, SI
CC APPLICANT: Kuo, Choon J.
CC APPLICANT: Jelmeberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Parrish, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/943,087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G.
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 553 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SEQUENCE 553 AA; 62533 MW; 1648042 CN;
SO

Query Match 1 6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 136 QIGPPEV 142
1111111
QY 127 QIGPPEV 133

RESULT 29
ID US-08-943-087-22 STANDARD; PRT; 553 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 22, Application US/08943087
XX
CC Sequence 22, Application US/08943087
CC Patent No. 5945511
CC GENERAL INFORMATION:
CC APPLICANT: Lok, Si
CC APPLICANT: Kho, Choon J.
CC APPLICANT: Jelmeberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Fairah, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943,087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:

CC NAME: Lunn, Paul G.
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 553 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SEQUENCE 553 AA; 62533 MW; 1648042 CN;
SO

Query Match 1 6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 136 QIGPPEV 142
1111111
QY 127 QIGPPEV 133

RESULT 30
ID US-08-943-087-42 STANDARD; PRT; 553 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 42, Application US/08943087
XX
CC Sequence 42, Application US/08943087
CC Patent No. 5945511
CC GENERAL INFORMATION:
CC APPLICANT: Lok, Si
CC APPLICANT: Kho, Choon J.
CC APPLICANT: Jelmeberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Fairah, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943,087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G.
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:

```
CC INFORMATION FOR SEQ ID NO: 42:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA; 62533 MW; 1648042 CM;  
  
Query Match 1.6%; Score 7; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
  
Db 136 QIGPPEV 142 *  
|||||  
OY 127 QIGPPEV 133  
  
RESULT 31  
ID US-08-943-087-28 STANDARD: PRT; 553 AA.  
AC xxxxxx  
AD  
DE Sequence 28, Application US/08943087  
XX  
XX  
XX  
XX  
XX  
XX  
Sequence 28, Application US/08943087  
Patent No. 5945511  
GENERAL INFORMATION:  
CC APPLICANT: Lok, S.I.  
CC APPLICANT: Kho, Choan J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Whitmore, Theodore E.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FastSeq for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G  
CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 28:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein
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CC FRAGMENT TYPE: Internal
SQ SEQUENCE 553 AA; 62553 MW; 1648042 CN;

Query Match 1.6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 136 OIGPEV 142
      |||||
OY 127 OIGPEV 133

RESULT 32
ID US-08-943-087-30 STANDARD: PRT; 553 AA.
XX xxxxxx
DT
XX
DE Sequence 30, Application US/08943087

Sequence 30, Application US/08943087
Patent No. 594511
GENERAL INFORMATION:
APPLICANT: Lok, Si
CC APPLICANT: Kho, Choon J.
CC APPLICANT: Jeimberg, Anna C.
CC APPLICANT: Adams, Rodyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Farrah, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943,087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: lunn, Paul G
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 30:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 553 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: Internal
CC SEQUENCE 553 AA; 62553 MW; 1648042 CN;

Query Match 1.6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE 553 AA; 62533 MW; 1648042 CN;
Query Match 1.6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db 136 QIGPEPV 142
1111111
QY 127 QIGPEPV 133
RESULT 39
ID US-08-943-087-34 STANDARD; PRT: 553 AA.
XX xxxxxx
DT
XX
DE
XX
XX
Sequence 34, Application US/08943087
Sequence 34, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, SI
APPLICANT: Kho, Choon J.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farhan, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 34:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 553 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SEQUENCE 553 AA; 6253 MW; 1648042 CN;

Query Match 1.6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 136 QIGPPEV 142
0Y 127 QIGPPEV 133

RESULT 40
ID US-08-943-087-38 STANDARD; PRT; 553 AA.

xxxxxx

Sequence 38, Application US/08943087

CC Sequence 38, Application US/08943087

CC Patent No. 5945511

CC GENERAL INFORMATION:

CC APPLICANT: Lok, Si

CC APPLICANT: Kho, Choon J.

CC APPLICANT: Jelmeberg, Anna C.

CC APPLICANT: Adams, Robyn L.

CC APPLICANT: Whitmore, Theodore E.

CC APPLICANT: Parrish, Theresa M.

CC TITLE OF INVENTION: CYTOKINE RECEPTOR

CC NUMBER OF SEQUENCES: 60

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: ZymoGenetics, Inc.

CC STREET: 1201 Eastlake Avenue East

CC CITY: Seattle

CC STATE: WA

CC COUNTRY: USA

CC ZIP: 98102

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette

CC COMPUTER: IBM Compatible

CC OPERATING SYSTEM: DOS

CC SOFTWARE: FASTSEQ for Windows Version 2.0

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/943,087

CC FILING DATE:

CC CLASSIFICATION: 536

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/803,305

CC FILING DATE: 20-FEB-1997

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Lunn, Paul G

CC REGISTRATION NUMBER: 32,743

CC REFERENCE/DOCKET NUMBER: 96-24C1

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 38:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 553 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
CC SEQUENCE 553 AA; 6253 MW; 1648042 CN;

Query Match 1.6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 136 QIGPPEV 142
0Y 127 QIGPPEV 133

RESULT 41
ID US-08-943-087-26 STANDARD; PRT; 553 AA.

xxxxxx

Sequence 26, Application US/08943087

CC Sequence 26, Application US/08943087

CC Patent No. 5945511

CC GENERAL INFORMATION:

CC APPLICANT: Lok, Si

CC APPLICANT: Kho, Choon J.

CC APPLICANT: Jelmeberg, Anna C.

CC APPLICANT: Adams, Robyn L.

CC APPLICANT: Whitmore, Theodore E.

CC APPLICANT: Parrish, Theresa M.

CC TITLE OF INVENTION: CYTOKINE RECEPTOR

CC NUMBER OF SEQUENCES: 60

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: ZymoGenetics, Inc.

CC STREET: 1201 Eastlake Avenue East

CC CITY: Seattle

CC STATE: WA

CC COUNTRY: USA

CC ZIP: 98102

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette

CC COMPUTER: IBM Compatible

CC OPERATING SYSTEM: DOS

CC SOFTWARE: FASTSEQ for Windows Version 2.0

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/943,087

CC FILING DATE:

CC CLASSIFICATION: 536

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/803,305

CC FILING DATE: 20-FEB-1997

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Lunn, Paul G

CC REGISTRATION NUMBER: 32,743

CC REFERENCE/DOCKET NUMBER: 96-24C1

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 206-442-6627

CC TELEFAX: 206-442-6678

CC TELEX:

CC INFORMATION FOR SEQ ID NO: 26:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 553 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
SQ SEQUENCE 553 AA; 62533 MW; 1648042 CN;

Query Match 1.68; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 136 QIGPPEV 142
1111111
OY 127 QIGPPEV 133

RESULT 42
ID US-08-943-087-14 STANDARD; PRT; 553 AA.
XX xxxxxx

Sequence 14, Application US/08943087

Sequence 14, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kho, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Rodyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Fairah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: IBM Compatible

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,087

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE 553 AA; 62533 MW; 1648042 CN;

Query Match 1.68; Score 7; DB 2; Length 553;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 136 QIGPPEV 142
1111111
OY 127 QIGPPEV 133

RESULT 43
ID US-08-943-087-36 STANDARD; PRT; 553 AA.
XX xxxxxx

Sequence 36, Application US/08943087

Sequence 36, Application US/08943087
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kho, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Rodyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Fairah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: IBM Compatible

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,087

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE 553 AA; 62533 MW; 1648042 CN;

Query Match 1.68; Score 7; DB 2; Length 553;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT	44				
ID	US-08-943-087-24	STANDARD:	PRT:	553 AA.	
XX	xxxxxx				
DE	Sequence 24, Application US/08943087				
CC	Sequence 24, Application US/08943087				
CC	Patent No. 5945511				
CC	GENERAL INFORMATION:				
CC	APPLICANT: Lok, SL				
CC	APPLICANT: Kho, Choon J				
CC	APPLICANT: Jeimberg, Anna C.				
CC	APPLICANT: Adams, Robyn L.				
CC	APPLICANT: Whitmore, Theodore E.				
CC	APPLICANT: Farrah, Theresa M.				
CC	TITLE OF INVENTION: CYTOKINE RECEPTOR				
CC	NUMBER OF SEQUENCES: 60				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: Zymogenetics, Inc.				
CC	STREET: 1201 Eastlake Avenue East				
CC	City: Seattle				
CC	STATE: WA				
CC	COUNTRY: USA				
CC	ZIP: 98102				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Diskette				
CC	COMPUTER: IBM Compatible				
CC	OPERATING SYSTEM: DOS				
CC	SOFTWARE: FastSeq for Windows Version 2.0				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/943,087				
CC	FILING DATE:				
CC	CLASSIFICATION: 536				
CC	Prior APPLICATION DATA:				
CC	APPLICATION NUMBER: 08/803,305				
CC	FILING DATE: 20-FEB-1997				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: Lunn, Paul G				
CC	REGISTRATION NUMBER: 32,743				
CC	REFERENCE/DOCKET NUMBER: 96-24C1				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: 206-442-6627				
CC	TELEFAX: 206-442-6678				
CC	TELEX:				
CC	INFORMATION FOR SEQ ID NO: 24:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 553 amino acids				
CC	TYPE: amino acid				
CC	STRANDEDNESS: single				
CC	TOPOLOGY: linear				
CC	MOLECULE TYPE: protein				
CC	FRAGMENT TYPE: internal				
SQ	SEQUENCE 553 AA; 62553 MM; 1648042 CN;				
DB	136 QIGPEPV 142				
OY	127 QIGPEPV 133				
Query Match	1.6%; Score 7; DB 2; Length 553;				
Best Local Similarity 100.0%;	Pred. No. 2.03e+01;				
Matches 7; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
RESULT	45				
ID	US-09-016-000-2	STANDARD:	PRT:	688 AA.	
AC	xxxxxx				
XX					
DT					

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XX      Sequence 2, Application US/09016000
DE
CC      Sequence 2, Application US/09016000
CC      Patent No. 5962232
CC      GENERAL INFORMATION:
CC      APPLICANT: Hillman, Jennifer L.
CC      APPLICANT: Lal, Preeti.
CC      APPLICANT: Bandman, Olga
CC      APPLICANT: Akerblom, Ingrid E.
CC      APPLICANT: Shah, Puri
CC      APPLICANT: Corley, Neil C.
CC      APPLICANT: Guegler, Karl G.
CC      TITLE OF INVENTION: PROTEIN KINASE MOLECULES
CC      NUMBER OF SEQUENCES: 12
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Incyte Pharmaceuticals, Inc.
CC      STREET: 3174 Porter Drive
CC      CITY: Palo Alto
CC      STATE: CA
CC      COUNTRY: USA
CC      ZIP: 94304
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette
CC      COMPUTER: IBM compatible
CC      OPERATING SYSTEM: DOS
CC      SOFTWARE: FastSeq for Windows Version 2.0
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/09/016,000
CC      FILING DATE: HEREWITH
CC      CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER:
CC      FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Billings, Lucy J
CC      REGISTRATION NUMBER: 36,749
CC      REFERENCE/DOCKET NUMBER: PF-0465 US
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 650-855-0555
CC      TELEFAX: 650-845-4166
CC      TELEX:
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 688 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      IMMEDIATE SOURCE:
CC      LIBRARY: HEARNOT01
CC      CLONE: 307624
SO      SEQUENCE 688 AA; 77471 MW; 2333783 CN;

Query Match      1.6%; Score 7; DB 2; Length 688;
Best Local Similarity 100.0%; Pred.No.2.03e+01;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Db      297 AERKITE 303
Oy      380 AERKITE 386

Search completed: Mon Aug 21 10:35:27 2000
Job time : 50 secs.

```

WFO-TV, Inc.
1000 W. Peachtree Street
Atlanta, Georgia 30308
404-525-1234

 WISE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit,
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MSearch: protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Aug 21 10:31:57 2000; MSPar time 14.09 Seconds
 Tabular output not generated. 958.880 Million cell updates/sec

Title: >US-09-240-675-2
 Description: (1-436) from US09240675.pep
 Perfect Score: 436
 Sequence: 1 MMYVLLGATTLVAVGPMV.....KSSVSDACEKTRKPGNTSK 436

Scoring table: TABLE uniprottable
 Gap 60

Searched: 85661 segs, 30989116 residues

Post-processing: Minimum Match 0%
 Listing first 1000 summaries

Database: swiss-prot
 1:swissprot

Statistics: Mean 3.766; Variance 0.410; scale 9.184

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	436	100.0	557	1	INRL_HUMAN INTERFERON-ALPHA/BETA	0.00e+00
2	15	3.4	560	1	INRL_SHEEP INTERFERON-ALPHA/BETA	1.71e-21
3	13	3.0	560	1	INRL_BOVIN INTERFERON-ALPHA/BETA	1.40e-15
4	11	2.5	590	1	INRL_MOUSE INTERFERON-ALPHA/BETA	5.20e-10
5	7	1.6	11	1	BRK_MERFL MEGASCOTILANTININ (6-TNR	1.63e+00
6	7	1.6	35	1	ATP8_COTUA ATP SYNTHASE PROTEIN 8	1.63e+00
7	7	1.6	195	1	AAAT_HDVMI DELTA ANTIGEN	1.63e+00
8	7	1.6	252	1	TRT3_COTUA TROPONIN T, FAST SKELE	1.63e+00
9	7	1.6	257	1	TRT3_HUMAN TROPONIN T, FAST SKELE	1.63e+00
10	7	1.6	258	1	TRT3_RAT TROPONIN T, FAST SKELE	1.63e+00
11	7	1.6	262	1	TRT3_CHICK TROPONIN T, FAST SKELE	1.63e+00
12	7	1.6	278	1	TRT3_RABIT TROPONIN T, FAST SKELE	1.63e+00
13	7	1.6	337	1	INOS_HUMAN INTERFERON-GAMMA RECEPTOR	1.63e+00
14	7	1.6	353	1	FIXB_RHIME INTERFERON-GAMMA RECEPTOR	1.63e+00
15	7	1.6	369	1	FIXB_RHISN INTERFERON-GAMMA RECEPTOR	1.63e+00
16	7	1.6	369	1	FIXB_RHISN INTERFERON-GAMMA RECEPTOR	1.63e+00
17	7	1.6	369	1	FIXB_RHISN INTERFERON-GAMMA RECEPTOR	1.63e+00
18	7	1.6	369	1	FIXB_RHISN INTERFERON-GAMMA RECEPTOR	1.63e+00
19	7	1.6	423	1	PUR6_CAEEL PROBABLE MULTIFUNCTIONAL PROTEIN	1.63e+00
20	7	1.6	425	1	PUR6_RAT MULTIFUNCTIONAL PROTEIN	1.63e+00
21	7	1.6	425	1	PUR6_HUMAN MULTIFUNCTIONAL PROTEIN	1.63e+00
22	7	1.6	442	1	YAL7_SYNY3 PUTATIVE AMONIDUM TRAN	1.63e+00
23	7	1.6	450	1	VGIM_HSVB GLYCOPROTEIN M.	1.63e+00

24	7	1.6	681	1	MAOC_ECOLI MAOC PROTEIN (PHENYLAC	1.63e+00
25	7	1.6	687	1	CATE_RHIME CATECHOLASE EC 1.11.1.1	1.63e+00
26	7	1.6	698	1	UVRB_MCTU UVRB_MCTU	1.63e+00
27	7	1.6	1051	1	IT3A_HUMAN INTEGRIN ALPHA-3 PRECU	1.63e+00
28	7	1.6	1053	1	IT3A_MOUSE INTEGRIN ALPHA-3 PRECU	1.63e+00
29	7	1.6	1091	1	MSH_MOUSE MSH_MOUSE	1.63e+00
30	7	1.6	2205	1	POLG_POL2M POLG_POL2M	1.63e+00
31	7	1.6	2206	1	POLG_POL3 POLG_POL3	1.63e+00
32	7	1.6	2206	1	POLG_POL3 POLG_POL3	1.63e+00
33	7	1.6	2214	1	POLG_POL2 POLG_POL2	1.63e+00
34	7	1.6	2214	1	POLG_POL2 POLG_POL2	1.63e+00
35	7	1.6	3744	1	YHP9_YEAST YHP9_YEAST	1.63e+00
36	7	1.4	53	1	RUBR_PIRFU RUBR_PIRFU	1.07e+02
37	7	1.4	75	1	YC61_PORPU YC61_PORPU	1.07e+02
38	7	1.4	80	1	LEFA_NPPOP LATE EXPRESSION FACTOR	1.07e+02
39	6	1.4	80	1	TYRO_FELCA TYROSINASE (EC 1.14.18	1.07e+02
40	6	1.4	84	1	DMP_BPT5 DMP PROTEIN (FRAGMENT	1.07e+02
41	6	1.4	85	1	CYC6_PLEBO CYC6_PLEBO	1.07e+02
42	6	1.4	86	1	CYC6_ANAVA CYC6_ANAVA	1.07e+02
43	6	1.4	98	1	CERA_CERCE CERASTORTIN (EC 3.4.21.	1.07e+02
44	6	1.4	105	1	NIPM_BOVIN NADH-UBIQUINONE OXIDOR	1.07e+02
45	6	1.4	110	1	YCX1_CHLPP CYC6_ANASP	1.07e+02
46	6	1.4	111	1	CYC6_ANASP CYC6_ANASP	1.07e+02
47	6	1.4	111	1	CYC6_ANASP CYC6_ANASP	1.07e+02
48	6	1.4	112	1	YPMC_ECOLI SHAL INDUCIBLE MOBILIZAT	1.07e+02
49	6	1.4	112	1	SYZ7_HUMAN SMC RIBOSOMAL PROTEIN	1.07e+02
50	6	1.4	115	1	OIT1_MOUSE UREASE ACCESSORY PROTE	1.07e+02
51	6	1.4	115	1	RLI9_THEMA EYES ABSENT HOMOLOG 4	1.07e+02
52	6	1.4	117	1	DRER_BACPA EYES ABSENT HOMOLOG 4	1.07e+02
53	6	1.4	119	1	EY4A_CHICK EYES ABSENT HOMOLOG 4	1.07e+02
54	6	1.4	119	1	EY4A_FUGRU EYES ABSENT HOMOLOG 4	1.07e+02
55	6	1.4	119	1	EY4A_CHICK EYES ABSENT HOMOLOG 3	1.07e+02
56	6	1.4	119	1	EY4A_CHICK EYES ABSENT HOMOLOG 3	1.07e+02
57	6	1.4	125	1	CHM5_PENIP CRUSTACEAN HYPERGICLYC	1.07e+02
58	6	1.4	127	1	TRBC_RHISN PROBABLE CONUTICAL TRAN	1.07e+02
59	6	1.4	129	1	C556_RHOPA GLUTAMYL AMINOPEPTIDAS	1.07e+02
60	6	1.4	133	1	AMPE_RAT CONUTICAL TRANSFER PROT	1.07e+02
61	6	1.4	134	1	TRBC_AGRT6 L-LACTATE DEHYDROGENAS	1.07e+02
62	6	1.4	134	1	LDH_LISMO L-LACTATE DEHYDROGENAS	1.07e+02
63	6	1.4	136	1	LYSE_MOUSE LYMPHOCYTE ANTIGEN LY-	1.07e+02
64	6	1.4	137	1	Y074_MYCGE HYPOHETICAL PROTEIN M	1.07e+02
65	6	1.4	142	1	YNER_BACSU HYPOHETICAL 17.0 KDA	1.07e+02
66	6	1.4	144	1	WAP3_PIG WAP-3 PROTEIN PRECURSO	1.07e+02
67	6	1.4	155	1	IL2_CANFA INTERLEUKIN-2 PRECURSO	1.07e+02
68	6	1.4	155	1	GRP_BOMOR GASTRIN-RELEASING PEPT	1.07e+02
69	6	1.4	156	1	Y015_BPT4 HYPOHETICAL 18.3 KDA	1.07e+02
70	6	1.4	157	1	Y015_METTH EPITHELIAL MEMBRANE PR	1.07e+02
71	6	1.4	157	1	EMPI_HUMAN 18.0 KDA CLASS. I HEAT	1.07e+02
72	6	1.4	159	1	HS12_DAOCA HYDROGENASE EXPRESSION	1.07e+02
73	6	1.4	161	1	HOXO_ALCEU C-PHYCOCYANIN ALPHA CH	1.07e+02
74	6	1.4	162	1	PHCA_CVACA TRANSCRIPTION ELONGATI	1.07e+02
75	6	1.4	164	1	GREX_MYCLE TRANSCRIPTION ELONGATI	1.07e+02
76	6	1.4	164	1	GREX_MYCLE TRANSCRIPTION ELONGATI	1.07e+02
77	6	1.4	166	1	Y021_BHPPI HYPOHETICAL 19.2 KDA	1.07e+02
78	6	1.4	167	1	CD3D_SHEEP T-CELL SURFACE GLYCOPR	1.07e+02
79	6	1.4	177	1	YDAB_MYCBO HYPOHETICAL 19.3 KDA	1.07e+02
80	6	1.4	179	1	Y053_SYNY3 HYPOHETICAL 20.1 KDA	1.07e+02
81	6	1.4	181	1	YMD6_YEAST HYPOHETICAL 20.7 KDA	1.07e+02
82	6	1.4	186	1	GREP_YEAST GRPE PROTEIN (HSP-70 C	1.07e+02
83	6	1.4	186	1	DNA_WOLSP CHROMOSOMAL REPLICATIO	1.07e+02
84	6	1.4	187	1	SPAI_PIG SODIUM/POTASSIUM ATPAS	1.07e+02
85	6	1.4	187	1	US51_YEAST U6 SNRNA-ASSOCIATED PR	1.07e+02
86	6	1.4	189	1	EXBI_HELPY PUTATIVE BIOPOLYMER TR	1.07e+02
87	6	1.4	192	1	Y210_AQUAE PEPTIDYL-TRNA HYDROLAS	1.07e+02
88	6	1.4	194	1	Y210_AQUAE HYPOHETICAL PROTEIN A	1.07e+02
89	6	1.4	194	1	RS7_ARCFU 30S RIBOSOMAL PROTEIN	1.07e+02
90	6	1.4	195	1	AAAT_HDVV2 DELTA ANTIGEN	1.07e+02
91	6	1.4	195	1	AAAT_HDVV2 DELTA ANTIGEN	1.07e+02
92	6	1.4	195	1	IBBR_OYRSA BOWMAN-BIRK TYPE BRAN	1.07e+02
93	6	1.4	195	1	RS7_SULAC 30S RIBOSOMAL PROTEIN	1.07e+02
94	6	1.4	199	1	Y186_MYCTU HYPOHETICAL 20.8 KDA	1.07e+02
95	6	1.4	199	1	R13B_YEAST 60S RIBOSOMAL PROTEIN	1.07e+02
96	6	1.4	199	1	R13A_YEAST 60S RIBOSOMAL PROTEIN	1.07e+02

97	6	1.4	201	1	OSMT_ECOLI	OSMOTICALLY INDUCIBLE	1.07e+02	170	6	1.4	317	1	FMT_BACSU	METHIONYL-TRNA FORMYL	1.07e+02
98	6	1.4	205	1	AAAT_HOYMO	DELTA ANTIGEN.	1.07e+02	171	6	1.4	322	1	YK02_YEAST	HYPOTHETICAL 36.6 KDA	1.07e+02
99	6	1.4	206	1	UPP_MDCPN	URACIL PHOSPHORIBOSYL	1.07e+02	172	6	1.4	322	1	R1R2_PLAAT	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
100	6	1.4	208	1	NU4M_MICPE	NADH-UBIQUINONE OXIDOR	1.07e+02	173	6	1.4	322	1	YFBL_ECOLI	HYPOTHETICAL 35.9 KDA	1.07e+02
101	6	1.4	213	1	H1X_HUMAN	HISTONE H1X.	1.07e+02	174	6	1.4	323	1	YFBL_ECOLI	HYPOTHETICAL 35.9 KDA	1.07e+02
102	6	1.4	214	1	AAAT_HOYNA	DELTA ANTIGEN.	1.07e+02	175	6	1.4	323	1	HFLC_ECOLI	HELC PROTEIN (EC 3.4.-	1.07e+02
103	6	1.4	214	1	AAAT_HOYIT	DELTA ANTIGEN (ALPHA A	1.07e+02	176	6	1.4	324	1	HME2_MOUSE	HOMEOBOX PROTEIN ENGRA	1.07e+02
104	6	1.4	218	1	IM23_SCHEA	23 KDA INTEGRAL MEMBRA	1.07e+02	177	6	1.4	326	1	Y16B_HUMAN	HYPOTHETICAL PROTEIN K	1.07e+02
105	6	1.4	218	1	IM23_SCHEA	23 KDA INTEGRAL MEMBRA	1.07e+02	178	6	1.4	331	1	PELB_COGL	PEPCATE LYSASE B PREC	1.07e+02
106	6	1.4	218	1	IM23_SCHEA	23 KDA INTEGRAL MEMBRA	1.07e+02	179	6	1.4	333	1	GLXP_HAEIN	GLXP PROTEIN HOMOLOG.	1.07e+02
107	6	1.4	218	1	GLNP_RICPR	POTATIVE GLUTAMINE TRA	1.07e+02	180	6	1.4	336	1	UL16_EBV	BGLF PROTEIN.	1.07e+02
108	6	1.4	219	1	ATP_OXONM	ATP SYNTHASE A CHAIN (1.07e+02	180	6	1.4	338	1	R1R2_DICD	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
109	6	1.4	221	1	EPD1_ONCMY	EPENDYMIN I PRECURSOR	1.07e+02	181	6	1.4	339	1	HXD9_MOUSE	HOMEOBOX PROTEIN HOX-D	1.07e+02
110	6	1.4	221	1	GCH1_ECOLI	GTP CYCLOHYDROLASE I (1.07e+02	182	6	1.4	343	1	PS8B_HUMAN	PROSTASIN PRECURSOR (E	1.07e+02
111	6	1.4	221	1	EPD1_ECOLI	EPENDYMIN PRECURSOR (E	1.07e+02	183	6	1.4	346	1	TAS_ECOLI	TAS PROTEIN.	1.07e+02
112	6	1.4	221	1	RAVZ_ARATH	GMP-RINING NUCLEAR PR	1.07e+02	184	6	1.4	346	1	DHAS_MYCOS	ASPARTATE-SEMIALDEHYDE	1.07e+02
113	6	1.4	222	1	CASB_SHEEP	BETA CASEIN PRECURSOR.	1.07e+02	185	6	1.4	348	1	TRPD_STN13	ANTHRANILATE PHOSPHORI	1.07e+02
114	6	1.4	222	1	CASB_CAPHI	BETA CASEIN PRECURSOR.	1.07e+02	186	6	1.4	349	1	R1R2_PLAFA	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
115	6	1.4	223	1	Y770_METTA	HYPOTHETICAL PROTEIN M	1.07e+02	187	6	1.4	349	1	TRPD_PSEAE	ANTHRANILATE PHOSPHORI	1.07e+02
116	6	1.4	223	1	CT14_RABIT	CYTOTOXIC T-LYMPHOCYTE	1.07e+02	188	6	1.4	353	1	VPL1_RDV	NONSTRUCTURAL PROTEIN	1.07e+02
117	6	1.4	223	1	ATP6_OXONM	ATP SYNTHASE A CHAIN (1.07e+02	189	6	1.4	358	1	AROB_AERPE	3-DEHYDOXYMATE SYNTH	1.07e+02
118	6	1.4	224	1	CASH_BOVIN	BETA CASEIN PRECURSOR.	1.07e+02	190	6	1.4	360	1	FLXB_AZOVI	FLXB PROTEIN.	1.07e+02
119	6	1.4	229	1	TRJ1_ECOLI	TRAJ PROTEIN.	1.07e+02	191	6	1.4	363	1	UL16_AZOVI	FLXB PROTEIN.	1.07e+02
120	6	1.4	231	1	CUT2_CAEEL	CUTICLIN 2 PRECURSOR.	1.07e+02	192	6	1.4	368	1	VAAC_DICD	VACUOLAR ATP SYNTHASE	1.07e+02
121	6	1.4	231	1	YDQO_ECOLI	HYPOTHETICAL 24.5 KDA	1.07e+02	193	6	1.4	369	1	TR15_BAJA	CYCLOHYDROME C-TYPE BIGO	1.07e+02
122	6	1.4	232	1	OVAX_CHICK	GENE X PROTEIN (OVALIN	1.07e+02	194	6	1.4	374	1	TR15_FUSSP	TRICHODIENE SYNTHASE (1.07e+02
123	6	1.4	238	1	ATP6_MYTED	ATP SYNTHASE A CHAIN (1.07e+02	195	6	1.4	375	1	TR15_GIBZE	TRICHODIENE SYNTHASE (1.07e+02
124	6	1.4	239	1	RS6_SCHPO	40S RIBOSOMAL PROTEIN	1.07e+02	196	6	1.4	377	1	TR15_FUSPO	TRICHODIENE SYNTHASE (1.07e+02
125	6	1.4	246	1	PRCA_ARCFU	PROTASONE ALPHA SUBUN	1.07e+02	197	6	1.4	378	1	LEIK_RAT	LEUKOSTALIN PRECURSOR	1.07e+02
126	6	1.4	246	1	TR1B_RAT	TRYPSINOGEN V-B PRECUR	1.07e+02	198	6	1.4	383	1	DEVA_HUMAN	DEMATIN (ERYTHROCYTE M	1.07e+02
127	6	1.4	246	1	MCBR_ECOLI	TRYPSINOGEN V-A PRECUR	1.07e+02	199	6	1.4	383	1	TR15_GIBPO	TRYPSINOGEN V-B PRECUR	1.07e+02
128	6	1.4	247	1	MCBR_ECOLI	TRYPSINOGEN V-A PRECUR	1.07e+02	200	6	1.4	384	1	NKR_R_MOUSE	SUBSTANACE-K RECEPTOR	1.07e+02
129	6	1.4	247	1	MCBR_ECOLI	TRYPSINOGEN V-A PRECUR	1.07e+02	201	6	1.4	384	1	NKR_R_MOUSE	SUBSTANACE-K RECEPTOR	1.07e+02
130	6	1.4	248	1	TRV1_RAT	TRYPSINOGEN IV PRECURS	1.07e+02	202	6	1.4	384	1	NKR_R_MOUSE	SUBSTANACE-K RECEPTOR	1.07e+02
131	6	1.4	248	1	TRV1_RAT	TRYPSINOGEN IV PRECURS	1.07e+02	203	6	1.4	384	1	NKR_R_MOUSE	SUBSTANACE-K RECEPTOR	1.07e+02
132	6	1.4	248	1	TRV1_RAT	TRYPSINOGEN IV PRECURS	1.07e+02	204	6	1.4	385	1	NKR_R_MOUSE	SUBSTANACE-K RECEPTOR	1.07e+02
133	6	1.4	249	1	TRV1_RAT	TRYPSINOGEN IV PRECURS	1.07e+02	205	6	1.4	385	1	NKR_R_MOUSE	SUBSTANACE-K RECEPTOR	1.07e+02
134	6	1.4	250	1	TRV1_RAT	TRYPSINOGEN IV PRECURS	1.07e+02	206	6	1.4	388	1	TR15_MIRO	TRICHODIENE SYNTHASE (1.07e+02
135	6	1.4	253	1	Y505_METTA	HYPOTHETICAL PROTEIN M	1.07e+02	207	6	1.4	390	1	MEKX_ACACA	S-ADENOSINETHIONINE S	1.07e+02
136	6	1.4	253	1	TRV1_RICPR	TRYPSINOGEN IV PRECURS	1.07e+02	208	6	1.4	390	1	SCC1_HUMAN	SQUAMOUS CELL CARCINOM	1.07e+02
137	6	1.4	253	1	TRV1_RICPR	TRYPSINOGEN IV PRECURS	1.07e+02	209	6	1.4	390	1	SCC2_HUMAN	SQUAMOUS CELL CARCINOM	1.07e+02
138	6	1.4	256	1	M3L_DICDI	CAMP-REGULATED M3L PRO	1.07e+02	210	6	1.4	392	1	NKR_RAT	SUBSTANACE-K RECEPTOR	1.07e+02
139	6	1.4	256	1	ATP6_HUMAN	ATP SYNTHASE B CHAIN,	1.07e+02	211	6	1.4	394	1	CCG1_YEAST	RUBREDONIN-NAD(+) REDU	1.07e+02
140	6	1.4	259	1	ATP6_HUMAN	ATP SYNTHASE B CHAIN,	1.07e+02	212	6	1.4	398	1	NKR_R_HUMAN	SUBSTANACE-K RECEPTOR	1.07e+02
141	6	1.4	259	1	ATP6_HUMAN	ATP SYNTHASE B CHAIN,	1.07e+02	213	6	1.4	399	1	NKR_R_HUMAN	SUBSTANACE-K RECEPTOR	1.07e+02
142	6	1.4	259	1	ATP6_HUMAN	ATP SYNTHASE B CHAIN,	1.07e+02	214	6	1.4	401	1	R1R2_YEAST	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
143	6	1.4	263	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	215	6	1.4	401	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
144	6	1.4	263	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	216	6	1.4	402	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
145	6	1.4	264	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	217	6	1.4	403	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
146	6	1.4	266	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	218	6	1.4	405	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
147	6	1.4	266	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	219	6	1.4	409	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
148	6	1.4	269	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	220	6	1.4	411	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
149	6	1.4	270	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	221	6	1.4	412	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
150	6	1.4	280	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	222	6	1.4	413	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
151	6	1.4	283	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	223	6	1.4	419	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
152	6	1.4	285	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	224	6	1.4	421	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
153	6	1.4	288	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	225	6	1.4	426	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
154	6	1.4	288	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	226	6	1.4	433	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
155	6	1.4	292	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	227	6	1.4	435	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
156	6	1.4	300	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	228	6	1.4	437	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
157	6	1.4	300	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	229	6	1.4	437	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
158	6	1.4	302	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	230	6	1.4	437	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
159	6	1.4	302	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	231	6	1.4	438	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
160	6	1.4	303	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	232	6	1.4	443	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
161	6	1.4	304	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	233	6	1.4	443	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
162	6	1.4	304	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	234	6	1.4	449	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
163	6	1.4	308	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	235	6	1.4	450	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
164	6	1.4	308	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	236	6	1.4	451	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
165	6	1.4	312	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	237	6	1.4	454	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
166	6	1.4	313	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	238	6	1.4	458	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
167	6	1.4	316	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	239	6	1.4	459	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
168	6	1.4	316	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	240	6	1.4	459	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
169	6	1.4	316	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	241	6	1.4	459	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02
	6	1.4	316	1	PPH_MYCPN	COMPLEMENT FACTOR D PR	1.07e+02	242	6	1.4	459	1	CHRA_ALCEA	CHROMATINE TRANSPORT PRO	1.07e+02

243	6	1.4	462	1	MUTL_CLOTT	MUTL PROTEIN	1.07e+02	316	6	1.4	574	1	CO9_ONCMY	COMPLEMENT COMPONENT C	1.07e+02
244	6	1.4	463	1	ZABA_SCHRO	PROTEIN PHOSPHATASE PP	1.07e+02	317	6	1.4	580	1	STCD_RHME	STACHYDRINE UTILIZATIO	1.07e+02
245	6	1.4	473	1	GUNB_YEAST	ENDOGLUCANASE B PRECUR	1.07e+02	318	6	1.4	584	1	LEU1_SCHPO	PROBABLE 2-ISOPROPYLAM	1.07e+02
246	6	1.4	473	1	ENG4_YEAST	C-24(28) STEROL REDUCT	1.07e+02	319	6	1.4	589	1	STEV_CANAL	SERINE/THREONINE PROTE	1.07e+02
247	6	1.4	474	1	NU4M_DIDMA	NADH-UBIQUINONE OXIDOR	1.07e+02	320	6	1.4	591	1	VG01_VACCV	PROTEIN G1	1.07e+02
248	6	1.4	474	1	DLDH_HALVO	DIHYDROLIPOAMIDE DEHYD	1.07e+02	321	6	1.4	591	1	VG01_VACCV	PROTEIN G1	1.07e+02
249	6	1.4	476	1	YCAM_ECOLI	HYPOTHETICAL 52.5 KDA	1.07e+02	322	6	1.4	591	1	VG01_VACCV	PROTEIN G1	1.07e+02
250	6	1.4	476	1	NIFD_SYNP8	NITROGENASE MOLIBDENUM	1.07e+02	323	6	1.4	591	1	VG01_VACCV	PROTEIN G1	1.07e+02
251	6	1.4	478	1	ATPB_AOUPY	ATP SYNTHASE BETA CHAI	1.07e+02	324	6	1.4	592	1	VG01_VACCV	PROTEIN G1	1.07e+02
252	6	1.4	478	1	ATPB_AOUPY	ATP SYNTHASE BETA CHAI	1.07e+02	325	6	1.4	594	1	VLI_HPV27	MAJOR CASID PROTEIN L	1.07e+02
253	6	1.4	481	1	LMRA_STRLN	LINCAMYCIN RESISTANCE	1.07e+02	326	6	1.4	597	1	MBHL_CIFER	HYDROGENASE-1 LARGE CH	1.07e+02
254	6	1.4	482	1	CATA_BACSU	VEGETATIVE CATALASE (E	1.07e+02	327	6	1.4	599	1	MTGS_YEAST	METHYLENTERAHRADROL	1.07e+02
255	6	1.4	482	1	TISD_HUMAN	TISID PROTEIN (BUTYRA	1.07e+02	328	6	1.4	602	1	MTGS_YEAST	METHYLENTERAHRADROL	1.07e+02
256	6	1.4	483	1	TRKH_ECOLI	TRK SYSTEM POTASSIUM U	1.07e+02	329	6	1.4	602	1	MTGS_YEAST	METHYLENTERAHRADROL	1.07e+02
257	6	1.4	484	1	QAR2_LOCM1	POTASSIUM TYRAMINE RECE	1.07e+02	330	6	1.4	606	1	SPB4_YEAST	ATP-DEPENDENT RNA HEL	1.07e+02
258	6	1.4	484	1	QAR2_LOCM1	POTASSIUM TYRAMINE RECE	1.07e+02	331	6	1.4	615	1	YED8_SCHPO	HYPOTHETICAL 70.4 KDA	1.07e+02
259	6	1.4	486	1	RBL1_RHOSH	RIBULOSE BIPHOSPHATE	1.07e+02	332	6	1.4	616	1	CIRK1_DROME	VOLTAGE-GATED POTASSIU	1.07e+02
260	6	1.4	486	1	RBLP_ALCEU	RIBULOSE BIPHOSPHATE	1.07e+02	333	6	1.4	616	1	EYAL_MOUSE	EYES ABSENT HOMOLOG 4	1.07e+02
261	6	1.4	486	1	RBLP_ALCEU	RIBULOSE BIPHOSPHATE	1.07e+02	334	6	1.4	621	1	GP63_LEIGU	LEISHMANOLYSIN PRECURS	1.07e+02
262	6	1.4	486	1	RBLP_ALCEU	RIBULOSE BIPHOSPHATE	1.07e+02	335	6	1.4	626	1	PM17_MOUSE	MELANOCYTE PROTEIN PME	1.07e+02
263	6	1.4	487	1	RK75_MYCTU	HYPOTHETICAL 51.6 KDA	1.07e+02	336	6	1.4	627	1	YK09_YEAST	HYPOTHETICAL 72.4 KDA	1.07e+02
264	6	1.4	488	1	RBL_XANPL	NITROGENASE MOLIBDENUM	1.07e+02	337	6	1.4	627	1	YK09_YEAST	HYPOTHETICAL 72.4 KDA	1.07e+02
265	6	1.4	489	1	NIFD_THIFE	NITROGENASE MOLIBDENUM	1.07e+02	338	6	1.4	627	1	YK09_YEAST	HYPOTHETICAL 72.4 KDA	1.07e+02
266	6	1.4	490	1	AGAL_RHIME	ALPHA-GALACTOSIDASE (E	1.07e+02	339	6	1.4	629	1	FLGK_BORBU	FLAGELLAR HOOK-ASSOCIA	1.07e+02
267	6	1.4	491	1	YF86_METUA	HYPOTHETICAL PROTEIN M	1.07e+02	340	6	1.4	632	1	LY9_MOUSE	ANTIGEN IX-9 PRECURSOR	1.07e+02
268	6	1.4	492	1	CPA1_RAT	CYTOCHROME P450 2A1 (E	1.07e+02	341	6	1.4	638	1	KU70_CHICK	ATP-DEPENDENT DNA HELI	1.07e+02
269	6	1.4	493	1	CPA9_MESAU	CYTOCHROME P450 2A9 (E	1.07e+02	342	6	1.4	638	1	VE1_HPV26	REPLICATION PROTEIN E1	1.07e+02
270	6	1.4	494	1	LIPH_RAT	TRIACYLGLYCEROL LIPASE	1.07e+02	343	6	1.4	638	1	KAL_HUMAN	PLASMA KALLIKREIN PREC	1.07e+02
271	6	1.4	495	1	CIRK1_MOUSE	VOLTAGE-GATED POTASSIU	1.07e+02	344	6	1.4	639	1	YHR2_YEAST	HYPOTHETICAL 71.9 KDA	1.07e+02
272	6	1.4	495	1	CIRK1_MOUSE	VOLTAGE-GATED POTASSIU	1.07e+02	345	6	1.4	639	1	YHR2_YEAST	HYPOTHETICAL 71.9 KDA	1.07e+02
273	6	1.4	495	1	CIRK1_MOUSE	VOLTAGE-GATED POTASSIU	1.07e+02	346	6	1.4	642	1	YBBD_HUMAN	EYES ABSENT HOMOLOG 4	1.07e+02
274	6	1.4	504	1	SYK2_ECOLI	LISYL-TRNA SYNTHETASE,	1.07e+02	347	6	1.4	644	1	CIRK2_DROME	VOLTAGE-GATED POTASSIU	1.07e+02
275	6	1.4	504	1	TPM5_DROME	TROPOMYOSIN 1, FUSION	1.07e+02	348	6	1.4	644	1	DB73_DROME	POTASSIUM ATP-DEPENDENT	1.07e+02
276	6	1.4	507	1	KROS_CHICK	ROS PROTO-ONCOGENE TYR	1.07e+02	349	6	1.4	647	1	CN16_ECOLI	2',3'-CYCLIC NUCLEOTID	1.07e+02
277	6	1.4	508	1	XO20_HUMAN	HYPOTHETICAL PROTEIN K	1.07e+02	350	6	1.4	651	1	NADO_THERR	NADO OXIDASE (EC 1.1.1.1)	1.07e+02
278	6	1.4	508	1	MURE_BORBU	UDP-N-ACETYLURACIDYL	1.07e+02	351	6	1.4	652	1	CN16_YEREN	2',3'-CYCLIC NUCLEOTID	1.07e+02
279	6	1.4	510	1	EYAL_MOUSE	EYES ABSENT HOMOLOG 3	1.07e+02	352	6	1.4	653	1	YB64_MCTU	DNA LIGASE (EC 6.5.1.2)	1.07e+02
280	6	1.4	514	1	Y4U1_RH1SN	POTASSIUM TRANSPORTASE	1.07e+02	353	6	1.4	656	1	DNL_HELPY	DNA LIGASE (EC 6.5.1.2)	1.07e+02
281	6	1.4	515	1	SIR2_CANAL	REGULATORY PROTEIN SIR	1.07e+02	354	6	1.4	656	1	CIRK4_DROME	VOLTAGE-GATED POTASSIU	1.07e+02
282	6	1.4	518	1	TPM4_DROME	TROPOMYOSIN 1, FUSION	1.07e+02	355	6	1.4	656	1	YVRB_MJGCE	EXCINCLINASE ABC SUBUN	1.07e+02
283	6	1.4	520	1	ITSN_HUMAN	INTERSECTIN (SH3 DOMAI	1.07e+02	356	6	1.4	657	1	YVRB_MJGCE	EXCINCLINASE ABC SUBUN	1.07e+02
284	6	1.4	522	1	YGF6_YEAST	HYPOTHETICAL 58.1 KDA	1.07e+02	357	6	1.4	657	1	YVRB_MJGCE	EXCINCLINASE ABC SUBUN	1.07e+02
285	6	1.4	529	1	TYRO_HUMAN	TYROSINASE PRECURSOR	1.07e+02	358	6	1.4	660	1	CSPI_CONGL	PSI PROTEIN PRECURSOR	1.07e+02
286	6	1.4	530	1	TRPG_SALTY	ANTHRANILATE SYNTHASE	1.07e+02	359	6	1.4	661	1	HS74_TRYBB	DNAK PROTEIN (HEAT SHO	1.07e+02
287	6	1.4	530	1	TRPG_SALTY	ANTHRANILATE SYNTHASE	1.07e+02	360	6	1.4	664	1	ALOX_PICAN	ALCOHOL OXIDASE (EC.1.	1.07e+02
288	6	1.4	532	1	EYAL_MOUSE	EYES ABSENT HOMOLOG 2	1.07e+02	361	6	1.4	667	1	YEO1_SCHPO	HYPOTHETICAL 76.4 KDA	1.07e+02
289	6	1.4	533	1	TYRO_MOUSE	TYROSINASE PRECURSOR	1.07e+02	362	6	1.4	667	1	SIX5_MOUSE	HOMEOBOX PROTEIN SIX5	1.07e+02
290	6	1.4	534	1	TYRL_HUMAN	5,6-DIHYDROXYINDOLE-2-	1.07e+02	363	6	1.4	667	1	VG09_BPP22	TAIL PROTEIN (LATE PRO	1.07e+02
291	6	1.4	535	1	SSDH_HUMAN	SUCCINATE SEMIALDEHYDE	1.07e+02	364	6	1.4	670	1	INVI_MAIZE	DNA POLYMERASE III SUB	1.07e+02
292	6	1.4	536	1	DIPI_YEAST	SPORE WALL MATURATION	1.07e+02	365	6	1.4	681	1	PIOT_SCHPO	SERINE/THREONINE-PROTE	1.07e+02
293	6	1.4	537	1	MYPH_CHICK	MYOSIN-BINDING PROTEIN	1.07e+02	366	6	1.4	683	1	NU5C_SESIN	NADH-PLASTOQUINONE OXI	1.07e+02
294	6	1.4	538	1	EYAL_HUMAN	EYES ABSENT HOMOLOG 2	1.07e+02	367	6	1.4	684	1	NU5C_SESIN	NADH-PLASTOQUINONE OXI	1.07e+02
295	6	1.4	540	1	TYRO_ORLTA	TYROSINASE PRECURSOR	1.07e+02	368	6	1.4	686	1	GYRB_STRCO	DNA GYRASE SUBUNIT B	1.07e+02
296	6	1.4	542	1	DAGA_ALPHA	NA(+)-LINKED D-ALANINE	1.07e+02	369	6	1.4	686	1	CTCL_HUMAN	KINESIN LIGHT CHAIN (K	1.07e+02
297	6	1.4	545	1	ICAI_RAT	INTERLEUKIN ADHESION	1.07e+02	370	6	1.4	687	1	CTCL_HUMAN	KINESIN LIGHT CHAIN (K	1.07e+02
298	6	1.4	547	1	IF37_MOUSE	EUKARYOTIC TRANSLATION	1.07e+02	371	6	1.4	690	1	PERO_DROME	PEROXIDASE PRECURSOR	1.07e+02
299	6	1.4	548	1	ILVIG_ECOLI	ACETOACETATE SYNTHASE	1.07e+02	372	6	1.4	693	1	SPAI_MOUSE	GPASE-ACTIVATING PROT	1.07e+02
300	6	1.4	548	1	FE37_HUMAN	EUKARYOTIC TRANSLATION	1.07e+02	373	6	1.4	695	1	NU5C_CAPBA	NADH-PLASTOQUINONE OXI	1.07e+02
301	6	1.4	551	1	REFR_SPKKA	RIFAMPICIN RESISTANCE	1.07e+02	374	6	1.4	695	1	NU5C_CAPBA	NADH-PLASTOQUINONE OXI	1.07e+02
302	6	1.4	551	1	REFR_SPKKA	RIFAMPICIN RESISTANCE	1.07e+02	375	6	1.4	696	1	Y012_CABEL	POTASSIUM ATP-DEPENDENT	1.07e+02
303	6	1.4	551	1	REFR_SPKKA	RIFAMPICIN RESISTANCE	1.07e+02	376	6	1.4	697	1	Y012_CABEL	POTASSIUM ATP-DEPENDENT	1.07e+02
304	6	1.4	551	1	REFR_SPKKA	RIFAMPICIN RESISTANCE	1.07e+02	377	6	1.4	699	1	NU5C_DIGGR	NADH-PLASTOQUINONE OXI	1.07e+02
305	6	1.4	553	1	MCPS2_SALTY	METHYL-ACCEPTING CHEMO	1.07e+02	378	6	1.4	702	1	PTA_HABIN	PHOSPHATE ACETILTRANSF	1.07e+02
306	6	1.4	554	1	YGS6_YEAST	HYPOTHETICAL 63.3 KDA	1.07e+02	379	6	1.4	710	1	Y012_CABEL	POTASSIUM ATP-DEPENDENT	1.07e+02
307	6	1.4	555	1	DCS3_GOSAR	(+)-DETA-CADINENE SYN	1.07e+02	380	6	1.4	716	1	Y012_CABEL	POTASSIUM ATP-DEPENDENT	1.07e+02
308	6	1.4	557	1	HLVB_SERMA	HEMOXYLIN ACTIVATOR PR	1.07e+02	381	6	1.4	724	1	HMNM_HUMAN	HEMALURANIN MEDIATED MO	1.07e+02
309	6	1.4	559	1	UROT_MOUSE	TISSUE PLASMINOGEN ACT	1.07e+02	382	6	1.4	727	1	NU5C_PROFR	METHANOLAMONT-COA MUTA	1.07e+02
310	6	1.4	559	1	UROT_MOUSE	TISSUE PLASMINOGEN ACT	1.07e+02	383	6	1.4	740	1	NU5C_TOBAC	NADH-PLASTOQUINONE OXI	1.07e+02
311	6	1.4	564	1	HCM1_YEAST	GLYCOPROTEIN H PRECURS	1.07e+02	384	6	1.4	742	1	VG1H_HCMVA	GLYCOPROTEIN H PRECURS	1.07e+02
312	6	1.4	566	1	UROT_BOVIN	GLYCOPROTEIN H PRECURS	1.07e+02	385	6	1.4	743	1	VG1H_HCMVA	GLYCOPROTEIN H PRECURS	1.07e+02
313	6	1.4	568	1	G6P1_CLAMI	GLUCOSE-6-PHOSPHATE IS	1.07e+02	386	6	1.4	746	1	NU5C_ARATH	NADH-PLASTOQUINONE OXI	1.07e+02
314	6	1.4	572	1	U125_ILVT	64.1 KDA VITON PROTEI	1.07e+02	387	6	1.4	746	1	NU5C_ARATH	NADH-PLASTOQUINONE OXI	1.07e+02
315	6	1.4	573	1	EYAL_HUMAN	EYES ABSENT HOMOLOG 3	1.07e+02	388	6	1.4	746	1	CLC5_HUMAN	CHLORIDE CHANNEL PROTE	1.07e+02

389	6	1.4	747	1	CIC4_RAT	CHLORIDE CHANNEL, PROTE	1.07e+02	462	6	1.4	1205	1	NCCL_MOUSE	BUNNETANIDE-SENSITIVE S	1.07e+02
390	6	1.4	747	1	VTBR_VZVD	PROBABLE DNA PACKAGING	1.07e+02	463	6	1.4	1209	1	DNBI_HSVB	MAJOR DNA-BINDING PROT S	1.07e+02
391	6	1.4	747	1	CIC4_MOUSE	CHLORIDE CHANNEL, PROTE	1.07e+02	464	6	1.4	1212	1	NCCL_HUMAN	BUNNETANIDE-SENSITIVE S	1.07e+02
392	6	1.4	760	1	CIC4_HUMAN	CHLORIDE CHANNEL, PROTE	1.07e+02	465	6	1.4	1275	1	TRP_DROME	TRANSIENT-RECEPTOR-POT	1.07e+02
393	6	1.4	762	1	TRPG_NEUCR	ANTHRANILATE SYNTHASE	1.07e+02	466	6	1.4	1315	1	CAIH_MOUSE	COLLAGEN ALPHA 1(XVII)	1.07e+02
394	6	1.4	763	1	IF39_YEAST	EUKARYOTIC TRANSLATION	1.07e+02	467	6	1.4	1325	1	YAB6_SCHRO	HYPOTHETICAL 145.8 KDA	1.07e+02
395	6	1.4	766	1	EVA_DROME	DEVELOPMENTAL PROTEIN	1.07e+02	468	6	1.4	1332	1	XKDO_SCHRO	PHASE-LIKE ELEMENT PBS	1.07e+02
396	6	1.4	768	1	TRPG_COCHIE	ANTHRANILATE SYNTHASE	1.07e+02	469	6	1.4	1358	1	MK5_YEAST	MITOGEN-ACTIVATED PROT	1.07e+02
397	6	1.4	795	1	P5CS_MOUSE	DELTA 1-PYRROLINE-5-CA	1.07e+02	470	6	1.4	1374	1	MK5_HUMAN	MITOGEN-ACTIVATED PROT	1.07e+02
398	6	1.4	795	1	AFSK_STRGR	SERINE/THREONINE PROTE	1.07e+02	471	6	1.4	1379	1	MK5_MOUSE	MITOGEN-ACTIVATED PROT	1.07e+02
399	6	1.4	807	1	AFSK_STRGR	SERINE/THREONINE PROTE	1.07e+02	472	6	1.4	1391	1	M157_YEAST	MITOGEN-ACTIVATED PROT	1.07e+02
400	6	1.4	814	1	POL_IPMAT	PROBABLE POLYPROTEIN	1.07e+02	473	6	1.4	1429	1	L112_CAEEL	LIN-12 PROTEIN PRECURS	1.07e+02
401	6	1.4	817	1	YGBL_YEAST	HYPOTHETICAL 95.4 KDA	1.07e+02	474	6	1.4	1444	1	ADP1_MYCE	ADHESIN P1 PRECURSOR (1.07e+02
402	6	1.4	830	1	YGBL_HSV62	GLYCOPROTEIN B PRECURS	1.07e+02	475	6	1.4	1473	1	TOP2_ARATH	DNA TOPOISOMERASE II (1.07e+02
403	6	1.4	830	1	YGBL_HSV60	GLYCOPROTEIN B PRECURS	1.07e+02	476	6	1.4	1495	1	A2MG_MOUSE	ALPHA-2-MACROGLOBULIN	1.07e+02
404	6	1.4	830	1	YGBL_HSV66	GLYCOPROTEIN B PRECURS	1.07e+02	477	6	1.4	1497	1	TRR2_CAEER	SEX-DETERMINING TRANSF	1.07e+02
405	6	1.4	830	1	PRN2_MYXXA	SERINE/THREONINE-PROTE	1.07e+02	478	6	1.4	1548	1	MOR_LEITR	MULTIDRUG RESISTANCE P	1.07e+02
406	6	1.4	831	1	IF2_RICPR	TRANSLATION INITIATION	1.07e+02	479	6	1.4	1589	1	CC25_YEAST	CELL DIVISION CONTROL	1.07e+02
407	6	1.4	831	1	SAS3_YEAST	SAS3 PROTEIN.	1.07e+02	480	6	1.4	1596	1	GL13_HUMAN	ZINC FINGER PROTEIN GL	1.07e+02
408	6	1.4	839	1	YDDB_HAEIN	HYPOTHETICAL PROTEIN H	1.07e+02	481	6	1.4	1678	1	CUH_MOUSE	CLATHRIN HEAVY CHAIN.	1.07e+02
409	6	1.4	845	1	YAP4_RHISN	PROBABLE CHEMORECEPTOR	1.07e+02	482	6	1.4	1738	1	CO4_MOUSE	COMPLEMENT C4 PRECURSO	1.07e+02
410	6	1.4	859	1	PM52_MOUSE	PM51 PROTEIN HOMOLOG 2	1.07e+02	483	6	1.4	1745	1	ZOI_MOUSE	TIGHT JUNCTION PROTEIN	1.07e+02
411	6	1.4	868	1	MCN2_YEAST	MINICHROMOSOME MAINTEN	1.07e+02	484	6	1.4	1763	1	POLN_PCE9	NON-STRUCTURAL POLYPRO	1.07e+02
412	6	1.4	869	1	YD95_YEAST	HYPOTHETICAL 98.7 KDA	1.07e+02	485	6	1.4	2139	1	CRB_DROME	CROMBS PROTEIN PRECURS	1.07e+02
413	6	1.4	872	1	ADHE_GLOAB	ALDEHYDE-ALCOHOL DEHID	1.07e+02	486	6	1.4	2292	1	POLG_EMCVB	GENOME POLYPROTEIN (CO	1.07e+02
414	6	1.4	877	1	DPOL_LACLC	DNA POLYMERASE 1 (EC 2	1.07e+02	487	6	1.4	2366	1	TOXB_CLODI	GENOME POLYPROTEIN (CO	1.07e+02
415	6	1.4	885	1	AR36_SCHPO	ARG11 PROTEIN PRECURSO	1.07e+02	488	6	1.4	2524	1	NOTC_XENIA	NEUROGENIC LOCUS NOTCH	1.07e+02
416	6	1.4	887	1	YAV5_SCHPO	PROBABLE ATP-DEPENDENT	1.07e+02	489	6	1.4	2663	1	CENE_HUMAN	CENTROMERIC PROTEIN E	1.07e+02
417	6	1.4	892	1	IF2_CHLTR	TRANSLATION INITIATION	1.07e+02	490	6	1.4	3411	1	POLG_YEY1	GENOME POLYPROTEIN (CO	1.07e+02
418	6	1.4	909	1	CT1A_FUSSO	CUTINASE TRANSCRIPTION	1.07e+02	491	6	1.4	3411	1	POLG_YEY2	GENOME POLYPROTEIN (CO	1.07e+02
419	6	1.4	909	1	MC2_YEAST	MC2 PROTEIN.	1.07e+02	492	6	1.4	3491	1	ERY1_SACER	ERYTHRONOIDE SYNTHASE	1.07e+02
420	6	1.4	919	1	GLK3_RAT	GLUTAMATE RECEPTOR, IO	1.07e+02	493	6	1.4	3672	1	LM2_CAEEL	LAMININ-LIKE PROTEIN K	1.07e+02
421	6	1.4	919	1	GLK3_HUMAN	GLUTAMATE RECEPTOR, IO	1.07e+02	494	6	1.4	3898	1	POLG_HCVB	GENOME POLYPROTEIN.	1.07e+02
422	6	1.4	919	1	EXL3_HUMAN	EXOSTOSIN-LIKE 3 (PUTA	1.07e+02	495	6	1.4	4036	1	RPRP_DUGCV	RNA-DIRECTED RNA POLYM	1.07e+02
423	6	1.4	922	1	LCN2_LACLA	LACTICIN 481/LACIOCCO	1.07e+02	496	6	1.4	4092	1	DYHC_YEAST	DYENIN HEAVY CHAIN, CY	1.07e+02
424	6	1.4	927	1	B3AT_CHICK	BAND 3 ANION TRANSPORT	1.07e+02	497	6	1.4	4568	1	DYHC_CAEEL	DYENIN HEAVY CHAIN, CY	1.07e+02
425	6	1.4	927	1	B3AT_RAT	BAND 3 ANION EXCHANGE	1.07e+02	498	6	1.4	4568	1	RYNC_RABIT	RYNADINE RECEPTOR, CA	1.07e+02
426	6	1.4	929	1	B3AT_MOUSE	BAND 3 ANION EXCHANGE	1.07e+02	499	6	1.4	4969	1	MCN2_HUMAN	MUCIN 2 PRECURSOR (INT	1.07e+02
427	6	1.4	932	1	SECA_SYNY3	PREPROTEIN TRANSLOCASE	1.07e+02	500	6	1.4	5179	1	VP18_CLOHE	MUCIN 2 PRECURSOR (INT	1.07e+02
428	6	1.4	932	1	HIRL_SCHPO	HISTONE TRANSCRIPTION	1.07e+02	501	6	1.4	55	1	YOR7_TTVI	HYPOTHETICAL 6.1 KDA P	3.04e+03
429	6	1.4	941	1	AMPN_SCHPO	MUTS. PROTEIN HOMOLOG 1	1.07e+02	502	6	1.4	56	1	YOR7_TTVI	HYPOTHETICAL 6.5 KDA P	3.04e+03
430	6	1.4	942	1	AMPN_MANSE	AMINOPEPTIDASE N (EC 3	1.07e+02	503	6	1.4	62	1	YLP_MYCHO	HYPOTHETICAL 6.5 KDA P	3.04e+03
431	6	1.4	944	1	VP35_YEAST	VACUOLAR PROTEIN SORTI	1.07e+02	504	6	1.4	67	1	TRPF_METO	HYPOTHETICAL PROTEIN I	3.04e+03
432	6	1.4	953	1	YC07_YEAST	HYPOTHETICAL 107.9 KDA	1.07e+02	505	6	1.4	72	1	YHEU_ECOLI	HYPOTHETICAL 8.5 KDA P	3.04e+03
433	6	1.4	956	1	GLK4_HUMAN	GLUTAMATE RECEPTOR, IO	1.07e+02	506	6	1.4	72	1	YF77_HAEIN	HYPOTHETICAL 8.9 KDA P	3.04e+03
434	6	1.4	956	1	GLK4_RAT	GLUTAMATE RECEPTOR, IO	1.07e+02	507	6	1.4	73	1	YOR6_TTVI	HYPOTHETICAL 8.9 KDA P	3.04e+03
435	6	1.4	984	1	KBP1_CHICK	NUCLEAR FACTOR NF-KAPB	1.07e+02	508	6	1.4	73	1	YOR6_TTVI	HYPOTHETICAL 8.9 KDA P	3.04e+03
436	6	1.4	985	1	ENV_ROMAY	ENV POLYPROTEIN (COAT	1.07e+02	509	6	1.4	74	1	YMOG_SALTY	HYPOTHETICAL PROTEIN I	3.04e+03
437	6	1.4	992	1	EBN6_EBV	EBNA-6 NUCLEAR PROTEIN	1.07e+02	510	6	1.4	78	1	YPUK_ECOLI	HYPOTHETICAL 7.7 KDA P	3.04e+03
438	6	1.4	1002	1	MMUA_MYCTU	PUTATIVE MEMBRANE PROT	1.07e+02	511	6	1.4	84	1	YV77_YEAST	HYPOTHETICAL 9.7 KDA P	3.04e+03
439	6	1.4	1005	1	MMUA_DICDI	LYSOSOMAL ALPHAN-MANNOS	1.07e+02	512	6	1.4	87	1	YVNC_ECOLI	HYPOTHETICAL 11.2 KDA	3.04e+03
440	6	1.4	1008	1	MMUA_MYCLE	PUTATIVE MEMBRANE PROT	1.07e+02	513	6	1.4	93	1	YVAL_RHISP	INSERTION ELEMENT ISR1	3.04e+03
441	6	1.4	1015	1	DNM3_MOUSE	DNA LIGASE-III (EC 6.5	1.07e+02	514	6	1.4	95	1	YV12_CLOHE	INSERTION ELEMENT ISR1	3.04e+03
442	6	1.4	1025	1	SLAP_CAUCR	S-LAYER PROTEIN (PARAC	1.07e+02	515	6	1.4	97	1	YHBY_ECOLI	HYPOTHETICAL 10.7 KDA	3.04e+03
443	6	1.4	1043	1	EF3A_YEAST	ELONGATION FACTOR 3A (1.07e+02	516	6	1.4	102	1	YHBY_ECOLI	HYPOTHETICAL 10.8 KDA	3.04e+03
444	6	1.4	1043	1	EF3B_YEAST	ELONGATION FACTOR 3B (1.07e+02	517	6	1.4	104	1	YH82_ECOLI	INSERTION ELEMENTS ISR1	3.04e+03
445	6	1.4	1049	1	EF3_CANAL	ELONGATION FACTOR 3 (E	1.07e+02	518	6	1.4	107	1	YV04_YEAST	HYPOTHETICAL 11.7 KDA	3.04e+03
446	6	1.4	1051	1	ITV3_CRISP	INTEGRIN ALPHA-3 PRECU	1.07e+02	519	6	1.4	113	1	YV65_MYCTU	HYPOTHETICAL 13.0 KDA	3.04e+03
447	6	1.4	1053	1	RROC_BROTH	DNA-DIRECTED RNA POLYM	1.07e+02	520	6	1.4	114	1	YVRS_CAEEL	HYPOTHETICAL 11.3 KDA	3.04e+03
448	6	1.4	1056	1	MUC5_HUMAN	TRACHEOBRONCHIAL MUCIN	1.07e+02	521	6	1.4	114	1	YVCA_YEREN	HYPOTHETICAL 13.1 KDA	3.04e+03
449	6	1.4	1070	1	RROB_TOBAC	DNA-DIRECTED RNA POLYM	1.07e+02	522	6	1.4	115	1	YV11_METO	HYPOTHETICAL PROTEIN M	3.04e+03
450	6	1.4	1072	1	CARB_ECOLI	CARBAMOYL-PHOSPHATE SY	1.07e+02	523	6	1.4	115	1	YVXA_BACSU	HYPOTHETICAL 13.0 KDA	3.04e+03
451	6	1.4	1073	1	ITAB_MOUSE	INTEGRIN ALPHA-6 PRECU	1.07e+02	524	6	1.4	116	1	YV92_YEAST	HYPOTHETICAL 13.4 KDA	3.04e+03
452	6	1.4	1074	1	CARB_SALTY	CARBAMOYL-PHOSPHATE SY	1.07e+02	525	6	1.4	119	1	YVJD_ECOLI	HYPOTHETICAL 13.9 KDA	3.04e+03
453	6	1.4	1076	1	HSEB_CAVPO	HEAT-STABLE ENTEROTOXI	1.07e+02	526	6	1.4	120	1	YVVS_YEAST	HYPOTHETICAL 13.9 KDA	3.04e+03
454	6	1.4	1081	1	PDR6_YEAST	PILOTROPIC DRUG RESIS	1.07e+02	527	6	1.4	120	1	YVBI_ECOLI	HYPOTHETICAL 14.0 KDA	3.04e+03
455	6	1.4	1087	1	XYNX_CLODM	EXOGLUCANASE XYNA PREC	1.07e+02	528	6	1.4	122	1	YH88_YEAST	VERY HYPOTHETICAL 14.2	3.04e+03
456	6	1.4	1118	1	YPT4_CAEEL	HYPOTHETICAL 127.3 KDA	1.07e+02	529	6	1.4	123	1	YV09_CAEEL	HYPOTHETICAL 14.8 KDA	3.04e+03
457	6	1.4	1132	1	JAK2_HUMAN	TYROSINE-PROTEIN KINAS	1.07e+02	530	6	1.4	123	1	YV89_YEAST	HYPOTHETICAL 14.8 KDA	3.04e+03
458	6	1.4	1132	1	JAK2_RAT	TYROSINE-PROTEIN KINAS	1.07e+02	531	6	1.4	123	1	YV89_YEAST	HYPOTHETICAL 14.8 KDA	3.04e+03
459	6	1.4	1141	1	MEM2_CAEEL	MEMBRANE-ASSOCIATED PR	1.07e+02	532	6	1.4	125	1	YV89_YEAST	HYPOTHETICAL 15.0 KDA	3.04e+03
460	6	1.4	1175	1	PTRNF_RAT	PROTEIN-TYROSINE PHOSP	1.07e+02	533	6	1.4	126	1	YV89_YEAST	HYPOTHETICAL 15.0 KDA	3.04e+03
461	6	1.4	1176	1	PTRNF_MOUSE	PROTEIN-TYROSINE PHOSP	1.07e+02	534	6	1.4	127	1	YV89_YEAST	HYPOTHETICAL 14.4 KDA	3.04e+03

535	5	1.1	129	1	YB2_YEAST	HYPOTHETICAL_14.4 KDA	3.04e+03	608	5	1.1	242	1	YURK_BACSU	HYPOTHETICAL_TRANSCRIP	3.04e+03
536	5	1.1	129	1	YOFX_BACSU	HYPOTHETICAL_13.9 KDA	3.04e+03	609	5	1.1	245	1	YOD1_CAEEL	HYPOTHETICAL_28.3 KDA	3.04e+03
537	5	1.1	132	1	YXEC_BACSU	HYPOTHETICAL_15.7 KDA	3.04e+03	610	5	1.1	246	1	YPT3_MYCU	HYPOTHETICAL_26.2 KDA	3.04e+03
538	5	1.1	134	1	YORD_TTV1	HYPOTHETICAL_15.4 KDA	3.04e+03	611	5	1.1	248	1	YIUL_LISMO	HYPOTHETICAL_OXIDOREU	3.04e+03
539	5	1.1	134	1	YNB2_YEAST	HYPOTHETICAL_14.7 KDA	3.04e+03	612	5	1.1	248	1	YIUNL_ECOLI	PROBABLE ARP-DEPENDENT	3.04e+03
540	5	1.1	135	1	YND4_METJA	HYPOTHETICAL_PROTEIN M	3.04e+03	613	5	1.1	250	1	YMI9_MYCU	HYPOTHETICAL_26.9 KDA	3.04e+03
541	5	1.1	138	1	YNC8_CAEEL	HYPOTHETICAL_15.3 KDA	3.04e+03	614	5	1.1	259	1	YG31_YEAST	HYPOTHETICAL_27.2 KDA	3.04e+03
542	5	1.1	143	1	YONH_TTV1	HYPOTHETICAL_16.6 KDA	3.04e+03	615	5	1.1	260	1	YQGR_BACSU	HYPOTHETICAL_ABC TRANS	3.04e+03
543	5	1.1	143	1	YPP9_MYCU	HYPOTHETICAL_15.0 KDA	3.04e+03	616	5	1.1	262	1	YXBG_BACSU	HYPOTHETICAL_OXIDOREU	3.04e+03
544	5	1.1	145	1	YPM6_YEAST	HYPOTHETICAL_16.9 KDA	3.04e+03	617	5	1.1	262	1	YKVA_CAEEL	HYPOTHETICAL_30.0 KDA	3.04e+03
545	5	1.1	145	1	YERC_SCHPO	HYPOTHETICAL_16.8 KDA	3.04e+03	618	5	1.1	265	1	YR44_CAEEL	HYPOTHETICAL_30.0 KDA	3.04e+03
546	5	1.1	148	1	YJBE_STRCO	HYPOTHETICAL_15.9 KDA	3.04e+03	619	5	1.1	270	1	YR44_MYCC	HYPOTHETICAL_31.5 KDA	3.04e+03
547	5	1.1	148	1	YPT3_STRCO	HYPOTHETICAL_15.9 KDA	3.04e+03	620	5	1.1	270	1	YOP1_BACSU	HYPOTHETICAL_30.3 KDA	3.04e+03
548	5	1.1	149	1	YQBN_BACSU	HYPOTHETICAL_17.1 KDA	3.04e+03	621	5	1.1	273	1	YGN8_YEAST	HYPOTHETICAL_30.7 KDA	3.04e+03
549	5	1.1	150	1	YVP3_AGR19	HYPOTHETICAL_16.1 KDA	3.04e+03	622	5	1.1	273	1	YGF0_YEAST	ZINC FINGER PROTEIN-80	3.04e+03
550	5	1.1	150	1	YQ24_BPH1	POTATIVE_TAIL_TUBE PRO	3.04e+03	623	5	1.1	273	1	ZNB0_PONPY	ZINC FINGER PROTEIN-80	3.04e+03
551	5	1.1	151	1	Y228_AQUAE	HYPOTHETICAL_PROTEIN A	3.04e+03	624	5	1.1	273	1	ZNB0_PANTR	ZINC FINGER PROTEIN 80	3.04e+03
552	5	1.1	151	1	YRC3_YEAST	HYPOTHETICAL_17.5 KDA	3.04e+03	625	5	1.1	273	1	ZNB0_GORGO	ZINC FINGER PROTEIN 80	3.04e+03
553	5	1.1	151	1	YPT3_ECOLI	HYPOTHETICAL_17.1 KDA	3.04e+03	626	5	1.1	274	1	YG15_YEAST	HYPOTHETICAL_32.1 KDA	3.04e+03
554	5	1.1	155	1	YHCH_HAEIN	HYPOTHETICAL_PROTEIN H	3.04e+03	627	5	1.1	275	1	YD84_YEAST	HYPOTHETICAL_30.0 KDA	3.04e+03
555	5	1.1	156	1	YMS6_CAEEL	HYPOTHETICAL_16.9 KDA	3.04e+03	628	5	1.1	276	1	YGBR_ECOLI	HYPOTHETICAL_32.4 KDA	3.04e+03
556	5	1.1	158	1	YNI9_YEAST	HYPOTHETICAL_17.1 KDA	3.04e+03	629	5	1.1	280	1	YG4_YEAST	HYPOTHETICAL_32.0 KDA	3.04e+03
557	5	1.1	159	1	YB21_MYCU	HYPOTHETICAL_16.4 KDA	3.04e+03	630	5	1.1	281	1	YH11_ABRPE	HYPOTHETICAL_PROTEIN A	3.04e+03
558	5	1.1	159	1	YB27_YEAST	HYPOTHETICAL_18.1 KDA	3.04e+03	631	5	1.1	281	1	YK45_STYH3	HYPOTHETICAL_30.4 KDA	3.04e+03
559	5	1.1	160	1	YGA0_PSEPU	HYPOTHETICAL_16.7 KDA	3.04e+03	632	5	1.1	281	1	YTKC_BACSU	HYPOTHETICAL_33.3 KDA	3.04e+03
560	5	1.1	167	1	YPT4_MYCU	HYPOTHETICAL_19.0 KDA	3.04e+03	633	5	1.1	282	1	YK05_YEAST	HYPOTHETICAL_32.1 KDA	3.04e+03
561	5	1.1	167	1	YQ20_HAEIN	HYPOTHETICAL_PROTEIN H	3.04e+03	634	5	1.1	284	1	YPV2_METTP	HYPOTHETICAL_33.2 KDA	3.04e+03
562	5	1.1	167	1	YPA2_ASCIM	HYPOTHETICAL_19.7 KDA	3.04e+03	635	5	1.1	285	1	YN26_YEAST	HYPOTHETICAL_32.3 KDA	3.04e+03
563	5	1.1	168	1	YH11_AZOBIR	HYPOTHETICAL_18.6 KDA	3.04e+03	636	5	1.1	286	1	YND3_CAEEL	HYPOTHETICAL_32.1 KDA	3.04e+03
564	5	1.1	169	1	YS4L_PNECA	POTATIVE_40S RIBOSOMAL	3.04e+03	637	5	1.1	286	1	YGBR_EDMIC	HYPOTHETICAL_30.6 KDA	3.04e+03
565	5	1.1	170	1	YHE3_YEAST	HYPOTHETICAL_19.8 KDA	3.04e+03	638	5	1.1	288	1	YOD5_CAEEL	HYPOTHETICAL_33.2 KDA	3.04e+03
566	5	1.1	175	1	YHIE_ECOLI	HYPOTHETICAL_20.6 KDA	3.04e+03	639	5	1.1	289	1	YRAN_BACSU	HYPOTHETICAL_TRANSCRIP	3.04e+03
567	5	1.1	175	1	YPEV_LACDL	HYPOTHETICAL_TRANSPORT	3.04e+03	640	5	1.1	289	1	YFK2_YEAST	HYPOTHETICAL_31.9 KDA	3.04e+03
568	5	1.1	179	1	YPOL_THERF	HYPOTHETICAL_PROTEIN I	3.04e+03	641	5	1.1	292	1	YKX2_YEAST	HYPOTHETICAL_32.1 KDA	3.04e+03
569	5	1.1	180	1	YXRI_HAEIN	HYPOTHETICAL_PROTEIN H	3.04e+03	642	5	1.1	292	1	YKX4_YEAST	HYPOTHETICAL_34.3 KDA	3.04e+03
570	5	1.1	183	1	ZEB2_MAIZE	ZEIN-BETA PRECURSOR (Z	3.04e+03	643	5	1.1	293	1	ZNB0_MACMO	ZINC FINGER PROTEIN 80	3.04e+03
571	5	1.1	188	1	YIAl_LACAC	HYPOTHETICAL_PROTEIN I	3.04e+03	644	5	1.1	293	1	YFIE_ECOLI	HYPOTHETICAL_TRANSCRIP	3.04e+03
572	5	1.1	189	1	YUVD_BACSU	HYPOTHETICAL_22.0 KDA	3.04e+03	645	5	1.1	295	1	YUST_BACSU	HYPOTHETICAL_TRANSCRIP	3.04e+03
573	5	1.1	189	1	YNOU_YEAST	VERY_HYPOTHETICAL_21.7	3.04e+03	646	5	1.1	295	1	YFIE_CANCR	HYPOTHETICAL_PROTEIN I	3.04e+03
574	5	1.1	189	1	YPT2_CAEEL	HYPOTHETICAL_21.6 KDA	3.04e+03	647	5	1.1	297	1	YMY9_YEAST	HYPOTHETICAL_34.0 KDA	3.04e+03
575	5	1.1	191	1	YGL2_STRCO	HYPOTHETICAL_20.1 KDA	3.04e+03	648	5	1.1	299	1	YKND_BACSU	HYPOTHETICAL_OXIDOREU	3.04e+03
576	5	1.1	193	1	YRBP_HAEIN	HYPOTHETICAL_PROTEIN H	3.04e+03	649	5	1.1	301	1	YND3_CAEEL	HYPOTHETICAL_33.7 KDA	3.04e+03
577	5	1.1	194	1	YMP9_CAEEL	HYPOTHETICAL_22.0 KDA	3.04e+03	650	5	1.1	301	1	YGL4_BACST	HYPOTHETICAL_31.5 KDA	3.04e+03
578	5	1.1	196	1	YKGR_ECOLI	HYPOTHETICAL_23.3 KDA	3.04e+03	651	5	1.1	301	1	YML6_MYCU	HYPOTHETICAL_35.7 KDA	3.04e+03
579	5	1.1	198	1	YMO3_YEAST	HYPOTHETICAL_22.7 KDA	3.04e+03	652	5	1.1	302	1	YUNT4_YEAST	HYPOTHETICAL_34.1 KDA	3.04e+03
580	5	1.1	200	1	YPT2_SCHPO	YPT1-RELATED PROTEIN 2	3.04e+03	653	5	1.1	302	1	YHCT_BACST	HYPOTHETICAL_33.7 KDA	3.04e+03
581	5	1.1	203	1	YR63_SCHPO	HYPOTHETICAL_23.2 KDA	3.04e+03	654	5	1.1	302	1	YR65_CAEEL	HYPOTHETICAL_34.8 KDA	3.04e+03
582	5	1.1	203	1	YH14_YEAST	HYPOTHETICAL_20.6 KDA	3.04e+03	655	5	1.1	303	1	YR65_CAEEL	HYPOTHETICAL_34.8 KDA	3.04e+03
583	5	1.1	204	1	YI18_YEAST	HYPOTHETICAL_22.8 KDA	3.04e+03	656	5	1.1	305	1	YHBU_HAEIN	HYPOTHETICAL_PROTEIN H	3.04e+03
584	5	1.1	207	1	YI0R_CVMT	HYPOTHETICAL_PROTEIN I	3.04e+03	657	5	1.1	307	1	YK55_YEAST	POTATIVE_AMINO-ACID AB	3.04e+03
585	5	1.1	208	1	YPD3_CAEEL	HYPOTHETICAL_24.4 KDA	3.04e+03	658	5	1.1	307	1	YML6_MYCU	HYPOTHETICAL_36.1 KDA	3.04e+03
586	5	1.1	210	1	YI1A_ECOLI	HYPOTHETICAL_GTP-BINDI	3.04e+03	659	5	1.1	308	1	YR05_HAEIN	HYPOTHETICAL_32.9 KDA	3.04e+03
587	5	1.1	212	1	YGBL_ECOLI	HYPOTHETICAL_23.2 KDA	3.04e+03	660	5	1.1	309	1	YHDS_BACSU	HYPOTHETICAL_PROTEIN H	3.04e+03
588	5	1.1	213	1	YH11_ARCPV	HYPOTHETICAL_PROTEIN A	3.04e+03	661	5	1.1	310	1	YHDC_ECOLI	HYPOTHETICAL_34.5 KDA	3.04e+03
589	5	1.1	214	1	Y2010_XENIA	COOCTE_ZINC FINGER PRO	3.04e+03	662	5	1.1	310	1	YK11_YEAST	36.1 KDA PROTEIN IN BU	3.04e+03
590	5	1.1	215	1	YG39_YEAST	HYPOTHETICAL_24.8 KDA	3.04e+03	663	5	1.1	315	1	YK16_CAEEL	HYPOTHETICAL_36.7 KDA	3.04e+03
591	5	1.1	216	1	YGB7_YEAST	HYPOTHETICAL_25.0 KDA	3.04e+03	664	5	1.1	319	1	YUMB_BACSU	HYPOTHETICAL_33.6 KDA	3.04e+03
592	5	1.1	217	1	YGD9_METTP	HYPOTHETICAL_PROTEIN M	3.04e+03	665	5	1.1	319	1	YH11_CRYPA	HYPOTHETICAL_33.6 KDA	3.04e+03
593	5	1.1	217	1	YRPA_BACSU	HYPOTHETICAL_25.1 KDA	3.04e+03	666	5	1.1	320	1	YH17_YEAST	HYPOTHETICAL_36.9 KDA	3.04e+03
594	5	1.1	218	1	YPT2_CAEEL	HYPOTHETICAL_24.2 KDA	3.04e+03	667	5	1.1	325	1	YOOD_BACSU	HYPOTHETICAL_36.4 KDA	3.04e+03
595	5	1.1	220	1	YPT3_YEAST	GTP-BINDING PROTEIN YP	3.04e+03	668	5	1.1	326	1	YR02_MYCN	HYPOTHETICAL_ABC TRANS	3.04e+03
596	5	1.1	222	1	YKGR_ECOLI	HYPOTHETICAL_25.6 KDA	3.04e+03	669	5	1.1	330	1	YERK_BACSU	HYPOTHETICAL_35.8 KDA	3.04e+03
597	5	1.1	225	1	YRNI_CAEEL	HYPOTHETICAL_25.2 KDA	3.04e+03	670	5	1.1	331	1	YU44_METJA	HYPOTHETICAL_PROTEIN M	3.04e+03
598	5	1.1	227	1	YRVA_METTE	HYPOTHETICAL_24.7 KDA	3.04e+03	671	5	1.1	332	1	YI1K_HAEIN	HYPOTHETICAL_PROTEIN H	3.04e+03
599	5	1.1	228	1	YR16_MYCU	HYPOTHETICAL_24.6 KDA	3.04e+03	672	5	1.1	338	1	YR1V_HAEIN	POTATIVE_ARSENICAL_POM	3.04e+03
600	5	1.1	229	1	YRNM_ECOLI	TRNA (GUANOSINE-2'-O-)	3.04e+03	673	5	1.1	338	1	YDHR_ECOLI	HYPOTHETICAL_38.0 KDA	3.04e+03
601	5	1.1	231	1	YR44_YEAST	HYPOTHETICAL_25.1 KDA	3.04e+03	674	5	1.1	340	1	YK65_CAEEL	HYPOTHETICAL_38.8 KDA	3.04e+03
602	5	1.1	232	1	YR23_YEAST	HYPOTHETICAL_26.3 KDA	3.04e+03	675	5	1.1	341	1	YK51_YEAST	HYPOTHETICAL_39.8 KDA	3.04e+03
603	5	1.1	238	1	YR23_AGRV1	HYPOTHETICAL_26.7 KDA	3.04e+03	676	5	1.1	342	1	YK52_BACSU	HYPOTHETICAL_40.6 KDA	3.04e+03
604	5	1.1	238	1	YRBN_ECOLI	HYPOTHETICAL_28.0 KDA	3.04e+03	677	5	1.1	344	1	YK20_YEAST	HYPOTHETICAL_39.6 KDA	3.04e+03
605	5	1.1	239	1	YK07_CAEEL	HYPOTHETICAL_26.6 KDA	3.04e+03	678	5	1.1	346	1	YK53_CAEEL	HYPOTHETICAL_38.8 KDA	3.04e+03
606	5	1.1	239	1	YK07_CAEEL	HYPOTHETICAL_26.6 KDA	3.04e+03	679	5	1.1	346	1	YK53_CAEEL	HYPOTHETICAL_38.8 KDA	3.04e+03
607	5	1.1	241	1	YI12_METJA	HYPOTHETICAL_PROTEIN M	3.04e+03	680	5	1.1	347	1	YBP7_YEAST	HYPOTHETICAL_38.1 KDA	3.04e+03

681	5	1.1	347	YPRC_ECOLI	HYPOTHETICAL 38.7 KDA	3.04e+03	754	449	1	YUCD_ECOLI	HYPOTHETICAL 45.7 KDA	3.04e+03
682	5	1.1	349	YHNT_ECOLI	HYPOTHETICAL 38.5 KDA	3.04e+03	755	452	1	YNA2_YEAST	HYPOTHETICAL 51.2 KDA	3.04e+03
683	5	1.1	352	Z1B5_MOUSE	ZINC FINGER PROTEIN 18	3.04e+03	756	452	1	Z1B5_MOUSE	ZINC FINGER PROTEIN 18	3.04e+03
684	5	1.1	360	YQFA_CAEEL	HYPOTHETICAL 39.7 KDA	3.04e+03	757	453	1	YWS5_CAEEL	HYPOTHETICAL 49.8 KDA	3.04e+03
685	5	1.1	361	YMO1_CAEEL	PROBABLE G PROTEIN-COU	3.04e+03	758	455	1	Y1I2_MYCTU	HYPOTHETICAL 48.1 KDA	3.04e+03
686	5	1.1	366	YQCC_BACSU	HYPOTHETICAL 41.5 KDA	3.04e+03	759	456	1	YMO5_CAEEL	HYPOTHETICAL 51.6 KDA	3.04e+03
687	5	1.1	366	YHKO_YEAST	HYPOTHETICAL 42.3 KDA	3.04e+03	760	456	1	YMO5_YEAST	HYPOTHETICAL 51.0 KDA	3.04e+03
688	5	1.1	367	YMI1_PASTE	HYPOTHETICAL 43.7 KDA	3.04e+03	761	457	1	YMO9_YEAST	HYPOTHETICAL 52.2 KDA	3.04e+03
689	5	1.1	367	YMP4_STRCO	HYPOTHETICAL 42.5 KDA	3.04e+03	762	457	1	YGO9_HAEIN	HYPOTHETICAL 51.8 KDA	3.04e+03
690	5	1.1	371	YHDX_BACSU	HYPOTHETICAL 42.9 KDA	3.04e+03	763	457	1	YK04_CAEEL	HYPOTHETICAL 51.8 KDA	3.04e+03
691	5	1.1	376	YHNC_YEAST	HYPOTHETICAL 42.0 KDA	3.04e+03	764	463	1	YNAJ_BACSU	HYPOTHETICAL 51.9 KDA	3.04e+03
692	5	1.1	376	YK03_CAEEL	HYPOTHETICAL 42.6 KDA	3.04e+03	765	464	1	YGSV_CAEEL	HYPOTHETICAL 51.9 KDA	3.04e+03
693	5	1.1	377	YPR8_BACSU	POU DOMAIN PROTEIN ZP-	3.04e+03	766	465	1	YQ18_RHME	HYPOTHETICAL 53.8 KDA	3.04e+03
694	5	1.1	384	ZP47_BRARE	HYPOTHETICAL 43.5 KDA	3.04e+03	767	468	1	YPS7_CAEEL	PUTATIVE SERINE/THREON	3.04e+03
695	5	1.1	385	YCG7_YEAST	HYPOTHETICAL 43.4 KDA	3.04e+03	768	469	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
696	5	1.1	387	YCT2_BACFI	HYPOTHETICAL 43.4 KDA	3.04e+03	769	471	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
697	5	1.1	397	YF20_METJA	HYPOTHETICAL 40.5 KDA	3.04e+03	770	471	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
698	5	1.1	389	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	771	472	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
699	5	1.1	390	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	772	472	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
700	5	1.1	392	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	773	474	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
701	5	1.1	393	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	774	474	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
702	5	1.1	394	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	775	477	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
703	5	1.1	396	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	776	477	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
704	5	1.1	397	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	777	482	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
705	5	1.1	398	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	778	484	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
706	5	1.1	398	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	779	486	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
707	5	1.1	399	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	780	488	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
708	5	1.1	400	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	781	491	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
709	5	1.1	402	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	782	491	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
710	5	1.1	403	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	783	491	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
711	5	1.1	403	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	784	497	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
712	5	1.1	403	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	785	497	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
713	5	1.1	404	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	786	498	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
714	5	1.1	404	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	787	498	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
715	5	1.1	405	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	788	499	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
716	5	1.1	405	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	789	500	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
717	5	1.1	407	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	790	501	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
718	5	1.1	408	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	791	503	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
719	5	1.1	408	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	792	503	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
720	5	1.1	411	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	793	504	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
721	5	1.1	411	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	794	505	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
722	5	1.1	413	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	795	514	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
723	5	1.1	413	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	796	516	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
724	5	1.1	413	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	797	519	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
725	5	1.1	414	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	798	520	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
726	5	1.1	414	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	799	520	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
727	5	1.1	415	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	800	523	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
728	5	1.1	419	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	801	527	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
729	5	1.1	419	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	802	529	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
730	5	1.1	421	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	803	533	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
731	5	1.1	421	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	804	533	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
732	5	1.1	422	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	805	534	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
733	5	1.1	423	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	806	535	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
734	5	1.1	423	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	807	536	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
735	5	1.1	423	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	808	539	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
736	5	1.1	424	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	809	540	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
737	5	1.1	425	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	810	541	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
738	5	1.1	425	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	811	541	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
739	5	1.1	428	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	812	543	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
740	5	1.1	428	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	813	543	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
741	5	1.1	430	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	814	544	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
742	5	1.1	431	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	815	547	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
743	5	1.1	431	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	816	551	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
744	5	1.1	432	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	817	552	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
745	5	1.1	432	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	818	552	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
746	5	1.1	437	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	819	558	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
747	5	1.1	438	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	820	562	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
748	5	1.1	438	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	821	564	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
749	5	1.1	439	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	822	568	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
750	5	1.1	439	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	823	568	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
751	5	1.1	443	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	824	571	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
752	5	1.1	446	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	825	575	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03
753	5	1.1	447	YH08_YEAST	HYPOTHETICAL 42.9 KDA	3.04e+03	826	577	1	YH05_CAEEL	PUTATIVE SERINE CARBOX	3.04e+03

827	5	1.1	581	1	YMF7_YEAST	HYPOTHETICAL 65.2 KDA	3.04e+03	900	5	1.1	776	1	YI4A_CAEEL	HYPOTHETICAL 86.9 KDA	3.04e+03
828	5	1.1	585	1	YMF7_CAEEL	HYPOTHETICAL 65.3 KDA	3.04e+03	901	5	1.1	780	1	YOM1_CAEEL	HYPOTHETICAL 88.3 KDA	3.04e+03
829	5	1.1	585	1	YK58_YEAST	HYPOTHETICAL 68.3 KDA	3.04e+03	902	5	1.1	782	1	YNN2_YEAST	HYPOTHETICAL 84.8 KDA	3.04e+03
830	5	1.1	587	1	YID6_YEAST	HYPOTHETICAL 65.3 KDA	3.04e+03	903	5	1.1	786	1	Y8A_CAEEL	HYPOTHETICAL 84.3 KDA	3.04e+03
831	5	1.1	587	1	YKRO_YEAST	HYPOTHETICAL 67.5 KDA	3.04e+03	904	5	1.1	796	1	YE2_YEAST	POTATIVE 90.2 KDA ZINC	3.04e+03
832	5	1.1	593	1	YK28_YEAST	POTATIVE TRANSPORTER Y	3.04e+03	905	5	1.1	799	1	ZEK1_MOUSE	ZINC FINGER X-CHROMOSOM	3.04e+03
833	5	1.1	597	1	YKPA_KLUFA	HYPOTHETICAL KILLER PL	3.04e+03	906	5	1.1	800	1	ZEK1_MOUSE	ZINC FINGER X-CHROMOSOM	3.04e+03
834	5	1.1	599	1	YV06_CAEEL	HYPOTHETICAL 66.2 KDA	3.04e+03	907	5	1.1	801	1	ZEK1_MOUSE	ZINC FINGER X-CHROMOSOM	3.04e+03
835	5	1.1	607	1	YK28_CAEEL	HYPOTHETICAL 66.2 KDA	3.04e+03	908	5	1.1	804	1	YNA4_CAEEL	HYPOTHETICAL 91.0 KDA	3.04e+03
836	5	1.1	607	1	YKRO_YEAST	HYPOTHETICAL 70.2 KDA	3.04e+03	909	5	1.1	805	1	ZEK1_MOUSE	ZINC FINGER X-CHROMOSOM	3.04e+03
837	5	1.1	610	1	YKRO_YEAST	PROBABLE ATP-DEPENDENT	3.04e+03	910	5	1.1	807	1	YNA1_MOUSE	HYPOTHETICAL 91 KDA PR	3.04e+03
838	5	1.1	610	1	YKRO_YEAST	POTATIVE ABC TRANSPORT	3.04e+03	911	5	1.1	811	1	Y96_YEAST	HYPOTHETICAL 92.0 KDA	3.04e+03
839	5	1.1	614	1	YK28_CAEEL	HYPOTHETICAL 69.0 KDA	3.04e+03	912	5	1.1	821	1	YK28_CAEEL	HYPOTHETICAL 93.4 KDA	3.04e+03
840	5	1.1	615	1	YK28_CAEEL	HYPOTHETICAL 69.0 KDA	3.04e+03	913	5	1.1	823	1	YK28_CAEEL	HYPOTHETICAL 95.6 KDA	3.04e+03
841	5	1.1	618	1	YK28_CAEEL	POTATIVE 70.4 KDA TRAN	3.04e+03	914	5	1.1	839	1	YK28_CAEEL	ZINC FINGER X-CHROMOSOM	3.04e+03
842	5	1.1	624	1	YK28_CAEEL	HYPOTHETICAL 71.4 KDA	3.04e+03	915	5	1.1	852	1	YK28_CAEEL	HYPOTHETICAL 96.0 KDA	3.04e+03
843	5	1.1	627	1	YK28_CAEEL	HYPOTHETICAL 70.9 KDA	3.04e+03	916	5	1.1	863	1	YK28_CAEEL	POTATIVE 101.8 KDA TRA	3.04e+03
844	5	1.1	630	1	YK28_CAEEL	HYPOTHETICAL 70.9 KDA	3.04e+03	917	5	1.1	873	1	YK28_CAEEL	HYPOTHETICAL 99.0 KDA	3.04e+03
845	5	1.1	632	1	YK28_CAEEL	HYPOTHETICAL 69.8 KDA	3.04e+03	918	5	1.1	876	1	YK28_CAEEL	HYPOTHETICAL 98.9 KDA	3.04e+03
846	5	1.1	633	1	YK28_CAEEL	HYPOTHETICAL 73.0 KDA	3.04e+03	919	5	1.1	881	1	YK28_CAEEL	HYPOTHETICAL 97.7 KDA	3.04e+03
847	5	1.1	633	1	YK28_CAEEL	HYPOTHETICAL 72.9 KDA	3.04e+03	920	5	1.1	881	1	YK28_CAEEL	HYPOTHETICAL 97.7 KDA	3.04e+03
848	5	1.1	636	1	YK28_CAEEL	HYPOTHETICAL 67.4 KDA	3.04e+03	921	5	1.1	886	1	YK28_CAEEL	HYPOTHETICAL 98.0 KDA	3.04e+03
849	5	1.1	638	1	YK28_CAEEL	HYPOTHETICAL 71.7 KDA	3.04e+03	922	5	1.1	887	1	YK28_CAEEL	TYROSINE-PROTEIN KINAS	3.04e+03
850	5	1.1	642	1	YK28_CAEEL	HYPOTHETICAL 71.2 KDA	3.04e+03	923	5	1.1	888	1	YK28_CAEEL	TYROSINE-PROTEIN KINAS	3.04e+03
851	5	1.1	644	1	YK28_CAEEL	TRANSPOSABLE ELEMENT H	3.04e+03	924	5	1.1	888	1	YK28_CAEEL	TYROSINE-PROTEIN KINAS	3.04e+03
852	5	1.1	644	1	YK28_CAEEL	HYPOTHETICAL 74.0 KDA	3.04e+03	925	5	1.1	892	1	YK28_CAEEL	HYPOTHETICAL 100.9 KDA	3.04e+03
853	5	1.1	646	1	YK28_CAEEL	HYPOTHETICAL 70.5 KDA	3.04e+03	926	5	1.1	893	1	YK28_CAEEL	HYPOTHETICAL 100.7 KDA	3.04e+03
854	5	1.1	648	1	YK28_CAEEL	ZINC FINGER PROTEIN 20	3.04e+03	927	5	1.1	898	1	YK28_CAEEL	HYPOTHETICAL 104.7 KDA	3.04e+03
855	5	1.1	653	1	YK28_CAEEL	HYPOTHETICAL 75.9 KDA	3.04e+03	928	5	1.1	904	1	YK28_CAEEL	HYPOTHETICAL 102.3 KDA	3.04e+03
856	5	1.1	653	1	YK28_CAEEL	HYPOTHETICAL 75.5 KDA	3.04e+03	929	5	1.1	906	1	YK28_CAEEL	HYPOTHETICAL 103.6 KDA	3.04e+03
857	5	1.1	655	1	YK28_CAEEL	HYPOTHETICAL 75.9 KDA	3.04e+03	930	5	1.1	915	1	YK28_CAEEL	ZDS1 PROTEIN (NCL) PRO	3.04e+03
858	5	1.1	660	1	YK28_CAEEL	HYPOTHETICAL 73.9 KDA	3.04e+03	931	5	1.1	915	1	YK28_CAEEL	HYPOTHETICAL 102.5 KDA	3.04e+03
859	5	1.1	667	1	YK28_CAEEL	HYPOTHETICAL 73.9 KDA	3.04e+03	932	5	1.1	923	1	YK28_CAEEL	HYPOTHETICAL 103.9 KDA	3.04e+03
860	5	1.1	676	1	YK28_CAEEL	HYPOTHETICAL 76.2 KDA	3.04e+03	933	5	1.1	925	1	YK28_CAEEL	HYPOTHETICAL 105.5 KDA	3.04e+03
861	5	1.1	678	1	YK28_CAEEL	HYPOTHETICAL 76.2 KDA	3.04e+03	934	5	1.1	926	1	YK28_CAEEL	HYPOTHETICAL 103.6 KDA	3.04e+03
862	5	1.1	678	1	YK28_CAEEL	HYPOTHETICAL 75.4 KDA	3.04e+03	935	5	1.1	936	1	YK28_CAEEL	HYPOTHETICAL 106.5 KDA	3.04e+03
863	5	1.1	679	1	YK28_CAEEL	HYPOTHETICAL 75.4 KDA	3.04e+03	936	5	1.1	942	1	YK28_CAEEL	ZDS2 PROTEIN	3.04e+03
864	5	1.1	683	1	YK28_CAEEL	ZINC FINGER PROTEIN 26	3.04e+03	937	5	1.1	952	1	YK28_CAEEL	HYPOTHETICAL 105.3 KDA	3.04e+03
865	5	1.1	683	1	YK28_CAEEL	HYPOTHETICAL 76.4 KDA	3.04e+03	938	5	1.1	958	1	YK28_CAEEL	HYPOTHETICAL 108.2 KDA	3.04e+03
866	5	1.1	688	1	YK28_CAEEL	HYPOTHETICAL 80.2 KDA	3.04e+03	939	5	1.1	965	1	YK28_CAEEL	HYPOTHETICAL 108.5 KDA	3.04e+03
867	5	1.1	689	1	YK28_CAEEL	HYPOTHETICAL OXIDOREDU	3.04e+03	940	5	1.1	971	1	YK28_CAEEL	HYPOTHETICAL 111.8 KDA	3.04e+03
868	5	1.1	689	1	YK28_CAEEL	HYPOTHETICAL 72.8 KDA	3.04e+03	941	5	1.1	983	1	YK28_CAEEL	HYPOTHETICAL 110.7 KDA	3.04e+03
869	5	1.1	691	1	YK28_CAEEL	HYPOTHETICAL 75.1 KDA	3.04e+03	942	5	1.1	986	1	YK28_CAEEL	HYPOTHETICAL 107.7 KDA	3.04e+03
870	5	1.1	692	1	YK28_CAEEL	PROBABLE G PROTEIN-COU	3.04e+03	943	5	1.1	989	1	YK28_CAEEL	HYPOTHETICAL 112.2 KDA	3.04e+03
871	5	1.1	697	1	YK28_CAEEL	HYPOTHETICAL ABC TRANS	3.04e+03	944	5	1.1	993	1	YK28_CAEEL	POTATIVE ATP-DEPENDENT	3.04e+03
872	5	1.1	701	1	YK28_CAEEL	HYPOTHETICAL 81.2 KDA	3.04e+03	945	5	1.1	997	1	YK28_CAEEL	HYPOTHETICAL 110.9 KDA	3.04e+03
873	5	1.1	713	1	YK28_CAEEL	ZONA PELLUCIDA SPEM-B	3.04e+03	946	5	1.1	1018	1	YK28_CAEEL	HYPOTHETICAL 115.2 KDA	3.04e+03
874	5	1.1	720	1	YK28_CAEEL	HYPOTHETICAL 82.1 KDA	3.04e+03	947	5	1.1	1036	1	YK28_CAEEL	HYPOTHETICAL 118.2 KDA	3.04e+03
875	5	1.1	721	1	YK28_CAEEL	HYPOTHETICAL 80.0 KDA	3.04e+03	948	5	1.1	1070	1	YK28_CAEEL	HYPOTHETICAL 123.0 KDA	3.04e+03
876	5	1.1	725	1	YK28_CAEEL	HYPOTHETICAL 80.0 KDA	3.04e+03	949	5	1.1	1073	1	YK28_CAEEL	HYPOTHETICAL 119.5 KDA	3.04e+03
877	5	1.1	732	1	YK28_CAEEL	HYPOTHETICAL 81.8 KDA	3.04e+03	950	5	1.1	1086	1	YK28_CAEEL	NAD(P) TRANSHYDROGENAS	3.04e+03
878	5	1.1	733	1	YK28_CAEEL	HYPOTHETICAL 81.0 KDA	3.04e+03	951	5	1.1	1086	1	YK28_CAEEL	NAD(P) TRANSHYDROGENAS	3.04e+03
879	5	1.1	735	1	YK28_CAEEL	HYPOTHETICAL 80.5 KDA	3.04e+03	952	5	1.1	1088	1	YK28_CAEEL	HYPOTHETICAL 126.6 KDA	3.04e+03
880	5	1.1	737	1	YK28_CAEEL	HYPOTHETICAL 84.6 KDA	3.04e+03	953	5	1.1	1095	1	YK28_CAEEL	PROBABLE ATP-DEPENDENT	3.04e+03
881	5	1.1	742	1	YK28_CAEEL	ZINC FINGER AUTOSOMAL	3.04e+03	954	5	1.1	1107	1	YK28_CAEEL	HYPOTHETICAL 123.8 KDA	3.04e+03
882	5	1.1	742	1	YK28_CAEEL	HYPOTHETICAL 84.2 KDA	3.04e+03	955	5	1.1	1110	1	YK28_CAEEL	HYPOTHETICAL 124.5 KDA	3.04e+03
883	5	1.1	743	1	YK28_CAEEL	HYPOTHETICAL 84.0 KDA	3.04e+03	956	5	1.1	1117	1	YK28_CAEEL	HYPOTHETICAL 121.1 KDA	3.04e+03
884	5	1.1	744	1	YK28_CAEEL	HYPOTHETICAL 80.2 KDA	3.04e+03	957	5	1.1	1118	1	YK28_CAEEL	HYPOTHETICAL 128.7 KDA	3.04e+03
885	5	1.1	745	1	YK28_CAEEL	ZONA PELLUCIDA SPEM-B	3.04e+03	958	5	1.1	1122	1	YK28_CAEEL	HYPOTHETICAL 128.8 KDA	3.04e+03
886	5	1.1	745	1	YK28_CAEEL	ZONA PELLUCIDA SPEM-B	3.04e+03	959	5	1.1	1130	1	YK28_CAEEL	HYPOTHETICAL 130.5 KDA	3.04e+03
887	5	1.1	747	1	YK28_CAEEL	HYPOTHETICAL 83.2 KDA	3.04e+03	960	5	1.1	1139	1	YK28_CAEEL	HYPOTHETICAL 122.2 KDA	3.04e+03
888	5	1.1	750	1	YK28_CAEEL	HYPOTHETICAL 81.0 KDA	3.04e+03	961	5	1.1	1187	1	YK28_CAEEL	PROBABLE CANTON-TRANSP	3.04e+03
889	5	1.1	754	1	YK28_CAEEL	HYPOTHETICAL 83.4 KDA	3.04e+03	962	5	1.1	1222	1	YK28_CAEEL	HYPOTHETICAL 136.3 KDA	3.04e+03
890	5	1.1	757	1	YK28_CAEEL	HYPOTHETICAL 83.4 KDA	3.04e+03	963	5	1.1	1223	1	YK28_CAEEL	POTATIVE TYROSINE-PROT	3.04e+03
891	5	1.1	757	1	YK28_CAEEL	HYPOTHETICAL 88.3 KDA	3.04e+03	964	5	1.1	1228	1	YK28_CAEEL	HYPOTHETICAL 143.6 KDA	3.04e+03
892	5	1.1	758	1	YK28_CAEEL	HYPOTHETICAL 88.3 KDA	3.04e+03	965	5	1.1	1231	1	YK28_CAEEL	HYPOTHETICAL 143.6 KDA	3.04e+03
893	5	1.1	759	1	YK28_CAEEL	HYPOTHETICAL 87.4 KDA	3.04e+03	966	5	1.1	1237	1	YK28_CAEEL	POTATIVE SERINE-THREON	3.04e+03
894	5	1.1	764	1	YK28_CAEEL	HYPOTHETICAL 87.2 KDA	3.04e+03	967	5	1.1	1238	1	YK28_CAEEL	HYPOTHETICAL 141.1 KDA	3.04e+03
895	5	1.1	765	1	YK28_CAEEL	HYPOTHETICAL 82.7 KDA	3.04e+03	968	5	1.1	1240	1	YK28_CAEEL	HYPOTHETICAL 141.5 KDA	3.04e+03
896	5	1.1	766	1	YK28_CAEEL	HYPOTHETICAL 86.9 KDA	3.04e+03	969	5	1.1	1244	1	YK28_CAEEL	HYPOTHETICAL 139.1 KDA	3.04e+03
897	5	1.1	767	1	YK28_CAEEL	POTATIVE CYSTEINYL-TRN	3.04e+03	970	5	1.1	1257	1	YK28_CAEEL	HYPOTHETICAL 143.2 KDA	3.04e+03
898	5	1.1	767	1	YK28_CAEEL	HYPOTHETICAL 86.6 KDA	3.04e+03	971	5	1.1	1264	1	YK28_CAEEL	HYPOTHETICAL 145.6 KDA	3.04e+03
899	5	1.1	770	1	YK28_CAEEL	HYPOTHETICAL 84.2 KDA	3.04e+03	972	5	1.1	1267	1	YK28_CAEEL	POTATIVE ATP-DEPENDENT	3.04e+03

973 5 1.1 1286 1 YKVS_YEAST HYPOTHETICAL 140.4 KDA 3.04e+03
 974 5 1.1 1308 1 YK2_XENLA TRANSPOSOM T11 HYPOHE 3.04e+03
 975 5 1.1 1328 1 YK5_YEAST TRANSPOSOM TY1 PROTEIN 3.04e+03
 976 5 1.1 1358 1 Z261_HUMAN ZINC FINGER PROTEIN 26 3.04e+03
 977 5 1.1 1361 1 YME9_YEAST HYPOTHETICAL 153.8 KDA 3.04e+03
 978 5 1.1 1391 1 YLDS_CAEEL HYPOTHETICAL 157.0 KDA 3.04e+03
 979 5 1.1 1403 1 YGN1_YEAST HYPOTHETICAL 163.2 KDA 3.04e+03
 980 5 1.1 1411 1 YM4_YEAST HYPOTHETICAL 162.7 KDA 3.04e+03
 981 5 1.1 1420 1 YMB8_YEAST HYPOTHETICAL 163.6 KDA 3.04e+03
 982 5 1.1 1541 1 YH6_YEAST HYPOTHETICAL 175.8 KDA 3.04e+03
 983 5 1.1 1585 1 YH0_BACSU HYPOTHETICAL 171.0 KDA 3.04e+03
 984 5 1.1 1592 1 YHDS_YEAST PROBABLE APP-DEPENDENT 3.04e+03
 985 5 1.1 1612 1 YP2B_CRILO DNA TOPOISOMERASE II, 3.04e+03
 986 5 1.1 1626 1 YP2B_HUMAN DNA TOPOISOMERASE II, 3.04e+03
 987 5 1.1 1636 1 YN7_YEAST HYPOTHETICAL 186.8 KDA 3.04e+03
 988 5 1.1 1679 1 YMF9_YEAST HYPOTHETICAL 187.1 KDA 3.04e+03
 989 5 1.1 1736 1 ZOI_HUMAN TIGHT JUNCTION PROTEIN 3.04e+03
 990 5 1.1 1748 1 YNR2_YEAST HYPOTHETICAL 196.1 KDA 3.04e+03
 991 5 1.1 1753 1 YEM2_YEAST HYPOTHETICAL 195.4 KDA 3.04e+03
 992 5 1.1 1769 1 YK9_YEAST HYPOTHETICAL 200.0 KDA 3.04e+03
 993 5 1.1 1941 1 YRM8_CAEEL HYPOTHETICAL 216.3 KDA 3.04e+03
 994 5 1.1 1967 1 YGSO_YEAST PUTATIVE HELICASE YGR2 3.04e+03
 995 5 1.1 2111 1 YP84_CAEEL HYPOTHETICAL ZINC FING 3.04e+03
 996 5 1.1 2298 1 C215_HUMAN 258.1 KDA PROTEIN C210 3.04e+03
 997 5 1.1 2717 1 ZEP1_HUMAN ZINC FINGER PROTEIN 40 3.04e+03
 998 5 1.1 3443 1 YOG7_CAEEL HYPOTHETICAL 375.7 KDA 3.04e+03
 999 5 1.1 4385 1 YP73_CAEEL HYPOTHETICAL 486.0 KDA 3.04e+03
 1000 5 1.1 4385 1 YP73_CAEEL HYPOTHETICAL 486.0 KDA 3.04e+03

ALIGNMENTS

RESULT 1 STANDARD: PRT: 557 AA.
 ID INRL HUMAN
 AC P17181:
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA-CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNARI OR IFNAR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90124632.
 RA Uze G., Lutfalla G., Gresser I.,
 RT "Genetic transfer of a functional human interferon" alpha receptor
 RT into mouse cells: cloning and expression of its cDNA.";
 RT Cell 60:225-234(1990).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 92129376.
 RX Lutfalla G., Gardiner K., Proudhon D., Vieh E., Uze G.,
 RT "The structure of the human interferon alpha/beta receptor gene.";
 RT J. Biol. Chem. 267:2802-2809(1992).
 RL [3]
 RN PHOSPHORYLATION BY TYR2.
 RP MEDLINE: 95059042.
 RX Coleman J. O., Yan H., Domanski P., Hande R., Smalley D.,
 RA Mullerstein J., Witte M., Krishnan K., Krolewski J.,
 RT "Direct binding to and tyrosine phosphorylation of the alpha subunit
 RT of the type I interferon receptor by p135tyk2 tyrosine kinase.";
 RT Mol. Cell. Biol. 14:8133-8142(1994).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I TRIPS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA AND BETA.
 CC SUBUNIT: THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
 CC EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
 CC -1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYR2 TYROSINE KINASE.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: J03171; AAA52730.1; -
 DR EMBL: X60459; CAA42892.1; -
 DR PIR: A32694; A32694.
 DR PIR: S17112; S17112.
 DR MIM: 107450; -
 KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 KW Phosphorylation.
 FT SIGNAL 1 27
 FT CHAIN 28 557
 FT POTENTIAL.
 FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT CHAIN.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM.
 FT CYTOPLASMIC (POTENTIAL).
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT PHOSPHORYLATION (BY TYR2) (PROBABLE).
 FT MOD_RES 481 481
 FT MOD_RES 50 50
 FT CARBOHYD 58 58
 FT CARBOHYD 81 81
 FT CARBOHYD 81 81
 FT CARBOHYD 88 88
 FT CARBOHYD 110 110
 FT CARBOHYD 110 110
 FT CARBOHYD 172 172
 FT CARBOHYD 254 254
 FT CARBOHYD 313 313
 FT CARBOHYD 314 314
 FT CARBOHYD 314 314
 FT CARBOHYD 376 376
 FT CARBOHYD 416 416
 FT CARBOHYD 433 433
 FT CARBOHYD 433 433
 FT VARIANT 168 168
 FT L -> V
 FT /FTID=VAR.002717.
 FT G -> A (IN REF. 2).
 FT CONFLICT 17 17
 FT SEQUENCE 557 AA; 63525 MW; 0F6744C8A1ADB273 CRC64;
 SQ
 Query Match 100.0%; Score 436; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MAAVLLGATTLVLAAGVFWVLSAAGGRNLSPOKVEVDIIDDFILKRNSSDSVGNVT 60
 Oy 1 MAAVLLGATTLVLAAGVFWVLSAAGGRNLSPOKVEVDIIDDFILKRNSSDSVGNVT 60
 Db 61 FSPDYORTGDMNWKLSGCCONITSTKCNFSSLAKNVEIKLRIRAEKENTSSVTEPDSF 120
 Oy 61 FSPDYORTGDMNWKLSGCCONITSTKCNFSSLAKNVEIKLRIRAEKENTSSVTEPDSF 120
 Db 61 FSPDYORTGDMNWKLSGCCONITSTKCNFSSLAKNVEIKLRIRAEKENTSSVTEPDSF 120
 Oy 61 FSPDYORTGDMNWKLSGCCONITSTKCNFSSLAKNVEIKLRIRAEKENTSSVTEPDSF 120
 Db 121 TPFRAOIGPEVLEAEADKAIVIHISPGTDSVMALDGLSFYSLILKRNSSGVEERI 180
 Oy 121 TPFRAOIGPEVLEAEADKAIVIHISPGTDSVMALDGLSFYSLILKRNSSGVEERI 180
 Db 181 ENIYSRRKIKYKLSPEYTYCLKVAALLTSMKIGVYSPVHCITKTYVEHELPPEPIEVSQ 240
 Oy 181 ENIYSRRKIKYKLSPEYTYCLKVAALLTSMKIGVYSPVHCITKTYVEHELPPEPIEVSQ 240
 Db 241 NONVYLRKMDTYAMTQVOMLAFLKRNNGNHLKAKOIPDCNVYVTCQVPOQNFQK 300
 Oy 241 NONVYLRKMDTYAMTQVOMLAFLKRNNGNHLKAKOIPDCNVYVTCQVPOQNFQK 300
 Db 241 NONVYLRKMDTYAMTQVOMLAFLKRNNGNHLKAKOIPDCNVYVTCQVPOQNFQK 300
 Oy 241 NONVYLRKMDTYAMTQVOMLAFLKRNNGNHLKAKOIPDCNVYVTCQVPOQNFQK 300
 Db 301 GYILVRQASDGNNTSFWSEIKFDTIOAFLLPVPVNISSLDSFPIYIGAPQSGNTP 360
 Oy 301 GYILVRQASDGNNTSFWSEIKFDTIOAFLLPVPVNISSLDSFPIYIGAPQSGNTP 360
 Db 361 VIODYPLIYEITFEWNTSNAERKIIERTDVYVNLRLTYVYCVKAAHATMDERLKNSSV 420

OY 361 VIADYPLIEILMENTSNMERKIIKKIDVYTPNKLPLTYCVKARAHMDKLKSSV 420
 DB 421 FSDVACEKTRPGNTSK 436
 OY 421 FSDVACEKTRPGNTSK 436

RESULT 2
 ID INRI-SHEEP STANDARD: PRT; 560 AA.
 AC 028589; 095206;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
 DE INTERFERON-ALPHA/BETA RECEPTOR-1)
 GN IFNAR1 OR IFNAR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ENDOMETRIUM;
 RX MEDLINE: 97135690.
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
 RT "Structure of an ovine interferon receptor and its expression in
 endometrium."
 RL J. Mol. Endocrinol. 17:207-215(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ENDOMETRIUM;
 RX MEDLINE: 98006426.
 RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
 RT "Molecular cloning of ovine and bovine type I interferon receptor
 subunits from uteri, and endometrial expression of messenger
 ribonucleic acid for ovine receptors during the estrous cycle and
 pregnancy."
 RL Endocrinology 138:4757-4767(1997).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA- AND BETA-
 SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
 CONCEPTUS AT DAY 15 OF PREGNANCY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC EMBL: X95939; CAA65183.1;
 DR EMBL: U65978; AAB84231.1;
 DR PFAM: PF00041; fn3; 1.
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 560
 FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT CHAIN 25 560
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 438 458
 FT DOMAIN 459 560
 FT DISULFID 76 84
 FT DISULFID 199 220
 FT CARBOHYD 47 47
 FT CARBOHYD 55 55
 FT CARBOHYD 85 85
 FT CARBOHYD 108 108
 FT POTENTIAL.

FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 222 222 POTENTIAL.
 FT CARBOHYD 285 285 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 359 359 POTENTIAL.
 FT CARBOHYD 377 377 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CONFLICT 352 352 S -> G (IN REF. 2).
 FT CONFLICT 522 522 A -> D (IN REF. 2).
 SO SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;
 Query Match 3.48; Score 15; DB 1; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1,71e-21;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 395 PNKLPLTYCVKARA 409
 OY 394 PNKLPLTYCVKARA 408
 RESULT 3
 ID INRI BOVIN STANDARD: PRT; 560 AA.
 AC 004730;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNAR1 OR IFNAR.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG;
 RX MEDLINE: 93076908.
 RA Mouchel-Vielh E., Lutfalla G., Mogenssen K.E., Uze G.;
 RT "Specific antiviral activities of the human alpha interferons are
 determined at the level of receptor (IFNAR) structure."
 RL FEBS Lett. 313:255-259(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 93305725.
 RA Lim J.-K., Langer J.A.;
 RT "Cloning and characterization of a bovine alpha interferon receptor."
 RT Blooming Biophys. Acta 1173:314-319(1993).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA- AND BETA-
 SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
 CONCEPTUS AT DAY 15 OF PREGNANCY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC EMBL: X68443; CAA48484.1;
 DR EMBL: I06320; AAO02571.1;
 DR PIR: S33770; S33770;
 DR PIR: S27387; S27387;
 DR PFAM: PF00041; fn3; 1.
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 560
 FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT CHAIN 25 560
 FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 438 458 POTENTIAL.
 FT DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 76 84 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 47 47 POTENTIAL.
 FT CARBOHYD 55 55 POTENTIAL.
 FT CARBOHYD 85 85 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 313 313 POTENTIAL.
 FT CARBOHYD 377 377 POTENTIAL.
 FT CARBOHYD 434 434 POTENTIAL.
 FT CONFLICT 422 422 F->V (IN REF. 2).
 SQ SEQUENCE 560 AA; 63818 MW; 66D76B72861E1D11 CRC64;

Query Match 3.0%; Score 13; DB 1; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1,40e-15;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 397 LKPLTVICVAKARA 409
 396 LKPLTVICVAKARA 408

RESULT 4
 ID INRLMOUSE STANDARD; PRT; 590 AA.
 AC P33896;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
 GN IFNAR1 OR IFNAR OR IFAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 92262522.
 RX Use G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
 RT "Behavior of a cloned murine interferon alpha/beta receptor expressed
 in homospicific or heterospicific background";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 I IFNS. TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 SUBUNITS THEMSELVES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II-CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II-CYTOKINE FAMILY OF RECEPTORS.
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 CC
 CC EMBL: M89641.1, AAA37890.1;
 DR PIR: A45283, A45283.
 DR MGD: MGI107658; IFNAR.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 590 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 CHAIN.
 FT DOMAIN 27 429 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 430 449 POTENTIAL.
 FT DOMAIN 450 590 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 78 86 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT CARBOHYD 43 43 POTENTIAL.
 FT CARBOHYD 109 109 POTENTIAL.

FT CARBOHYD 181 181 POTENTIAL.
 FT CARBOHYD 214 214 POTENTIAL.
 FT CARBOHYD 314 314 POTENTIAL.
 FT CARBOHYD 370 370 POTENTIAL.
 FT CARBOHYD 409 409 POTENTIAL.
 FT CARBOHYD 413 413 POTENTIAL.
 SQ SEQUENCE 590 AA; 65776 MW; 7EC6FEF370185D2A CRC64;

Query Match 2.5%; Score 11; DB 1; Length 590;
 Best Local Similarity 100.0%; Pred. No. 5,20e-10;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 363 YEIFMENTSN 373
 369 YEIFMENTSN 379

RESULT 5
 ID BRK_MEGFL STANDARD; PRT; 11 AA.
 AC P12797;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MEGASCOLIAKININ (6-THR-BRADYKININ-LYS-ALA) [CONTAINS: BRADYKININ-LIKE
 PEPTIDE (THR-6-BRADYKININ)].
 OS Megascollia flavifrons (Garden dagger wasp) (Solitary wasp).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Scolioidea; Scollidae; Megascollia.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE; 87293024.
 RX Yasubara T., Mantel P., Nakajima T., Plek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 solitary wasp Megascollia flavifrons.";
 RL Toxicon 25:527-535(1987).
 CC [2]
 RN
 RP SEQUENCE.
 RA Nakajima T., Plek T., Yasunara T., Mantel P.;
 RT "Two kinins isolated from the venom of Megascollia flavifrons.";
 RL Toxicon 26:34-34(1988).
 CC -1- FUNCTION: BOTH PROTEINS HAVE BRADYKININ-LIKE, ALTHOUGH LOWER
 ACTIVITIES (E.G. SMOOTH MUSCLE CONTRACTION).
 CC -1- SUBCELLULAR LOCATION: WASP VENOM RESERVOIRS.
 DR PIR: A26744; A26744.
 DR PIR: B26744; B26744.
 DR PIR: A28609; A28609.
 KW Bradykinin; Vasodilator.
 FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
 FT PEPTIDE 1 11 MEGASCOLIAKININ.
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1,63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 5 FTPEPKA 11
 120 FTPEPKA 126

RESULT 6
 ID APP8_COTVA STANDARD; PRT; 55 AA.
 AC P50682;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
 GN ATP8 OR APP8.
 OS Coturnix coturnix japonica (Japanese quail).
 OC Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Coturnix.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Ramirez V., Morals R.;
 RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBUNIT OF THE CHAINS OF THE NONMEMBRANIC COMPONENT
 CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
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 CC or send an email to license@sib-sib.ch)
 CC
 CC EMBL: U36794; AAA76731.1;
 DR PFAA: PF00895; ATP-synt_8; 1;
 KM Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
 FT TRANSMEM 8
 RL
 SQ SEQUENCE: 55 AA; 6494 MW; B284AFD91399AE1B CRC64;

Query Match 1.6%; Score 7; DB 1; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 FTYSLI 24
 OY 163 FTYSLI 169

RESULT 7
 ID AANT HDVMI STANDARD; PRT; 195 AA.
 AC P25881;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last annotation update)
 DE DELTA ANTIGEN.
 CC Hepatitis delta virus (Isolate Japanese M-1) (HDV).
 CC Viruses; Deltavirus.
 CC [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 91012805.
 RA Imazeki F., Omata M., Ono M.
 RL "Heterogeneity and evolution rates of delta virus RNA sequences."
 RL J. Virol. 64:5594-5599(1990).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- DISEASE: BINDS SPECIFICALLY TO ANTISERA FROM PATIENTS WITH CHRONIC
 CC HEPATITIS DELTA VIRAL INFECTIONS.
 CC -1- MISCELLANEOUS: DELTA ANTIGEN BINDS SPECIFICALLY TO HDV RNA.
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 CC
 CC EMBL: D90190; BAA14214.1;
 DR PIR: A36409; SAVIDM;
 DR PFAA: PF01517; HDV_ag; 1;
 KM Antigen; RNA-binding; Nuclear protein; Phosphorylation.
 SQ SEQUENCE: 195 AA; 21811 MW; FOAF63C16F746F1 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 AAGKRL 122
 OY 24 AAGKRL 30

RESULT 8
 ID TRT3_COTJA STANDARD; PRT; 252 AA.
 AC P06398; P06397;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE TROPONIN T, FAST SKELETAL MUSCLE ISOFORM.
 OS Coturnix coturnix japonica (Japanese quail).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Coturnix.
 CC [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 89308680.
 RA Bucher E.A., de la Brousse F.C., Emerson C.P. Jr.;
 RT "Developmental and muscle-specific regulation of avian fast skeletal
 RT tropomyosin T isoform expression by mRNA splicing."
 RL J. Biol. Chem. 264:12482-12491(1989).
 CC [2]
 RP SEQUENCE OF 108-252 FROM N.A.
 RX MEDLINE: 86033836.
 RA Hastings K.E.M., Bucher E.A., Emerson C.P. Jr.;
 RT "Generation of tropomyosin T isoforms by alternative RNA splicing in
 RT avian skeletal muscle. Conserved and divergent features in birds and
 RT mammals."
 RL J. Biol. Chem. 260:13699-13703(1985).
 CC -1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
 CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONTERS
 CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
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 CC
 CC EMBL: M26600; AAA49506.1;
 DR EMBL: M26599; AAA49505.1;
 DR EMBL: M11685; AAA49504.1;
 DR EMBL: M11684; AAA49503.1;
 DR PIR: A03084; TPQJ72.
 DR PIR: A03084; TPQJ71.
 DR PFAA: PF00992; Tropoin; 1.
 KM Muscle protein; Alternative splicing; Multigene family;
 FT Phosphorylation.
 FT INIT MET 0
 FT MOD. RES 1 1
 FT VARSPPLIC 27 30
 FT VARSPPLIC 225 237
 FT
 SQ SEQUENCE: 252 AA; 29967 MW; 67BED1A595C3C997 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 252;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 104 RIRAEK 110
 OY 103 RIRAEK 109

RESULT 9
 ID TRT3_HUMAN STANDARD; PRT; 257 AA.

AC P45378;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE TROPONIN T, FAST SKELETAL MUSCLE ISOFORM BETA (BETA TMTF).
 GN TMTF3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FETAL SKELETAL MUSCLE;
 RX MEDLINE; 94226695.
 RA Wu O.-L., Jha P.K., Raychowdhury M.K., Du Y., Leavis P.C.,
 SA Sarker S.;
 RT "Isolation and characterization of human fast skeletal beta tropoin
 T cDNA: comparative sequence analysis of isoforms and insight into
 the evolution of members of a multigene family.";
 RL DNA Cell Biol. 13:217-233(1994).
 CC -1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
 CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS
 CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
 CC -1- TISSUE SPECIFICITY: IN FETAL AND ADULT FAST SKELETAL MUSCLES, WITH
 CC A HIGHER LEVEL EXPRESSION IN FETAL THAN IN ADULT MUSCLE.
 CC -----
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 CC -----
 DR EMBL; M21984; AAA36777.1;
 DR MIM; 6006932;
 DR PFM; PF00992; Tropoin; 1.
 DR Muscle protein; Multigene family; Phosphorylation.
 KW INT_MET 0 0
 FT MOD_RES 1 1
 FT PHOSPHORYLATION (BY CK2)
 FT (BY SIMILARITY).
 SQ SEQUENCE 257 AA; 30465 MW; FA33B3626BE597D9 CRC64;
 Query Match 1 68; Score 7; DB 1; Length 257;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RX MEDLINE; 85201690.
 RA Bretthart R.E., Nguyen H.T., Medford R.M., Destree A.T., Mahdavi V.,
 RT "Indicate combinatorial patterns of exon splicing generate multiple
 regulated tropoin T isoforms from a single gene.";
 RL Cell 41:67-82(1985).
 CC -1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
 CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS
 CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 44 ISOFORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING. THE ALPHA AND BETA FORMS ARE PRODUCED BY THE
 CC USE OF MUTUALLY EXCLUSIVE EXONS.
 CC -----
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 CC -----
 DR EMBL; M15202; CAB24794.1;
 DR EMBL; M15202; AAA96446.1;
 DR EMBL; M15202; CAB24796.1;
 DR EMBL; M15202; CAB24802.1;
 DR EMBL; M15202; CAB24798.1;
 DR EMBL; M15202; CAB24789.1;
 DR EMBL; M15202; CAB24800.1;
 DR EMBL; M15202; CAB24809.1;
 DR EMBL; M15202; CAB24803.1;
 DR EMBL; M15202; CAB24793.1;
 DR EMBL; M15202; AAA96447.1;
 DR EMBL; M15202; AAA96442.1;
 DR EMBL; M15202; AAA96461.1;
 DR EMBL; M15202; AAA96443.1;
 DR EMBL; M15202; CAB24810.1;
 DR EMBL; M15202; CAB24806.1;
 DR EMBL; M15202; AAA96452.1;
 DR EMBL; M15202; CAB24797.1;
 DR EMBL; M15202; CAB24801.1;
 DR EMBL; M15202; AAA96455.1;
 DR EMBL; M15202; AAA96457.1;
 DR EMBL; M15202; AAA96458.1;
 DR EMBL; M15202; AAA96459.1;
 DR EMBL; M15202; CAB24790.1;
 DR EMBL; M15202; CAB24804.1;
 DR EMBL; M15202; CAB24808.1;
 DR EMBL; M15202; CAB24805.1;
 DR EMBL; M15202; AAA96460.1;
 DR EMBL; M15202; CAB24795.1;
 DR EMBL; M15202; AAA96462.1;
 DR EMBL; M15202; CAB24791.1;
 DR EMBL; M15202; CAB24807.1;
 DR EMBL; M15202; AAA96469.1;
 DR EMBL; M15202; CAB24792.1;
 DR EMBL; M15202; AAA96466.1;
 DR EMBL; M15202; AAA96470.1;
 DR EMBL; M15202; AAA96478.1;
 DR EMBL; M15202; AAA96479.1;
 DR EMBL; M15202; AAA96480.1;
 DR PIR; A24824; A24824.
 DR PFM; PF00992; Tropoin; 1.
 DR Muscle protein; Alternative splicing; Multigene family;
 KW Phosphorylation.
 FT INT_MET 0 0
 FT MOD_RES 1 1
 FT PHOSPHORYLATION (BY CK2)
 FT (BY SIMILARITY).
 VARSPIC 9 14 MISSING (IN SOME CLASS 1 ISOFORMS).

SQ SEQUENCE 262 AA; 31010 MM; F6B867C9ACEE77ED CRC64;
 Query Match 1.6%; Score 7; DB 1; Length 262;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 114 RIRAKE 120
 111111
 0Y 103 RIRAKE 109
 RESULT 12
 ID TRGT_RABIT STANDARD; PRT; 278 AA.
 AC P02641; P19349; P19350;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS.
 GN TNNT3.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE OF 1-10: 17-43 AND 56-278.
 RX MEDLINE; 77118575.
 RA Pearlstone J.R., Johnson P., Carpenter M.R., Smillie L.B.;
 RT "Primary structure of rabbit skeletal muscle troponin-T. Sequence
 RT determination of the NH2-terminal fragment CB3 and the complete
 RT sequence of troponin-T";
 RL J. Biol. Chem. 252:983-989(1977).
 RN [2]
 RP SEQUENCE OF 1-66 FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-SKELETAL MUSCLE;
 RX MEDLINE; 93345743.
 RA Briggs M.M., Schachet F.;
 RT "Origin of fetal troponin T: developmentally regulated splicing of a
 RT new exon in the fast troponin T gene";
 RL Dev. Biol. 158:503-509(1993).
 RN [3]
 RP SEQUENCE OF 1-66 FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-SKELETAL MUSCLE;
 RX MEDLINE; 90323375.
 RA Briggs M.M., McIntosh H.D., Schachet F.;
 RT "Transitions from fetal to fast troponin T isoforms are coordinated
 RT with changes in tropomyosin and alpha-actinin isoforms in developing
 RT rabbit skeletal muscle";
 RL Dev. Biol. 140:253-260(1990).
 RN [4]
 RP SEQUENCE OF 1-66 FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-SKELETAL MUSCLE;
 RA Briggs M.M., Schachet F.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-43 AND 56-65.
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-SKELETAL MUSCLE;
 RX MEDLINE; 89199646.
 RA Briggs M.M., Schachet F.;
 RT "N-terminal, amino acid sequences of three functionally different
 RT troponin T isoforms from rabbit fast skeletal muscle";
 RL J. Mol. Biol. 206:245-249(1989).
 RN [6]
 RP PHOSPHORYLATION SITES.
 RC MEDLINE; 77157104.
 RA Moir A.J.G., Cole H.A., Perry S.V.;
 RT "The phosphorylation sites of troponin T from white skeletal muscle
 RT and the effects of interaction with troponin C on their
 RT phosphorylation by phosphorylase kinase";
 RL Biochem. J. 161:371-382(1977).
 CC -1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
 CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS
 CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
 CC -1- ALTERNATIVE PRODUCTS: MANY DIFFERENT ISOFORMS ARE GENERATED BY A
 CC DIFFERENTIAL MNA SPLICING MECHANISM. THE FORM TNNT1 IS SHOWN

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CC IN VITRO BY PHOSPHORYLASE KINASE.
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DR EMBL: U04970; AAA16023.1; -
DR EMBL: U04971; AAA16024.1; -
DR EMBL: U04972; AAA16025.1; -
DR EMBL: U04973; AAA16026.1; -
DR EMBL: U04974; AAA16027.1; -
DR EMBL: U04975; AAA16028.1; -
DR EMBL: U04976; AAA16029.1; -
DR EMBL: U04977; AAA16030.1; -
DR EMBL: U04978; AAA16031.1; -
DR PIR: A03083; TPPTS.
DR PIR: S03590; S03590.
DR PIR: S03591; S03591.
DR PIR: S03592; S03592.
DR PIR: PF00992; Tropoin. 1.
DR PIR: PF00992; Tropoin. 1.
DR Muscle protein; Multigene family; Phosphorylation; Acetylation;
DR Alternative splicing.
FT INIT MET 0
FT MOD RES 1 1 ACETYLATION.
FT MOD RES 1 1 PHOSPHORYLATION (BY CK2).
FT VASPLIC 11 16 MISSING (IN TMT2F, TMT2.5F AND TMT4F).
FT VASPLIC 22 38 MISSING (IN TMT3, TMT3F AND TMT4F).
FT VASPLIC 32 38 MISSING (IN TMT3, TMT3F AND TMT4F).
FT VASPLIC 44 55 MISSING (IN TMT1F, TMT2F, TMT2FA, TMT2.5F).
FT VASPLIC 44 55 TMT2.5F, TMT3F AND TMT4F.
FT CONFLICT 19 19 O -> E (IN REF. 1).
FT CONFLICT 35 36 VH -> HV (IN REF. 1 AND 5).
FT CONFLICT 61 61 MISSING (IN REF. 1).
FT SEQUENCE 278 AA; 32903 MM; 3D5A7E5F61E4CA9 CMC64;
Query Match 1.6%; Score 7; DB 1; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.63e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 128 RIRAEKE 134
DB 103 RIRAEKE 109

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RX MEDLINE: 97067142.
RX Rhee S., Ebersperger C., Dembic Z., Pestka S.;
RX "The structure of the gene for the second chain of the human
RX Interferon gamma receptor."
RX J. Biol. Chem. 271:28947-28952(1996).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR
CC SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
CC THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO
CC INTERACT WITH GAF, JAK1, AND/OR JAK2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL: U05875; AAA16955.1; -
DR EMBL: U05877; AAA16956.1; -
DR EMBL: U06875; AAC52066.1; -
DR MIM: 147369; -
DR PIR: PF00041; fn3. 1.
DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 27
FT CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.
FT DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 269 337 POTENTIAL.
FT CARBOHYD 56 56 POTENTIAL.
FT CARBOHYD 85 85 POTENTIAL.
FT CARBOHYD 110 110 POTENTIAL.
FT CARBOHYD 137 137 POTENTIAL.
FT CARBOHYD 219 219 POTENTIAL.
FT CARBOHYD 231 231 POTENTIAL.
FT VARIANT 64 64 R -> Q.
FT SEQUENCE 337 AA; 37834 MM; 18C61B10AD90E509 CMC64;
Query Match 1.6%; Score 7; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.63e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 142 PENIEV 148
DB 231 PENIEV 237

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CC -1- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE ETF ALPHA-SUBUNIT / FIXB FAMILY.
CC
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CC
CC EMBL: M15546; AAA21769.1; -
CC PIR: B26952; B26952.
CC PFAM: PF00766; ETF_alpha.1.
CC PROSITE: P500696; ETF_ALPHA.1.
CC Electron transport; Flavoprotein; FAD; Nitrogen fixation;
CC Plasmid.
CC NP_BIND 283 311 FAD (ADP PART) (POTENTIAL).
CC SEQUENCE 353 AA; 37786 MW; 8142B04B4C08546 CRC64;
CC
CC Query Match 1.6%; Score 7; DB 1; Length 353;
CC Best Local Similarity 100.0%; Pred. No. 1.63e+00;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 109 LGATTL 115
CC
CC OY 5 LGATTL 11
CC
CC RESULT 15
CC ID FIXA_RHISN STANDARD; PRT; 369 AA.
CC AC 053209;
CC DT 01-NOV-1997 (Rel. 35; Created)
CC DT 01-NOV-1997 (Rel. 35; Last sequence update)
CC DT 15-FEB-2000 (Rel. 39; Last annotation update)
CC DE FIXB PROTEIN.
CC GN FIXB OR Y4YA.
CC OS Rhizobium sp. (strain NGR234).
CC OC Plasmid sym pNGR234a.
CC OG Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC CC Rhizobiaceae; Rhizobium.
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE: 97305956.
CC RA Freilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
CC Perret X.;
CC RT "Molecular basis of symbiosis between Rhizobium and legumes.";
CC RL Nature 387:394-401(1997).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE: 96389014.
CC RA Freilberg C., Perret X., Broughton W.J., Rosenthal A.;
CC RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
CC NGR334 using dye terminators and a thermostable 'sequenase' : a
CC beginning.";
CC RL Genome Res. 6:590-600(1996).
CC CC
CC -1- FUNCTION: MAY PLAY A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN
CC FIXATION.
CC
CC -1- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE ETF ALPHA-SUBUNIT / FIXB FAMILY.
CC
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CC
CC EMBL: Z68203; CAA92416.1; -
CC EMBL: AF000100; AAB91889.1; -
CC PFAM: PF00766; ETF_alpha.1.
CC PROSITE: P500696; ETF_ALPHA.1.
CC PROSITE: P500696; ETF_ALPHA.1.

KW Electron transport; Flavoprotein; FAD; Nitrogen fixation; Plasmid.
FT NP_BIND 299 327 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 369 AA; 39851 MW; C4B5DB56FA1C08A CRC64;
CC
CC Query Match 1.6%; Score 7; DB 1; Length 369;
CC Best Local Similarity 100.0%; Pred. No. 1.63e+00;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 125 LGATTL 131
CC
CC OY 5 LGATTL 11
CC
CC RESULT 16
CC ID FIXB_AZOCA STANDARD; PRT; 369 AA.
CC AC P26483;
CC DT 01-AUG-1992 (Rel. 23; Created)
CC DT 01-AUG-1992 (Rel. 23; Last sequence update)
CC DT 15-FEB-2000 (Rel. 39; Last annotation update)
CC DE FIXB PROTEIN.
CC GN FIXB.
CC OS Azorhizobium caulinodans.
CC OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC CC Hyphomicrobium group; Azorhizobium.
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN-OR5571;
CC RX MEDLINE: 91203829.
CC RA Argion F., Kaminski P.A., Hennecke H., Elmerich C.;
CC RT "Nucleotide sequence of the fixABC region of Azorhizobium caulinodans
CC OR5571: similarity of the fixB product with eukaryotic flavoproteins,
CC characterisation of fixB, and identification of nifH.";
CC RL Mol. Gen. Genet. 225:514-520(1991).
CC CC
CC -1- FUNCTION: MAY PLAY A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN
CC FIXATION.
CC
CC -1- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE ETF ALPHA-SUBUNIT / FIXB FAMILY.
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CC
CC EMBL: X55450; CAA39092.1; -
CC PIR: S14071; S14071.
CC DR HSPD: P13804; LEFV.
CC DR PFAM: PF00766; ETF_alpha.1.
CC DR PROSITE: P500696; ETF_ALPHA.1.
CC KW Electron transport; Flavoprotein; FAD; Nitrogen fixation.
CC FT NP_BIND 289 327 FAD (ADP PART) (POTENTIAL).
CC SQ SEQUENCE 369 AA; 39712 MW; F73BA68B40C751BB CRC64;
CC
CC Query Match 1.6%; Score 7; DB 1; Length 369;
CC Best Local Similarity 100.0%; Pred. No. 1.63e+00;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 125 LGATTL 131
CC
CC OY 5 LGATTL 11
CC
CC RESULT 17
CC ID FIXB_BRAJA STANDARD; PRT; 369 AA.
CC AC P10449;
CC DT 01-MAR-1999 (Rel. 10; Created)
CC DT 01-OCT-1996 (Rel. 34; Last sequence update)
CC DT 15-FEB-2000 (Rel. 39; Last annotation update)
CC DE FIXB PROTEIN.
CC GN FIXB.
CC OS Bradyrhizobium japonicum.

CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Bradyrhizobium group; Bradyrhizobium.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN-USDA 31B110;
 CC MEDLINE: 96172413.
 CC RA Weidenhaupt M., Rossi P., Beck C., Fischer H.M., Hennecke H.;
 CC "Bradyrhizobium japonicum possesses two discrete sets of electron
 CC transfer flavoprotein genes: fixA, fixB and etfA, etfB, etfL";
 CC Arch. Microbiol. 165:169-178(1996).
 CC [2]
 CC SEQUENCE OF 1-45 FROM N.A.
 CC STRAIN-110SPC4;
 CC MEDLINE: 89343618.
 CC RA Gubler M., Zurcher T., Hennecke H.;
 CC "The Bradyrhizobium japonicum fixBCX operon: identification of fixX
 CC and of a 5' mRNA region affecting the level of the fixBCX
 CC transcript";
 CC Mol. Microbiol. 3:141-148(1989).
 CC -1- FUNCTION: MAY PLAY A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN
 CC FIXATION.
 CC -1- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE ETF ALPHA-SUBUNIT / FIXB FAMILY.
 CC -----
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 CC -----
 CC EMBL: U32227; AAB00903.1; -;
 CC DR EMBL: X13143; CAA31538.1; -;
 CC DR PIR: S04183; S04183.
 CC DR HSP: P13804; IEV.
 CC DR PFAM: PF00766; ETF_ALPHA.1.
 CC DR PROSITE: PS00696; ETF_ALPHA.1.
 CC KW Electron transport; flavoprotein; FAD; Nitrogen fixation.
 CC NP_BIND 299 327 FAD (ADP PART) (POTENTIAL).
 CC SQ SEQUENCE 369 AA; 39526 MW; FAC273384769553B CRC64;
 CC -----
 CC Query Match 1.6%; Score 7; DB 1; Length 369;
 CC Best Local Similarity 100.0%; Pred.No. 1.63e+00;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Db 125 LIGATTL 131
 CC 5 LIGATTL 11
 CC RESULT 18
 CC ID PUR6_CABEL STANDARD; PRT; 423 AA.
 CC AC Q10457;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 15-FEB-2000 (Rel. 39, Last annotation update)
 CC DE PROBABLE MULTIFUNCTIONAL PROTEIN ADE2 [INCLUDES:
 CC PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (EC 6.3.2.6)
 CC (SAICAR SYNTHETASE); PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE
 CC (EC 4.1.1.21) (AIR CARBOXYLASE) (AIRC)].
 CC GN B0286.3;
 CC OS Eukaryotes; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC OC Rhabditidae; Pelodermidae; Caenorhabditis.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-BRISTOL N2;
 CC RA Waterston R.;
 CC RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC CC CATALYTIC ACTIVITY: ATP + 1-(5-PHOSPHORIBOSYL)-4-CARBOXY-5-
 CC AMINOIMIDAZOLE + L-ASPARTATE -> ADP + ORTHOPHOSPHATE + 1-(5-
 CC PHOSPHORIBOSYL)-4-(N-SUCCINO-CARBOXAMIDE)-5-AMINOIMIDAZOLE.

CC -1- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-5-AMINO-4-IMIDAZOLE-
 CC CARBOXYLATE - 1-(5-PHOSPHORIBOSYL)-5-AMINOIMIDAZOLE + CO(2).
 CC -1- PATHWAY: SIXTH AND SEVENTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SAICAR
 CC SYNTHETASE FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE AIR
 CC CARBOXYLASE FAMILY.
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 CC -----
 CC EMBL: U39848; AAA80690.1; -;
 CC DR WORMPEP: B0286.3; CE03863.
 CC DR PFAM: PF00731; AIRC.1.
 CC DR PFAM: PF01259; SAICAR_SYNTH.1.
 CC DR PROSITE: PS01057; SAICAR_SYNTHETASE_1; 1.
 CC DR PROSITE: PS01058; SAICAR_SYNTHETASE_2; 1.
 CC KW Hypothetical protein; Multifunctional enzyme; Purine biosynthesis;
 CC Lyase; Ligase; Decarboxylase.
 CC FT DOMAIN 1 263 SAICAR_SYNTHETASE.
 CC FT DOMAIN 264 423 AIR CARBOXYLASE.
 CC SQ SEQUENCE 423 AA; 46978 MW; 101CD65318C4804A CRC64;
 CC -----
 CC Query Match 1.6%; Score 7; DB 1; Length 423;
 CC Best Local Similarity 100.0%; Pred.No. 1.63e+00;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Db 112 FLKRNPG 118
 CC 265 FLKRNPG 271
 CC RESULT 19
 CC ID PUR6_RAT STANDARD; PRT; 425 AA.
 CC AC P51583;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 15-FEB-2000 (Rel. 39, Last annotation update)
 CC DE MULTIFUNCTIONAL PROTEIN ADE2 [INCLUDES: PHOSPHORIBOSYLAMINOIMIDAZOLE-
 CC SUCCINOCARBOXAMIDE SYNTHASE (EC 6.3.2.6) (SAICAR SYNTHETASE);
 CC PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21) (AIR
 CC CARBOXYLASE) (AIRC)].
 CC GN PAICS OR ADE2 OR AIRC.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-FISCHER.
 CC RX MEDLINE: 95260861.
 CC RA Iwahana H., Honda S., Tsujisawa T., Takahashi Y., Adzuma K.,
 CC Kawahana R., Yamoka T., Moritani M., Yoshimoto K., Itakura M.;
 CC "rat genomic structure of amidophosphoribosyltransferase, cDNA
 CC sequence of aminoimidazole ribonucleotide carboxylase, and cell
 CC cycle-dependent expression of these two physically linked genes";
 CC Biochim. Biophys. Acta 1261:369-380(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + 1-(5-PHOSPHORIBOSYL)-4-CARBOXY-5-
 CC AMINOIMIDAZOLE + L-ASPARTATE -> ADP + ORTHOPHOSPHATE + 1-(5-
 CC PHOSPHORIBOSYL)-4-(N-SUCCINO-CARBOXAMIDE)-5-AMINOIMIDAZOLE.
 CC -1- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-5-AMINO-4-IMIDAZOLE-
 CC CARBOXYLATE + 1-(5-PHOSPHORIBOSYL)-5-AMINOIMIDAZOLE + CO(2).
 CC -1- PATHWAY: SIXTH AND SEVENTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SAICAR
 CC SYNTHETASE FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE AIR
 CC CARBOXYLASE FAMILY.
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DR PROSITE: PS01057; SAICAR SYNTHETASE.1; 1.
DR PROSITE: PS01058; SAICAR SYNTHETASE.2; 1.
KW Multifunctional enzyme; Purine biosynthesis; Ligase; Lyase;
KW Decarboxylase.
FT DOMAIN 1 260 SAICAR SYNTHETASE.
FT DOMAIN 261 425 AIR CARBOXYLASE.
SO SEQUENCE 425 AA; 47079 MW; E08CF19BC8980F29 CNC64;

Query Match 1.6%; Score 7; DB 1; Length 425;
Best Local Similarity 100.0%; Pred. No. 1,636+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 108 FLKRNPG 114
|||||
QY 265 FLKRNPG 271

RESULT 21

ID PURB_CHICK STANDARD; PRT; 426 AA.
AC P38024; P87465;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-FEB-2000 (Rel. 39; Last annotation update)
DE MULTIFUNCTIONAL PROTEIN ADE2 [LINDUES; PHOSPHORIBOSYLAMINOIMIDAZOLE-
DE SUCCINOCARBOXAMIDE SYNTHASE (EC 6.3.2.6) (SAICAR SYNTHETASE)];
DE PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21) (AIR
DE CARBOXYLASE) (AIRC)].
GN AIRC.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER.
RX MEDLINE; 90222176.
RA Chen Z.D., Dixon J.E., Zalkin H.;
RT "Cloning of a chicken liver cDNA encoding 5-aminomidazole
RT ribonucleotide carboxylase and
RT 5-aminomidazole-4-N-succinocarboxamide ribonucleotide synthetase by
RT functional complementation of Escherichia coli pur mutants.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3097-3101(1990).
[2]
RN SEQUENCE OF 1-30 FROM N.A.
RX MEDLINE; 93330273.
RA Gavalas A., Dixon J.E., Brayton K.A., Zalkin H.;
RT "Expression of two closely linked avian genes for purine nucleotide
RT synthesis from a bidirectional promoter.";
RL Mol. Cell. Biol. 13:4784-4792(1993).
CC 1- CATALYTIC ACTIVITY: ATP + 1-(5'-PHOSPHORIBOSYL)-4-CARBOXY-5-
CC AMINOIMIDAZOLE-4-(N-SUCCINO-CARBOXAMIDE)-5-AMINOIMIDAZOLE-
CC PHOSPHORIBOSYL-4-(N-SUCCINO-CARBOXAMIDE)-5-AMINO-4-IMIDAZOLE-
CC 1- CATALYTIC ACTIVITY: 1-(5'-PHOSPHORIBOSYL)-5-AMINO-4-IMIDAZOLE-
CC CARBOXYLATE + 1-(5'-PHOSPHORIBOSYL)-5-AMINOIMIDAZOLE + CO(2).
CC 1- PATHWAY: SIXTH AND SEVENTH STEP IN DE NOVO PURINE BIOSYNTHESIS.
CC 1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SAICAR
CC SYNTHETASE FAMILY.
CC 1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE AIR
CC CARBOXYLASE FAMILY.

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CC -----
DR EMBL: M31764; AAA48601.1; -
DR EMBL: L12533; AAA17894.1; -
DR PIR: A35641; A35641.
DR PFAM: PF00731; AIRC; 1.
DR PFAM: PF01259; SAICAR_synth; 1.

DR PROSITE: PS01057; SAICAR SYNTHETASE.1; 1.
 DR PROSITE: PS01058; SAICAR SYNTHETASE.2; 1.
 KM Multifunctional enzyme; Purine biosynthesis; Ligase; Lyase;
 KM Decarboxylase.
 FT DOMAIN 1 261 SAICAR SYNTHETASE.
 FT DOMAIN 262 426 AIR CARBOXYLASE.
 SQ SEQUENCE 426 AA; 47240 MW; BAA90AE32AD360C CRC64;

Query Match 1.6%; Score 7; DB 1; Length 426;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 109 FLKRNPG 115
 |||||
 OY 265 FLKRNPG 271

RESULT 22
 ID YAL1 SYN3 STANDARD; PRT; 442 AA.
 AC P72935;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PUTATIVE AMMONIUM TRANSPORTER SL1017.
 GN SL1017.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97061201.
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K.,
 RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT *Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.;
 RL DNA Res. 3:109-136(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE AMT1/MEP/NRGA FAMILY OF AMMONIUM
 CC TRANSPORTERS (TC 2.49).
 CC
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CC
 CC EMBL: D90901; BAA16952.1;
 DR PFM: PF00909; Ammonium.transp. 1.
 DR PROSITE: PS01219; AMMONIUM.TRANSP. 1.
 KW Hypothetical protein; Transport; Transmembrane.
 FT TRANSMEM 5 25 POTENTIAL.
 FT TRANSMEM 44 64 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 104 124 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.
 FT TRANSMEM 155 175 POTENTIAL.
 FT TRANSMEM 193 213 POTENTIAL.
 FT TRANSMEM 240 260 POTENTIAL.
 FT TRANSMEM 269 289 POTENTIAL.
 FT TRANSMEM 299 319 POTENTIAL.
 FT TRANSMEM 325 345 POTENTIAL.
 FT TRANSMEM 354 374 POTENTIAL.
 FT TRANSMEM 386 406 POTENTIAL.
 SQ SEQUENCE 442 AA; 47172 MW; F3683BF3D96539E CRC64;

Query Match 1.6%; Score 7; DB 1; Length 442;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 277 LSAAAG 283
 |||||
 OY 21 LSAAAG 27

RESULT 23
 ID VGLM_HSVB STANDARD; PRT; 450 AA.
 AC P28948;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE GLYCOPROTEIN M.
 GN GM OR 52.
 OS Equine herpesvirus type 1 (strain Abap) (EHV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92295566.
 RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
 RT *The DNA sequence of equine herpesvirus-1.*;
 RL Virology 189:304-316(1992).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN M.
 CC
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CC
 CC EMBL: M86664; AAB02487.1;
 DR PIR: G36800; WZBER4.
 DR PFM: PF01528; Herpes-glycop. 1.
 DR PRINTS: PR00333; HSVINTEGRIMP.
 KW Transmembrane; Glycoprotein.
 FT TRANSMEM 37 53 POTENTIAL.
 FT TRANSMEM 111 127 POTENTIAL.
 FT TRANSMEM 156 173 POTENTIAL.
 FT TRANSMEM 179 195 POTENTIAL.
 FT TRANSMEM 241 257 POTENTIAL.
 FT TRANSMEM 271 287 POTENTIAL.
 FT TRANSMEM 297 314 POTENTIAL.
 FT TRANSMEM 341 358 POTENTIAL.
 FT CARBOHYD 75 75 POTENTIAL.
 SQ SEQUENCE 450 AA; 49221 MW; 5F1271CBDA9B0E6 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 450;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 109 TTVLVA 115
 |||||
 OY 9 TTVLVA 15

RESULT 24
 ID MAOC_ECOLI STANDARD; PRT; 681 AA.
 AC P77455; O53009;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MAOC PROTEIN (PHENYLACETIC ACID DEGRADATION PROTEIN PAZ).
 GN MAOC OR PAZ.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;

RX MEDLINE: 97426617.
 RA Blatter F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Colado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.,
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R12;
 RX MEDLINE: 97251357.
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitagawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nagahimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sasaki G., Seki Y., Sivasubramanian S., Tagami H., Takeda J.,
 RA Takeuchi K., Takeuchi Y., Wada C., Yamamoto Y., Horinouchi T.,
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
 corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 11105;
 RA Diaz E.,
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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 CC
 DR EMBL: AEO00236; AAC74469.1;
 DR EMBL: D90777; CAB20913.1;
 DR EMBL: X87452; CAA66088.1;
 DR EMBL: E613735; MAOC.
 DR PFAM: PF01575; MAOC_1like; 1.
 DR PROSITE: PS00070; ALDEHYDE DEHYDR. CYS; FALSE NEG.
 DR PROSITE: PS00687; ALDEHYDE DEHYDR. GLU; FALSE NEG.
 KW Oxidoreductase.
 FT ACT_SITE 256 BY SIMILARITY.
 FT ACT_SITE 295 BY SIMILARITY.
 FT ACT_SITE 143 L -> V (IN REF. 3).
 FT CONFLICT 440 A -> T (IN REF. 3).
 FT CONFLICT 611 S -> N (IN REF. 3).
 FT SEQUENCE: 681 AA; 73002 MW; A631B97AA37A1C3E CRC64;
 SO
 Query Match 1.68; Score: 7; DB 1; Length 681;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 587 VLSAAG 593
 OY 20 VLSAAG 26
 RESULT 25
 ID CATE_RHIME STANDARD; PRT; 687 AA.
 AC 09X576;
 DT 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DE CATALASE C (EC 1.11.1.6) (KAT2).
 GN KATC OR KATC.
 OS *Rhizobium meliloti* (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-RCR011 / SM47;
 RX MEDLINE: 99214118;
 RA Sigaud S., Becquet V., Frendo P., Puppo A., Herouart D.,
 RT "Differential regulation of two divergent *Sinorhizobium meliloti* genes
 for HPII-like catalases during free-living growth and protective role
 of both catalases during symbiosis.";
 RL J. Bacteriol. 181:2634-2639(1999).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE: 98295987;
 RA Cole S.T., Brosch R., Parthill J., Gantier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Ralindream M.A., Rogers J.,
 RA Rutter S., Seeger K., Shelton S., Squares S., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrett B.G.,
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 complete genome sequence.";
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AF121348; AAD21077.1;
 DR PROSITE: PS00437; CATALASE_1; 1.
 DR PROSITE: PS00438; CATALASE_2; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
 FT ACT_SITE 88 BY SIMILARITY.
 FT ACT_SITE 161 BY SIMILARITY.
 FT BINDING 375 PROXIMAL HEME LIGAND (BY SIMILARITY).
 FT SEQUENCE: 687 AA; 76553 MW; E0C11305DB59BA3F CRC64;
 SO
 Query Match 1.68; Score: 7; DB 1; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 430 KLRIRAE 436
 OY 101 KLRIRAE 107
 RESULT 26
 ID VVRB_MYCTU STANDARD; PRT; 698 AA.
 AC 006150;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE EXCINUCLEASE ABC SUBUNIT B.
 GN VVRB OR RV1633 OR MYC01B2.25.
 OS *Mycobacterium tuberculosis*.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.

	CC	COMPOSED OF AN HEAVY AND LIGHT CHAINS LINKED BY A DISULFIDE BOND.
	CC	ALPHA-3 ASSOCIATES WITH BETA-1.
	CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
	CC	-1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
	CC	-1- DATABASE: NAME=PROV; NOTE=CD guide CD49c.htm".
	CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd49c.htm".
	CC	-----
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	CC	use by non-profit institutions as long as its content is in no way
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	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
	CC	or send an email to license@isb.sib.ch).
	CC	-----
	DR	EMBL: M59911: AAA36120.1;
	DR	EMBL: D01038: BAA00845.1; -
	DR	PIR: JX0161; JX0161.
	DR	HSSP: P1215; 1A8X.
	DR	Pfam: PF01839; FG-GAP; 5.
	DR	Pfam: PF00357; Integrin.A; 1.
	DR	PRINTS: PR01185; INTEGRINA
	DR	PROSITE: PS00242; INTEGRIN_ALPHA.1.
	KM	Cell adhesion; Glycoprotein; Transmembrane; signal; Integrin;
	RW	Extracellular matrix; Cytoskeleton; Repeat.
	FT	SIGNAL 1 32
	FT	CHAIN 33 1051
	FT	CHAIN 33 872
	FT	CHAIN 876 1051
	FT	DOMAIN 33 991
	FT	TRANSMEM 992 1019
	FT	DOMAIN 1020 1051
	FT	DOMAIN 49 461
	FT	REPEAT 49 94
	FT	REPEAT 120 165
	FT	REPEAT 195 227
	FT	REPEAT 246 279
	FT	REPEAT 304 345
	FT	REPEAT 366 402
	FT	REPEAT 426 461
	FT	DISULFID 94 103
	FT	DISULFID 140 162
	FT	DISULFID 185 197
	FT	DISULFID 485 490
	FT	DISULFID 496 550
	FT	DISULFID 615 621
	FT	DISULFID 694 702
	FT	DISULFID 911 916
	FT	CARBOHYD 86 86
	FT	CARBOHYD 107 107
	FT	CARBOHYD 265 265
	FT	CARBOHYD 500 500
	FT	CARBOHYD 511 511
	FT	CARBOHYD 573 573
	FT	CARBOHYD 605 605
	FT	CARBOHYD 656 656
	FT	CARBOHYD 697 697
	FT	CARBOHYD 841 841
	FT	CARBOHYD 857 857
	FT	CARBOHYD 926 926
	FT	CARBOHYD 935 935
	FT	CARBOHYD 969 969
	SQ	SEQUENCE 1051 AA; 116612 MW; ERAFA778BFL7B21 CRC64;

	Db	994 LVLYANG 1000
	Oy	
		11 LVLYANG 17
		Query Match 1.68; Score 7; DB 1; Length 1051;
		Best local Similarity 100.08; Pred. No. 1.63e+00;
		Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 28
ID ITA3_MOUSE STANDARD; PRT; 1053 AA.
AC 062470; 008441; 008442;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTEGRIN ALPHA-3 PRECURSOR (GALACTOPROTEIN B3) (GAPB3) (VLA-3 ALPHA CHAIN) (CD49C).
GN ITG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA MEDLINE: 95279462.
RA Takeuchi K., Hirano K., Taji T., Osawa T., Irimura T.;
RT "CDN cloning of mouse VLA-3 alpha subunit.";
RL J. Cell. Biochem. 57:371-377(1995).
RN [2]
RP SEQUENCE OF 913-1053 FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE: 92052235.
RA Tamura R.N., Cooper H.M., Collo G., Quaranta V.;
RT "Cell type-specific integrin variants with alternative alpha chain cytoplasmic domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10183-10187(1991).
CC -1- FUNCTION: ACTS AS RECEPTOR FOR FIBRONECTIN, LAMININ AND COLLAGEN.
CC -1- SUBUNIT: DIMER OF AN ALPHA AND BETA CHAINS. THE ALPHA CHAIN IS COMPOSED OF AN HEAVY AND LIGHT CHAINS LINKED BY A DISULFIDE BOND.
CC ALPHA-3 ASSOCIATES WITH BETA-1.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS: ALPHA-3A (SHOWN HERE) AND ALPHA-3B; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
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CC
CC EMBL: D13867; BAA02980.1;
CC EMBL: S66292; CAB32673.1;
CC EMBL: S66294; CAB32675.1;
CC HSSP: P11215; 1A8X.
CC MGD: MGI:96602; TRCA3.
CC PFM: PFO1839; PG-GAP. 5.
CC PFM: PFO0357; Integrin_A. 1.
CC PRINTS: PRO1185; INTEGRIN.
CC PROSITE: PS00242; INTEGRIN ALPHA. 1.
CC Cell adhesion; Glycoprotein; Transmembrane; Signal; Integrin;
CC Extracellular matrix; Cytoskeleton; Repeat; Alternative splicing.
CC SIGNAL
CC 1 32
CC BY SIMILARITY.
CC CHAIN 33 1053
CC CHAIN 33 874
CC CHAIN 878 1053
CC DOMAIN 33 993
CC TRANSMEM. 996 1021
CC DOMAIN 1022 1053
CC REPEAT 49 94
CC REPEAT 120 155
CC REPEAT 195 227
CC REPEAT 246 280
CC REPEAT 305 346
CC REPEAT 367 403
CC REPEAT 427 462
CC DISULFID 94 103
CC DISULFID 140 162
CC DISULFID 185 197
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.

FT DISULFID 486 491 BY SIMILARITY.
FT DISULFID 497 551 BY SIMILARITY.
FT DISULFID 616 622 BY SIMILARITY.
FT DISULFID 695 704 BY SIMILARITY.
FT DISULFID 848 906 INTERCHAIN (BY SIMILARITY).
FT DISULFID 913 918 BY SIMILARITY.
FT CARBOHYD 86 86 POTENTIAL.
FT CARBOHYD 501 501 POTENTIAL.
FT CARBOHYD 512 512 POTENTIAL.
FT CARBOHYD 574 574 POTENTIAL.
FT CARBOHYD 606 606 POTENTIAL.
FT CARBOHYD 657 657 POTENTIAL.
FT CARBOHYD 699 699 POTENTIAL.
FT CARBOHYD 843 843 POTENTIAL.
FT CARBOHYD 859 859 POTENTIAL.
FT CARBOHYD 925 925 POTENTIAL.
FT CARBOHYD 928 928 POTENTIAL.
FT CARBOHYD 937 937 POTENTIAL.
FT CARBOHYD 971 971 POTENTIAL.
FT VARSPLIC 1023 1053 POTENTIAL.
FT
FT
FT CONFLICT 975 975 W -> C (IN REF. 2).
FT CONFLICT 979 979 D -> N (IN REF. 2).
FT CONFLICT 1002 1002 G -> S (IN REF. 2).
SQ SEQUENCE 1053 AA; 116745 MW; 6A5E0FBDA86D6E5 CRC64;
Query Match 1.68; Score 7; DB 1; Length 1053;
Best Local Similarity 100.08; Pred. No. 1.63e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 996 LVLAWG 1002
QY 11 LVLAWG 17
RESULT 29
ID MSH3_MOUSE STANDARD; PRT; 1091 AA.
AC P13705;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DNA MISMATCH REPAIR PROTEIN MSH3 (REPAIR-3 PROTEIN) (REP-1).
DE MSH3 OR REP-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Liu K., Niu L., Linton J.P., Crouse G.F.;
RL Submitted (Apr-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95011610
RA Liu K., Niu L., Linton J.P., Crouse G.F.;
RT Characterization of the mouse Rep-3 gene: sequence similarities to bacterial and yeast mismatch-repair proteins.";
RL Gene 147:169-177(1994).
RP [3]
RP SEQUENCE OF 1-917 FROM N.A.
RX MEDLINE: 89384567.
RA Linton J.P., Yen J.-Y.J., Selby E., Chen Z., Chinsky J.M., Liu K., Kellems R.E., Crouse G.F.;
RT "Dual bidirectional promoters at the mouse dhfr locus: cloning and characterization of two mRNA classes of the divergently transcribed Rep-1 gene.";
RL Mol. Cell. Biol. 9:3058-3072(1989).
CC -1- FUNCTION: NOT KNOWN. PROBABLE DNA-REPAIR PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
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DR EMBL: M80360; AAA40052.1; -

DR EMBL: L10319; AAB60711.1; JOINED.

DR EMBL: L10295; AAB60711.1; JOINED.

DR EMBL: L10296; AAB60711.1; JOINED.

DR EMBL: L10297; AAB60711.1; JOINED.

DR EMBL: L10298; AAB60711.1; JOINED.

DR EMBL: L10299; AAB60711.1; JOINED.

DR EMBL: L10300; AAB60711.1; JOINED.

DR EMBL: L10301; AAB60711.1; JOINED.

DR EMBL: L10302; AAB60711.1; JOINED.

DR EMBL: L10303; AAB60711.1; JOINED.

DR EMBL: L10304; AAB60711.1; JOINED.

DR EMBL: L10305; AAB60711.1; JOINED.

DR EMBL: L10306; AAB60711.1; JOINED.

DR EMBL: L10307; AAB60711.1; JOINED.

DR EMBL: L10308; AAB60711.1; JOINED.

DR EMBL: L10309; AAB60711.1; JOINED.

DR EMBL: L10310; AAB60711.1; JOINED.

DR EMBL: L10311; AAB60711.1; JOINED.

DR EMBL: L10312; AAB60711.1; JOINED.

DR EMBL: L10313; AAB60711.1; JOINED.

DR EMBL: L10314; AAB60711.1; JOINED.

DR EMBL: L10315; AAB60711.1; JOINED.

DR EMBL: L10316; AAB60711.1; JOINED.

DR EMBL: L10317; AAB60711.1; JOINED.

DR EMBL: L10318; AAB60711.1; JOINED.

DR EMBL: M24919; AAA40051.1; ALT_SEQ.

DR PIR: A30939; A30939.

DR PIR: A32495; A32495.

DR PIR: B32495; B32495.

DR MGD: MGI:109519; MSH3.

DR PFAM: PF00488; Muts_C; 1.

DR PFAM: PF01624; Muts_N; 1.

DR PROSITE: PS00486; DNA_MISMATCH_REPAIR_2; 1.

DR NP_BIND: 850 857 ATP (POTENTIAL).

FT CONFLICT 505 506 MV -> IL (IN REF. 2).

FT CONFLICT 864 864 T -> A (IN REF. 2).

SO SEQUENCE 1091 AA; 123074 MW; 822BF422436F513 CRC64;

Query Match: 1.6%; Score 7; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. NO. 1.63e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 279 NKSSVS 285
|||||||
QY 416 NKSSVS 422

RESULT: 30
ID POLG_POL2W STANDARD; PRT: 2205 AA.
AC P23069;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS P2A TO P2C, P3A; GENOME-LINKED PROTEIN VP3; PICORNAIN 3C (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D (EC 2.7.7.48)].
OS Poliovirus type 2 (strain W-2).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
NC Enterovirus.
RN [1].
RP SEQUENCE FROM N.A.
RX MEDLINE; 90155230.
RA Peñar D.C., Oh C.K., Cunningham L.L., Calenoff M., Jubelt B.;
RT "Localization of genomic regions specific for the attenuated, mouse-adapted poliovirus type 2 strain W-2."
RL J. Gen. Virol. 71:43-55(1990).
CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN

O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

-1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS, EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2, VP3, AND VP4.

-1- FUNCTION: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

-1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

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DR EMBL: D00625; BAA00516.1; ALT_SEQ.

DR PIR: A34032; GNNV2W.

DR HSSP: P03299; IBOV.

DR PFAM: PF00548; Cys-protease-3c; 1.

DR PFAM: PF00947; P1co_P2B; 1.

DR PFAM: PF01552; P1co_P2B; 1.

DR PFAM: PF00680; RNA_dep_RNA_pol; 1.

DR PFAM: PF00910; RNA_helicase; 1.

DR PFAM: PF00073; rhv; 3.

DR KAM: Poliovirus; Coat protein; Core protein; Transferrase; RNA-directed RNA polymerase; Hydrolyase; Thiol protease; Myristate.

FT CHAIN 2 69

FT CHAIN 70 340 COAT PROTEIN VP4 (PIA).

FT CHAIN 341 578 COAT PROTEIN VP2 (PIB).

FT CHAIN 579 879 COAT PROTEIN VP3 (PIC).

FT CHAIN 880 1028 COAT PROTEIN VP1 (PID).

FT CHAIN 1029 1125 PROTEASE 2A.

FT CHAIN 1126 1454 CORE PROTEIN 2B.

FT CHAIN 1455 1541 CORE PROTEIN 2C.

FT CHAIN 1542 1563 CORE PROTEIN 3A.

FT CHAIN 1564 1746 GENOME-LINKED PROTEIN VP3.

FT CHAIN 1747 2205 PICORNAIN 3C.

FT LIPID 2 2205 RNA-DIRECTED RNA POLYMERASE 3D.

FT ACT_SITE 1710 1710 MYRISTATE (BY SIMILARITY).

FT ACT_SITE 1724 1724 PROTEASE (POTENTIAL).

SO SEQUENCE 2205 AA; 245701 MW; 2A2A0D39E0254AD CRC64;

Query Match: 1.6%; Score 7; DB 1; Length 2205;
Best Local Similarity 100.0%; Pred. NO. 1.63e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1272 AEKENTS 1278
|||||||
QY 106 AEKENTS 112

RESULT: 31
ID POLG_POL32 STANDARD; PRT: 2206 AA.
AC P06209;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS P2A TO P2C, P3A; GENOME-LINKED PROTEIN VP3; PICORNAIN 3C (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D (EC 2.7.7.48)].
OS Poliovirus type 3 (strain 23127).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
NC Enterovirus.
RN [1].
RP SEQUENCE FROM N.A.
RX MEDLINE; 87010550.
RA Hughes P.J., Evans D.M.A., Minor P.D., Schild G.C., Almond J.W., Stanley G.;
RT "The nucleotide sequence of a type 3 poliovirus isolated during a recent outbreak of poliomyelitis in Finland."
RL J. Gen. Virol. 67:2093-2102(1986).
CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN

CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 Icosahedral units,
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
 CC VP3, AND VP4.
 CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
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 CC or send an email to license@isb-sdb.ch).
 CC
 CC EMBL: X04468; CAA28155.1; J.
 CC
 CC DR PIR: A27245; GNNY27.
 CC DR HSSP: P03302; LPIV.
 CC DR PFAM: PF00548; Cys-protease-3C; 1.
 CC DR PFAM: PF00947; Pico_P2A; 1.
 CC DR PFAM: PF01552; Pico_P2B; 1.
 CC DR PFAM: PF00680; RNA_dep_RNA_pol; 1.
 CC DR PFAM: PF00910; RNA_helicase; 1.
 CC DR PFAM: PF00073; rhy; 3.
 CC
 CC KM Polypeptide, Coat protein; Core protein; Transferase;
 CC RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.
 CC
 CC FT CHAIN 2
 CC FT CHAIN 340
 CC FT CHAIN 341
 CC FT CHAIN 578
 CC FT CHAIN 579
 CC FT CHAIN 878
 CC FT CHAIN 1027
 CC FT CHAIN 1028
 CC FT CHAIN 1125
 CC FT CHAIN 1125
 CC FT CHAIN 1454
 CC FT CHAIN 1454
 CC FT CHAIN 1562
 CC FT CHAIN 1562
 CC FT CHAIN 1745
 CC FT CHAIN 1746
 CC FT CHAIN 2206
 CC FT CHAIN 2
 CC FT ACT_SITE 1709
 CC FT ACT_SITE 1723
 CC FT ACT_SITE 1723
 CC SQ SEQUENCE 2206 AA; 245731 MW; F226AD85403C37BA CRC64;
 CC
 CC Query Match 1.68; Score 7; DB 1; Length 2206;
 CC Best Local Similarity 100.00; Pred. No. 1.63e+00;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Db 1271 AERENTS 1277
 CC OY 106 AERENTS 112
 CC
 CC RESULT 32.
 CC ID POLG.POL3L STANDARD: PRT; 2206 AA.
 CC AC P03302; 084783; 084784; 084785; 084786; 084787; 084788; 084789;
 CC AC 084790; 098592; 098593; 098594;
 CC DT 21-JUL-1986 (Rel. 01, Created)
 CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
 CC DT 15-FEB-2000 (Rel. 39, Last annotation update)
 CC DE GENOME POLYPROTEIN [COMPARISON: COAT PROTEINS VP1 TO VP4, CORE PROTEINS
 CC P2A TO P2C, P3A; GENOME-LINKED PROTEIN VP6; PICORNAIN 3C
 CC (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
 CC (EC 3.4.22.28)].
 CC OS Poliovirus type 3 (strains P3/Leon/37 and P3/Leon 12A11B).
 CC OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 CC OC Enterovirus.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-P3/LEON/37;
 CC RX MEDLINE; 84170338.
 CC RA Stanway G.C., Hughes P.J., Mountford R.C., Reeve P., Minor P.D.,
 CC RA Schild G.C., Almond J.W.;
 CC RT Comparison of the complete nucleotide sequences of the genomes of
 CC RT the neuroinfectant poliovirus P3/Leon/37 and its attenuated Sabin

RT vaccine derivative P3/Leon 12a1b.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:1539-1543(1984).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-P3/LEON 12A11B;
 RX MEDLINE; 83299239.
 RA Stanway G.C., Cann A.J., Hauptmann R., Hughes P., Clarke L.D.,
 RA Mountford R.C., Minor P.D., Schild G.C., Almond J.W.;
 RT "The nucleotide sequence of poliovirus type 3 Leon 12 alb: comparison
 RL with poliovirus type 1.";
 RL Nucleic Acids Res. 11:5629-5643(1983).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 1-878.
 RX MEDLINE; 95120467.
 RA Grant R.A., Hlrmath C.N., Filman D.J., Syed R., Andries K.,
 RA Hogle J.M.;
 RT Structures of poliovirus complexes with anti-viral drugs:
 RT implications for viral stability and drug design.";
 RL Curr. Biol. 4:784-797(1994).
 RL [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-878.
 RA Syed R., Filman D.J., Hogle J.M.;
 RT Submitted (MAR-1995) to the PDB data bank.
 RL
 CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
 CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 Icosahedral units,
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
 CC VP3, AND VP4.
 CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
 CC
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 CC
 CC EMBL: K01392; AAA46914.1;
 CC EMBL: X00925; CAA25444.1;
 CC DR PIR: A03900; GNNY4P.
 CC DR PDB: 1PIV; 20-JUL-95.
 CC DR PDB: 1PYC; 15-SEP-95.
 CC DR PDB: 1VBA; 11-JUL-96.
 CC DR PDB: 1VBB; 11-JUL-96.
 CC DR PDB: 1VBC; 11-JUL-96.
 CC DR PDB: 1VBE; 11-JUL-96.
 CC DR PFAM: PF00548; Cys-protease-3C; 1.
 CC DR PFAM: PF00947; Pico_P2A; 1.
 CC DR PFAM: PF01552; Pico_P2B; 1.
 CC DR PFAM: PF00680; RNA_dep_RNA_pol; 1.
 CC DR PFAM: PF00910; RNA_helicase; 1.
 CC DR PFAM: PF00073; rhy; 3.
 CC KM Polypeptide, Coat protein; Core protein; Transferase;
 CC RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate;
 CC 3D-structure.
 CC FT CHAIN 2
 CC FT CHAIN 69
 CC FT CHAIN 70
 CC FT CHAIN 340
 CC FT CHAIN 341
 CC FT CHAIN 578
 CC FT CHAIN 579
 CC FT CHAIN 878
 CC FT CHAIN 1027
 CC FT CHAIN 1028
 CC FT CHAIN 1125
 CC FT CHAIN 1125
 CC FT CHAIN 1454
 CC FT CHAIN 1454
 CC FT CHAIN 1562
 CC FT CHAIN 1562
 CC FT CHAIN 1745
 CC FT CHAIN 1746
 CC FT CHAIN 2206
 CC FT CHAIN 2
 CC FT ACT_SITE 1709
 CC FT ACT_SITE 1723
 CC FT ACT_SITE 1723
 CC SQ SEQUENCE 2206 AA; 245731 MW; F226AD85403C37BA CRC64;
 CC
 CC Query Match 1.68; Score 7; DB 1; Length 2206;
 CC Best Local Similarity 100.00; Pred. No. 1.63e+00;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Db 1271 AERENTS 1277
 CC OY 106 AERENTS 112
 CC
 CC RESULT 32.
 CC ID POLG.POL3L STANDARD: PRT; 2206 AA.
 CC AC P03302; 084783; 084784; 084785; 084786; 084787; 084788; 084789;
 CC AC 084790; 098592; 098593; 098594;
 CC DT 21-JUL-1986 (Rel. 01, Created)
 CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
 CC DT 15-FEB-2000 (Rel. 39, Last annotation update)
 CC DE GENOME POLYPROTEIN [COMPARISON: COAT PROTEINS VP1 TO VP4, CORE PROTEINS
 CC P2A TO P2C, P3A; GENOME-LINKED PROTEIN VP6; PICORNAIN 3C
 CC (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
 CC (EC 3.4.22.28)].
 CC OS Poliovirus type 3 (strains P3/Leon/37 and P3/Leon 12A11B).
 CC OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 CC OC Enterovirus.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-P3/LEON/37;
 CC RX MEDLINE; 84170338.
 CC RA Stanway G.C., Hughes P.J., Mountford R.C., Reeve P., Minor P.D.,
 CC RA Schild G.C., Almond J.W.;
 CC RT Comparison of the complete nucleotide sequences of the genomes of
 CC RT the neuroinfectant poliovirus P3/Leon/37 and its attenuated Sabin

FT ACT_SITE 1709 1709 PROTEASE (POTENTIAL).
 FT ACT_SITE 1723 1723 PROTEASE (POTENTIAL).
 FT VARIANT 431 431 S -> F (IN P3/LEON 12A11B).
 FT VARIANT 864 864 K -> R (IN P3/LEON 12A11B).
 FT VARIANT 908 908 T -> A (IN P3/LEON 12A11B).
 SO SEQUENCE 2206 AA; 246163 MW; 4766B15C861F66D3 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 2206;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1271 AKEKENTS 1277
 |||||
 106 AKEKENTS 112

RESULT 33
 ID POLG_POL2L STANDARD; PRT; 2207 AA.
 AC P06210;
 DT 01-JUN-1988 (Rel. 06, Last sequence update)
 DT 01-JUN-1988 (Rel. 06, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEIN VP1 TO VP4; CORE PROTEINS
 DE P2A TO P2C, P3A; GENOME-LINKED PROTEIN VP6; PICORNAIN 3C
 DE (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
 DE (EC 2.7.7.48)].
 OS Poliovirus type 2 (strain Lansing).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Enterovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86115399.
 RA La Monica N., Meriam C., Racanelli V.R.;
 RT Mapping of sequences required for mouse neurovirulence of poliovirus
 RT type 2 Lansing".
 RL J. Virol. 57:515-525(1986).
 CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
 CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
 CC SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
 CC VP3, AND VP4.
 CC -1- PPM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
 CC
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DR EMBL; M12197; AAA46912.1;
 DR PIR; A29507; GNNY5P.
 DR HSSP; P03299; IPOV.
 DR PRAM; PF00548; Cys-protease-3C; 1.
 DR PRAM; PF00947; Pico_P2A; 1.
 DR PRAM; PF01552; Pico_P2B; 1.
 DR PRAM; PF00680; RNA_dep_RNA_pol; 1.
 DR PRAM; PF00910; RNA_helicase; 1.
 DR PRAM; PF00073; rhv; 3.
 KW Polypeptide; Coat protein; Core protein; Transferrase;
 KM RNA-directed RNA polymerase; Hydrolyase; Thiol protease; Myristate.
 FT CHAIN 2 69;
 FT CHAIN 70 340
 FT CHAIN 341 578
 FT CHAIN 579 878
 FT CHAIN 880 1028
 FT CHAIN 1029 1125
 FT CHAIN 1126 1454
 FT CHAIN 1455 1541
 FT CHAIN 1542 1563
 FT CHAIN 1564 1746
 GENOME-LINKED PROTEIN VP6.
 PICORNAIN 3C.

FT CHAIN 1747 2207 RNA-DIRECTED RNA POLYMERASE 3D.
 FT LIPID 2 MYRISTATE.
 FT ACT_SITE 1710 1710 PROTEASE (POTENTIAL).
 FT ACT_SITE 1724 1724 PROTEASE (POTENTIAL).
 SO SEQUENCE 2207 AA; 245829 MW; 2B1E2070B1D44F99 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 2207;
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1272 AKEKENTS 1278
 |||||
 106 AKEKENTS 112

RESULT 34
 ID POLG_CXA24 STANDARD; PRT; 2214 AA.
 AC P36290;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEIN VP1 TO VP4; CORE PROTEINS
 DE P2A TO P2C, P3A; GENOME-LINKED PROTEIN VP6; PICORNAIN 3C
 DE (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D
 DE (EC 2.7.7.48)].
 OS Coxsackievirus A24 (strain EH24/70).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Enterovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92271460.
 RA Supanaranond K., Takeda N., Yamazaki S.;
 RT The complete nucleotide sequence of a variant of Coxsackievirus A24,
 RT an agent causing acute hemorrhagic conjunctivitis".
 RL Virus Genes 6:149-158(1992).
 CC -1- FUNCTION: IT IS THOUGHT THAT THE P2C PROTEIN ATTACHES TO VESICULAR
 CC MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.
 CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
 CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
 CC SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
 CC VP3, AND VP4.
 CC -1- PPM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
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DR EMBL; D90457; -; NOT_ANNOTATED_CDS.
 DR PIR; A48548; A48548.
 DR HSSP; P03300; IAR8.
 DR PRAM; PF00548; Cys-protease-3C; 1.
 DR PRAM; PF00947; Pico_P2A; 1.
 DR PRAM; PF01552; Pico_P2B; 1.
 DR PRAM; PF00680; RNA_dep_RNA_pol; 1.
 DR PRAM; PF00910; RNA_helicase; 1.
 DR PRAM; PF00073; rhv; 3.
 KW Polypeptide; Coat protein; Core protein; Thiol protease; Myristate.
 KM RNA-directed RNA polymerase; Hydrolyase; Thiol protease; Myristate.
 FT CHAIN 1 69;
 FT CHAIN 70 340
 FT CHAIN 341 577
 FT CHAIN 578 888
 FT CHAIN 889 1035
 FT CHAIN 1036 1132
 FT CHAIN 1133 1461
 FT CHAIN 1462 1548
 FT CHAIN 1549 1570
 GENOME-LINKED PROTEIN VP6 (P3B).

DR PROSITE; PS00202; RUBREDOXIN; 1.
KW Electron transport; Iron; Metal-binding; 3D-structure.
FT METAL. 5 5 IRON (BY SIMILARITY)

FT METAL 8 8 IRON (BY SIMILARITY)
 FT METAL 38 38 IRON (BT SIMILARITY)
 FT METAL 41 41 IRON (BT SIMILARITY)
 FT STRAND 2 5
 FT TURN 6 8
 FT STRAND 11 13
 FT TURN 14 16
 FT STRAND 18 18
 FT HELIX 19 21
 FT TURN 22 22
 FT STRAND 23 23
 FT TURN 25 26
 FT HELIX 29 31
 FT TURN 34 35
 FT TURN 37 37
 FT TURN 39 41
 FT STRAND 44 44
 FT HELIX 45 47
 FT STRAND 48 50
 SQ SEQUENCE 53 AA; 5895 MW; 9CCCBBA4A391EC1E CRC64;

Query Match 1.4%; Score 6; DB 1; Length 53;
 Best Local Similarity 100.0%; Pred. No. 1.07e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 23 ISPGTK 28
 111111
 146 ISPGTK 151

RESULT 37
 ID YC61_PORPU STANDARD; PRT; 75 AA.
 AC P51376;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE HYPOTHETICAL 8.7 KDA PROTEIN YC61 (ORF75).
 GN YC61.
 OS Porphyra purpurea.
 OG Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AVONPORT.
 RA Reith M.E., Munrolland J.;
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast genome."
 RL Plant Mol. Biol. Rep. 13:333-335(1995).
 CC -1- SIMILARITY: BELONGS TO THE YC61 FAMILY.

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CC EMBL: U38804; AAC08262.1;
 KM Hypothetical protein; Chloroplast;
 SQ SEQUENCE 75 AA; 8742 MW; 21E2375D9E3B19B CRC64;

Query Match 1.4%; Score 6; DB 1; Length 75;
 Best Local Similarity 100.0%; Pred. No. 1.07e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 45 VDIIDD 50
 111111
 38 VDIIDD 43

RESULT 38
 ID LEPA_NPVOP STANDARD; PRT; 80 AA.

AC O10311;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE LATE EXPRESSION FACTOR 10.
 GN LEF-10.
 OS Orygia pseudotsugata multicapsid polyhedrosis virus (OPMNPV).
 CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 CC Nucleopolyhedrovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97271300.
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 RA Rohmann G.F.;
 RT "The sequence of the Orygia pseudotsugata multinnucleocapsid nuclear
 RT polyhedrosis virus genome."
 RL Virology 229:381-399(1997).
 CC -1- FUNCTION: INVOLVED IN LATE/VERY LATE GENE ACTIVATION (BY
 CC SIMILARITY).

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DR EMBL: U75930; AAC59056.1;
 KM Transcription regulation.
 SQ SEQUENCE 80 AA; 8255 MW; 07AC5B3BAC095658 CRC64;

Query Match 1.4%; Score 6; DB 1; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.07e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 VLSAAA 9
 111111
 20 VLSAAA 25

RESULT 39
 ID TYRO_FELCA STANDARD; PRT; 80 AA.
 AC P55033;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE TYROSINASE (EC 1.14.18.1) (MONOPHENOL MONOOXYGENASE) (FRAGMENT).
 GN TYR.
 OS Felis silvestris catus (Cat).
 CC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EUROPEAN SHORTHAIR; TISSUE-MELANOMA;
 RA Vander J.S., Molendijk R.F., de Wit M.M.L., Garderen E.,
 RA Vander Velde D., de Weger R.A., Dille A.;
 RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
 CC THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
 CC COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO
 CC DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO
 CC INDOLE-5,6 QUINONE.
 CC -1- CATALYTIC ACTIVITY: L-TYROSINE + L-DOPA + O(2) -> L-DOPA +
 CC DOPACQUINONE + H(2)O.
 CC -1- COFACTOR: BINDS TWO COPPER IONS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MELANOSOMAL.
 CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.

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DR EMBL: U40716; AAB08729.1; -
 DR PFAM: PF00264; tyrosinase.1.
 DR PROSITE: PS00497; TYROSINASE_1; PARTIAL.
 DR PROSITE: PS00498; TYROSINASE_2; PARTIAL.
 KW Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Transmembrane;
 KW Melanin biosynthesis.
 FT NON_TER 1
 FT CARBOHYD 59
 FT METAL 80
 FT NON_TER 80
 SQ SEQUENCE 80 AA; 8693 MW; 926D7C99D49B74D3 CRC64;

Query Match 1.4%; Score 6; DB 1; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.07e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 RNPENH 26
 111111
 OY 268 RNPENH 273

RESULT 40
 ID DMP_BPT5 STANDARD; PRT; 84 AA.
 AC Q38167;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE DMP PROTEIN (FRAGMENT).
 GN DMP.
 OS Bacteriophage T5.
 OS Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
 RN [1].
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 94335651.
 RA Decker K., Krauel V., Meesmann A., Heller K.J.
 RT "Lytic conversion of Escherichia coli by bacteriophage T5: blocking
 RT of the FhuA receptor protein by a lipoprotein expressed early during
 RT infection."
 RL Mol. Microbiol. 12:321-332(1994).

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DR EMBL: X75922; CAA53525.1; -
 DR NON_TER 1
 FT SEQUENCE 84 AA; 9408 MW; E3D0C184A8271A6D CRC64;

Query Match 1.4%; Score 6; DB 1; Length 84;
 Best Local Similarity 100.0%; Pred. No. 1.07e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 VLSAAA 10
 111111
 OY 20 VLSAAA 25

RESULT 41
 ID CYC6_PLEBO STANDARD; PRT; 85 AA.
 AC P00117;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAR-1989 (Rel. 10, Last annotation update)
 DE CYTOCHROME C6 (SOLUBLE CYTOCHROME F) (CYTOCHROME C553).
 OS Plectonema boryanum.
 OS Bacteria; Cyanobacteria; Oscillatoriales; Plectonema.

RN [1]
 SEQUENCE.
 RP STRAIN-CCAP 1462/2;
 RC MEDLINE; 78023897.
 RA Alken A.;
 RT "Purification and primary structure of cytochrome f from the
 RT cyanobacterium, Plectonema boryanum."
 RL Eur. J. Biochem. 78:273-279(1977).

CC -1- FUNCTION: CYTOCHROME C6 IS A MONOHEME MONOMER. IT FUNCTIONS AS AN
 CC ELECTRON CARRIER BETWEEN MEMBRANE-BOUND CYTOCHROME F AND P700 IN
 CC THE PHOTOPHOSPHORYLATION CHAIN IN CHLOROPLASTS AND ALGAE. IT
 CC SUBSTITUTES FOR PLASTOCYANIN IN COPPER-DEFICIENT BLUE-GREEN ALGAE
 CC AND IN THE CHLOROPLASTS OF SOME EUKARYOTE ALGAE.
 CC PIR: A00109; CCPB6.
 DR HSSP: P56534; 1C6S.
 DR PFAM: PF00034; cytochrome_c_1.
 DR PRINTS: PR00605; CYTOCHROME_C1.
 DR PROSITE: PS00190; CYTOCHROME_C_1.

KW Electron transport; Photosynthesis; Heme.
 FT BINDING 14
 FT BINDING 17
 FT METAL 18
 FT METAL 58
 FT METAL 58
 SQ SEQUENCE 85 AA; 8576 MW; B9C0E4042A505B4 CRC64;

Query Match 1.4%; Score 6; DB 1; Length 85;
 Best Local Similarity 100.0%; Pred. No. 1.07e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 AAAGK 8
 111111
 OY 23 AAAGK 28

RESULT 42
 ID CYC6_ANAVA STANDARD; PRT; 86 AA.
 AC P00113;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CYTOCHROME C6 (SOLUBLE CYTOCHROME F) (CYTOCHROME C553).
 GN PCTJ.
 OS Anabaena variabilis.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 RN [1].
 RP SEQUENCE.
 RA MEDLINE; 82265568.
 RA Beecher J., Margolish E.;
 RL Unpublished results, cited by:
 RL Ulrich E.L., Krogmann D.W., Martley J.L.;
 RL J. Biol. Chem. 257:9356-9364(1982).

RN [2]
 RP SEQUENCE OF 1-22; 30-39 AND 56-86.
 RA MEDLINE; 77056395.
 RA Alken A.;
 RT "Protein evolution in cyanobacteria."
 RT Nature 263:793-796(1976).

CC -1- FUNCTION: CYTOCHROME C6 IS A MONOHEME MONOMER. IT FUNCTIONS AS AN
 CC ELECTRON CARRIER BETWEEN MEMBRANE-BOUND CYTOCHROME F AND P700 IN
 CC THE PHOTOPHOSPHORYLATION CHAIN IN CHLOROPLASTS AND ALGAE. IT
 CC SUBSTITUTES FOR PLASTOCYANIN IN COPPER-DEFICIENT BLUE-GREEN ALGAE
 CC AND IN THE CHLOROPLASTS OF SOME EUKARYOTE ALGAE.
 CC PIR: A00105; CCA16.
 DR HSSP: P56534; 1C6S.
 DR PFAM: PF00034; cytochrome_c_1.
 DR PRINTS: PR00605; CYTOCHROME_C1.
 DR PROSITE: PS00190; CYTOCHROME_C_1.

KW Electron transport; Photosynthesis; Heme.
 FT BINDING 14
 FT BINDING 17
 FT METAL 18
 FT METAL 58
 FT METAL 58
 SQ SEQUENCE 82
 E -> D (IN REF. 2).

RESULT	43	STANDARD;	PRT;	98 AA.
ID	CERA_CERCE			
AC	PS1038;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	CERASTOTIN (EC 3.4.21.-) (FRAGMENTS).			
OS	Cerastes cerastes (Horned desert viper).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Viperidae; Viperinae; Cerastes.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE-VENOM;			
RC	MEDLINE; 97390078.			
RA	Marickchi N., Barbouche R., Guermazi S., Karoui H., Bon C.,			
RA	el AyeB M.;			
RT	Cerastotin, a serine protease from Cerastes cerastes venom, with			
RT	platelet-aggregating and agglutinating properties.?			
RL	Eur. J. Biochem. 247:121-128(1997).			
CC	-1- FUNCTION: THROMBIN-LIKE SNAKE VENOM SERINE PROTEASE. POSSESSES			
CC	*ESTERASE AND AMIDOLYTIC ACTIVITIES. CLOTS HUMAN PLASMA AND			
CC	PREFERENTIALLY CLEAVES THE ALPHA CHAIN OF FIBRINOGEN.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE			
CC	*TRYPSIN FAMILY. SNAKE VENOM SUBFAMILY.			
DR	HSSP; P00761; 1EPT.			
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.			
DR	PROSITE; PS00135; TRYPSIN_SER; PARTIAL.			
KM	Hydrolase; Serine protease; Venom; Glycoprotein.			
FT	ACT_SITE 41 41 CHARGE RELAY SYSTEM (BY SIMILARITY).			
FT	ACT_SITE 85 85 CHARGE RELAY SYSTEM (BY SIMILARITY).			
FT	CARBOHYD 94 94 POTENTIAL.			
FT	NON_TER 98 98			
SO	SEQUENCE 98 AA; 11156 MW; 36AF696ABF074012 CRC64;			
Query Match	1.48; Score 6; DB 1; Length 98;			
Best Local Similarity	100.0%; Pred. No. 1.07e+02;			
Matches	6; Conservative	0; Mismatches	0; Indels	0; Caps
Db	35 WVLSSA 40			
Db				
Qy	19 WVLSSA 24			
RESULT	44	STANDARD;	PRT;	105 AA.
ID	NIPM_BOVIN			
AC	002379;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	NADH-UBIQUINONE-OXIDOREDUCTASE 15 KDA SUBUNIT (EC 1.6.5.3)			
DE	(EC 1.6.99.3) (COMPLEX I-15 KDA) (CI-15 KDA).			
GN	NDUP55.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OC	Bovidae; Bovinae; Bos.			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.			
RC	TISSUE-HEART;			
RC	MEDLINE; 92389317.			

	Query Match	1.4%	Score 6;	DB 1;	Length 105;	
	Best Local Similarity	100.0%	Pred. No.	1.07e+02;		
Dy	Matches	6;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
	49 IRAEKE 54					
Oy	104 IRAEKE 109					
RESULT	45					
ID	YCX1_CHLPHY	STANDARD;	PRT;	110 AA.		
AC	P05720;					
DT	01-NOV-1988 (Rel. 09, Created)					
DT	01-NOV-1988 (Rel. 09, Last sequence update)					
DT	01-FEB-1996 (Rel. 33, Last annotation update)					
DE	HYPOTHETICAL 12.7 KDA PROTEIN IN 16S-23S DNA SPACER.					
OS	Chlorella pyrenoidosa.					
OC	Eukaryotes; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;					
ON	Chlorellaceae; Chlorella.					
RC	[1]					
RX	SEQUENCE FROM N.A.					
RX	MEDLINE; 86232622.					
RA	Yamada T., Shimaji M.					
RT	"Peculiar feature of the organization of rRNA genes of the Chlorella					
RL	chloroplast DNA."					
CC	Nucleic Acids Res. 14:3827-3839(1986).					
CC						
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DR	EMBL; X03848; CAA27477.1; -					
DR	PIR; A24444; A24444.					
KW	Chloroplast; Hypothetical protein.					
SO	SEQUENCE 110 AA; 12782 MW; IFFSA6055A1A377 CRC64;					
Query Match	1.4%; Score 6; DB 1; Length 110;					
Best Local Similarity	100.0%; Pred. No. 1.07e+02;					
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					

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US-09-240-675-2.rsp

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Db 95 IENIYS 100
| | | | |
QY 180 IENIYS 185

Search completed: Mon Aug 21 10:32:48 2000
Job time : 51 secs.

